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(54) Title: **BAX-RESPONSIVE GENES FOR DRUG TARGET IDENTIFICATION IN YEAST AND FUNGI**

(57) Abstract: The invention describes the use of nucleic acids and polypeptides which are involved in a pathway eventually leading to programmed cell death of yeast or fungi for the preparation of a medicament for treating diseases associated with yeast or fungi or for the treatment of proliferative disorders or for preventing apoptosis in certain diseases. Methods are provided to identify compounds which selectively modulate the expression or functionality of said polypeptides in the same or a parallel pathway. Also provided are compounds as well as pharmaceutical compositions, medicaments and vaccines. The invention also comprises new nucleic acid sequences, probes and primers derived thereof, expression vectors and host cells transformed with said vectors, polypeptides and antibodies raised against said polypeptides.

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BAX-RESPONSIVE GENES FOR DRUG TARGET IDENTIFICATION IN YEAST AND FUNGI

Field of the invention

5 The present invention relates to the identification of genes and proteins encoded thereof from yeast and fungi whose expression is modulated upon programmed cell death and which genes, proteins or functional fragments and equivalents thereof may be used as selective targets for drugs to treat infections caused by or associated with yeast and fungi or for the treatment of proliferative disorders or for the prevention of apoptosis in certain diseases.

10

Background to the invention

Invasive fungal infections (e.g. *Candida* spp., *Aspergillus* spp., *Fusarium* spp., *Zygomycetes* spp.) (Walsh, 1992) have emerged during the past two decades as important pathogens causing formidable morbidity and mortality in an increasingly diverse and progressively
15 expanding population of immunocompromised patients. Those with the acquired immune deficiency syndrome (AIDS) constitute the most rapidly growing group of patients at risk for life-threatening mycosis. But fungal infections have also increased in frequency in several populations of other susceptible hosts, including very-low-birth-weight infants, cancer patients receiving chemotherapy, organ transplant recipients, burn patients and surgical patients with
20 complications.

These fungal infections are not limited to humans and other mammals, but are also important in plants where they can cause diseases or cause the production of unwanted compounds (e.g. *Fusarium* spp., *Aspergillus* spp., *Botrytis* spp., *Cladosporium* spp.).

Although recent advances in antifungal chemotherapy have had an impact on these mycoses,
25 expanding populations of immunocompromised patients will require newer approaches to antifungal therapy. The discovery of novel antifungal agents is thus an essential element of any new antifungal therapy.

Classical approaches for identifying antifungal compounds have relied almost exclusively on inhibition of fungal or yeast growth as an endpoint. Libraries of natural products, semi-synthetic,
30 or synthetic chemicals are screened for their ability to kill or arrest growth of the target pathogen or a related nonpathogenic model organism. These tests are cumbersome and provide no information about a compound's mechanism of action. The promising lead compounds that emerge from such screens must then be tested for possible host-toxicity and detailed mechanism of action studies must subsequently be conducted to identify the affected molecular
35 target.

Cells from multicellular organisms can commit suicide in response to specific signals or injury by an intrinsic program of cell death. Apoptosis is a form of programmed cell death which leads to elimination of unnecessary or damaged cells. Cells that are either unwanted or potentially harmful to the organism undergo the apoptotic process and show events like cell shrinkage, chromatin condensation, cytoplasmic condensation, digestion of nuclear DNA, loss of mitochondrial membrane potential, plasma membrane blebbing and phagocytosis of the cell debris (Schwartz, *et al.* 1993). The Bcl-2 family of proteins is centrally involved in the control of the programmed cell death process (PCD). Proteins of this group belong either to the inhibitors of cell death (Bcl-2, Bcl-X_L) or to the group of proteins promoting apoptosis (Bax, Bak) (Oltvai and Korsmeyer 1994; Knudson and Korsmeyer 1997; Reed *et al.* 1998). The ability of the Bcl-2 family of proteins to regulate life and death of a cell is conserved across evolution. Finding of homologues of PCD regulatory genes in plants and animals suggests the possibility that some functions involved in this process may originally have evolved in unicellular organisms, before a divergent development between the plant and the animal kingdom had happened (Apte *et al.* 1995).

Expression of the pro-apoptotic human or mouse Bax protein in *Saccharomyces cerevisiae* did induce cell death in this budding yeast (Sato *et al.* 1994; Greenhalf *et al.* 1996; Zha *et al.* 1996). It was initially described as a process that resembled autophagy with dissolution of the internal organelles and vacuolisation. The apoptotic features characteristic for multicellular eucaryotic cells like morphological changes in nuclear shape and chromatin condensation, were not observed in this yeast (Zha *et al.* 1996). It was therefore suggested that Bax-induced cell death in *S. cerevisiae* is due to the toxicity of the Bax protein itself, mediated by a hypothetical pore-formation without any involvement of a death program (Muchmore *et al.* 1996).

Bax expression in the fission yeast *Schizosaccharomyces pombe* did in contrast show some of the typical apoptotic changes like DNA fragmentation, chromatin condensation, dissolution of the nuclear envelope and cytosolic vacuolisation, suggesting the presence of the evolutionary conserved PCD pathway in this unicellular eucaryote (Ink *et al.* 1997; Jurgensmeier *et al.* 1997). Since it is very unlikely that species dependent differences in the toxicity of the Bax protein are the reason for this observed difference between the two yeasts, a bona fide cell death pathway may well be present in *S. cerevisiae*.

Recent findings of a yeast mutant in the cell division cycle gene *CDC48* show a number of morphological and molecular features that are considered typical indicators of apoptosis markers in metazoan cells: exposure of phosphatidylserine on the outer leaflet of the cytoplasmic membrane, DNA breakage as well as chromatin condensation and fragmentation, supporting the existence of a basic PCD machinery in this unicellular yeast. This theory was

supported by the analysis of a wild type yeast cell expressing the human Bax protein. Comprehensive tests for morphological markers of apoptosis did show a series of changes, identical to morphological markers defining apoptosis (Ligr, Madeo *et al.* 1998). Recent findings from the same group (Madeo *et al.*, 1999) implicate oxygen stress as a general regulator of apoptosis in yeast but the actual mechanism of Bax lethality in *S. cerevisiae* remains unclear.

5 It is an aim of the present invention to provide new *bax* sequences for expression in yeast and fungi and tools for identifying yeast and candida functions in the pathways leading to programmed cell death.

10 It is an aim of the present invention to provide nucleic acids as well as polypeptides which represent potential molecular targets for the identification of new compounds which can be used in alleviating diseases or conditions associated with yeast or fungal infections.

It is a further aim of the present invention to provide uses of these nucleic acid and polypeptide molecules for treating diseases associated with yeast or fungi or for the preparation of (a) medicament(s) for treating said diseases.

15 It is also an aim of the invention to provide pharmaceutical compositions and vaccines comprising these nucleic acids or polypeptides.

It is also an aim of the present invention to provide vectors comprising these nucleic acids, as well as host cells transfected or transformed with said vectors.

20 It is also an aim of the invention to provide antibodies against these polypeptides, which can be used as such, or in a composition as a medicament for treating diseases associated with yeast and fungi.

It is another aim of the invention to provide methods to selectively identify compounds or polypeptides capable of inhibiting or activating expression of the polypeptides of the invention or capable of selectively modulating expression or functionality of such polypeptides. The nucleic acid and polypeptide molecules alternatively can be incorporated into an assay or kit to identify these compounds or polypeptides.

25 It is also an aim of the invention to provide methods for preventing infection with yeast or fungi.

It is a further aim of the invention to provide human homologues for the nucleic acids and polypeptides of the invention for use in treating proliferative disorders, such as cancer, or for the prevention of apoptosis in certain diseases, or for the preparation of a medicament for treating such disorders or diseases.

30 All the aims of the present invention have been met by the embodiments as set out below.

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All the aims of the present invention have been met by the embodiments as set out below.

Summary of the invention

Since it has been discovered that the mammalian *bax* gene triggers apoptotic changes in yeast (Ligr *et al.*, 1998), this can be an indication that the molecular pathways eventually leading to programmed cell death may also be partially present in yeast cells and other unicellular eukaryotes. Identification of genes involved in this process could be important for the development of new antifungal therapeutics.

The present inventors overexpressed the Bax protein in the pathogenic yeast *Candida albicans* and found that this leads to a similar phenotype. However these results could only be received after having constructed a new synthetic *BAX* gene which could be adequately expressed in this pathogenic organism.

Furthermore, the present inventors identified a range of specific nucleic acids which are involved in the molecular pathways eventually leading to programmed cell death. The present inventors were able to identify via macro array screening a range of genes involved in a pathway eventually leading to programmed cell death in the yeast *Saccharomyces cerevisiae*.

Genes which were differentially expressed (analysed using the Pathways™ software) at different time points after Bax expression are envisaged as candidate genes in the present invention.

Additionally, the invention also relates to *Candida spp.* homologues of the *S. cerevisiae* candidate genes and their uses in stimulating or preventing cell death in yeast and fungi, especially pathogenic yeast and fungi are herewith envisaged.

Furthermore, also part of the invention are the human homologues of these apoptosis-associated *S. cerevisiae* nucleic acids and polypeptides and their potential use in treating proliferative disorders in human and other mammals.

Detailed description of the invention

The present invention relates to the use of a nucleic acid molecule encoding a polypeptide which is involved in a pathway eventually leading to programmed cell death of yeast or fungi and which nucleic acid sequence is selected from:

(a) a nucleic acid encoding a protein having an amino acid sequence as represented in any of

SEQ ID NOs 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248,

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662, 664, 666, 668, 670, 672, 674, 688, 692, 694, 696, 698, 700, 702, 704, 706, 708, 710,
712, 714, 716, 718, 720, 722, 724, 726, 728, 730 and 732, or encoding a functional
15 equivalent, derivative or bioprecursor of said protein,

(b) a nucleic acid encoding a protein having an amino acid sequence which is more than 70%
similar, preferably more than 75% or 80% similar, more preferably more than 85%, 90% or
95% similar and most preferably more than 97% similar to any of the amino acid sequences
as represented by any of SEQ ID NOs 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44,
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35 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614,

616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 692, 694, 696, 698, 700, 702, 704, 706, 708, 710, 712, 714, 716, 718, 720, 722, 724, 726, 728, 730 and 732,

(c) a nucleic acid encoding a protein having an amino acid sequence which is more than 70% identical, preferably more than 75% or 80% identical, more preferably more than 85%, 90% or 95% identical and most preferably more than 97% identical to any of the amino acid sequences as represented by any of SEQ ID NOs 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 299, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 324, 326, 328, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 569, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 692, 694, 696, 698, 700, 702, 704, 706, 708, 710, 712, 714, 716, 718, 720, 722, 724, 726, 728, 730 and 732,

(d) a nucleic acid comprising a sequence as represented in any of SEQ ID NOs 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295,

- 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481, 483, 485, 487, 489, 491, 493, 495, 497, 499, 501, 503, 505, 507, 509, 511, 513, 515, 517, 519, 521, 523, 525, 527, 529, 531, 533, 535, 537, 539, 541, 543, 545, 547, 549, 551, 553, 555, 557, 559, 561, 563, 565, 567, 569, 571, 573, 575, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, 627, 629, 631, 633, 635, 637, 639, 641, 643, 645, 647, 649, 651, 653, 655, 657, 659, 661, 663, 665, 667, 669, 671, 673, 687, 691, 693, 695, 697, 699, 701, 703, 705, 707, 709, 711, 713, 715, 717, 719, 721, 723, 725, 727, 729 and 731,
- (e) a nucleic acid which is more than 70% identical, preferably more than 75 or 80% identical, more preferably more than 85%, or 90% or 95% identical and most preferably more than 97% identical to any of the nucleic acid sequences as represented by any of SEQ ID NOs 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481, 483, 485, 487, 489, 491, 493, 495, 497, 499, 501, 503, 505, 507, 509, 511, 513, 515, 517, 519, 521, 523, 525, 527, 529, 531, 533, 535, 537, 539, 541, 543, 545, 547, 549, 551, 553, 555, 557, 559, 561, 563, 565, 567, 569, 571, 573, 575, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, 627, 629, 631, 633, 635, 637, 639, 641, 643, 645, 647, 649, 651, 653, 655, 657, 659, 661, 663, 665, 667, 669, 671, 673, 687, 691, 693, 695, 697, 699, 701, 703, 705, 707, 709, 711, 713, 715, 717, 719, 721, 723, 725, 727, 729 and 731,

(f) a nucleic acid encoding a functional fragment of any of the nucleic acids as specified in a) to e); and

(g) the complement of any of the nucleic acids as specified in a) to f),

for the preparation of a medicament for treating diseases associated with yeast or fungi.

5 Sequence similarity searches were performed using the BLAST software package version 2. Identity and similarity percentages were calculated using BLOSUM62 as a scoring matrix.

As known in the art, "similarity" between two polypeptides is determined by comparing the amino acid sequence and its conserved amino acid substitutes of one polypeptide to the sequence of a second polypeptide. Moreover, also known in the art is "identity" which means
10 the degree of sequence relatedness between two polypeptide or two polynucleotide sequences as determined by the identity of the match between two strings of such sequences. Both identity and similarity can be readily calculated. While there exist a number of methods to measure identity and similarity between two polynucleotide or polypeptide sequences, the terms "identity" and "similarity" are well known to skilled artisans (Carillo and Lipton, 1988). Methods commonly
15 employed to determine identity or similarity between two sequences include, but are not limited to, those disclosed in "Guide to Huge Computers (Bishop, 1994) and Carillo and Lipton (1988). Preferred methods to determine identity are designed to give the largest match between the two sequences tested. Methods to determine identity and similarity are codified in computer programs. Preferred computer program methods to determine identity and similarity between
20 two sequences include, but are not limited to, GCG program package (Devereux *et al.*, 1984), BLASTP, BLASTN and FASTA (Altschul *et al.*, 1990).

The expression "functional fragment of a nucleic acid" as used herein means the minimal nucleic acid which is necessary to encode a functional protein (or polypeptide). For instance, in situations where a nucleic acid is provided comprising at the 5' end and at the 3' end more
25 nucleotides than the actual open reading frame, the invention also relates to fragments of the nucleic acid which are smaller but which still contain the workable open reading frame. Also meant are parts of the open reading frame encoding a polypeptide having the same properties as the polypeptide encoded by the complete open reading frame.

The expression "a pathway eventually leading to programmed cell death" refers to a sequence
30 of steps ultimately leading to cell death and which can be triggered at various steps in this pathway by various agents, such as Bax, Bak, CED4, hydrogen peroxide, diamide and farnesol. The nucleic acid sequences to be used according to this aspect of the invention from *Saccharomyces cerevisiae* are defined in SEQ ID NOs 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85,
35 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125,

127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 5 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 691, 693, 695, 697, 699, 701, 703, 705, 707, 709, 711, 713 and 715; from *Candida albicans* are defined in SEQ ID NOs 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 10 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481, 483, 485, 487, 489, 491, 493, 495, 497, 499, 501, 503, 505, 507, 509, 511, 513, 515, 517, 519, 521, 523, 525, 527, 529, 531, 533, 535, 537, 539, 541, 543, 545, 547, 549, 551, 553, 555, 557, 559, 561, 563, 565, 567, 569, 571, 573, 575, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 15 609, 611, 613, 615, 617, 619, 621, 623, 625, 627, 629, 631, 633, 635, 637, 639, 641, 643, 645, 647, 649, 651, 653, 655, 657, 659, 661, 663, 665, 667, 669, 671, 673, 687, 718, 720, 722, 724, 726, 728, 730 and 732.

The yeast or fungi according to the invention may be, but are not restricted to, pathogenic yeast or fungi. As such, yeast or fungi may cause infections in healthy individuals as well as in 20 immunocompromised patients.

The expression "treating diseases associated with yeast and fungi" not only refers to diseases or infections caused by said organisms but also refers to allergic reactions caused by said organisms, such as the so-called "professional diseases" in, for instance, bakery and brewery and that are caused by yeast or fungi which are commonly known as "non-pathogenic". Some 25 examples of specific diseases associated with yeast or fungi are further exemplified.

The invention further relates to the use of nucleic acid sequence homologues of SEQ ID NOs 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 30 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 35 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377,

379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481, 483, 485, 487, 489, 491, 493, 495, 497, 499, 501, 503, 505, 507, 509, 511, 513, 515, 517, 519, 521, 523, 525, 527, 529, 531, 533, 535, 537, 539, 541, 543, 545, 547, 549, 551, 553, 555, 557, 559, 561, 563, 565, 567, 569, 571, 573, 575, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, 627, 629, 631, 633, 635, 637, 639, 641, 643, 645, 647, 649, 651, 653, 655, 657, 659, 661, 663, 665, 667, 669, 671, 673, 687, 691, 693, 695, 697, 699, 701, 703, 705, 707, 709, 711, 713, 715, 717, 719, 721, 723, 725, 727, 729 and 731 but isolated from other yeast and fungi strains which are also involved in a pathway eventually leading to programmed cell death. According to a more specific embodiment, these nucleic acid sequences are derived from *Aspergillus fumigatus*.

In a more specific embodiment the invention relates to a nucleic acid encoding a polypeptide which is involved in a pathway eventually leading to programmed cell death of yeast or fungi selected from:

(a) a nucleic acid encoding a protein having an amino acid sequence as represented in any of SEQ ID NOs 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 718, 720, 722, 724, 726, 728, 730 and 732, or encoding a functional equivalent, derivative or bioprecursor of said protein;

(b) a nucleic acid encoding a protein having an amino acid sequence which is more than 70% similar, preferably more than 75% or 80% similar, more preferably more than 85%, 90% or 95% similar and most preferably more than 97% similar to any of the amino acid sequences as represented by any of SEQ ID NOs 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586,

588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 718, 720, 722, 724, 726, 728, 730 and 732,

(c) a nucleic acid encoding a protein having an amino acid sequence which is more than 70% identical, preferably more than 75% or 80% identical, more preferably more than 85%, 90% or 95% identical and most preferably more than 97% identical to any of the amino acid sequences as represented by any of SEQ ID NOs 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 718, 720, 722, 724, 726, 728, 730 and 732,

(d) a nucleic acid comprising a sequence as represented in any of SEQ ID 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481, 483, 485, 487, 489, 491, 493, 495, 497, 499, 501, 503, 505, 507, 509, 511, 513, 515, 517, 519, 521, 523, 525, 527, 529, 531, 533, 535, 537, 539, 541, 543, 545, 547, 549, 551, 553, 555, 557, 559, 561, 563, 565, 567, 569, 571, 573, 575, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, 627, 629, 631, 633, 635, 637, 639, 641, 643, 645, 647, 649, 651, 653, 655, 657, 659, 661, 663, 665, 667, 669, 671, 673, 687, 717, 719, 721, 723, 725, 727, 729 and 731;

(e) a nucleic acid which is more than 70% identical, preferably more than 75% or 80% identical, more preferably more than 85%, 90% or 95% identical and most preferably more than 97% identical to any of the nucleic acid sequences as represented by any of SEQ ID NO 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481, 483, 485, 487, 489, 491, 493, 495, 497, 499, 501, 503, 505, 507, 509, 511, 513, 515, 517, 519, 521, 523, 525, 527, 529, 531, 533, 535, 537, 539, 541, 543, 545, 547, 549, 551, 553, 555, 557, 559, 561, 563, 565, 567, 569, 571, 573, 575, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613,

615, 617, 619, 621, 623, 625, 627, 629, 631, 633, 635, 637, 639, 641, 643, 645, 647, 649, 651, 653, 655, 657, 659, 661, 663, 665, 667, 669, 671, 673, 687, 717, 719, 721, 723, 725, 727, 729 and 731,

5 (f) a nucleic acid encoding a functional fragment of any of the nucleic acid sequences as specified in a) to e), and,

(g) the complement of any of the nucleic acids as specified in a) to f).

In a preferred embodiment the invention relates to nucleic acids from *Candida albicans*, as represented by the SEQ ID NOs 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 10 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481, 483, 485, 487, 489, 491, 493, 495, 497, 499, 501, 503, 505, 507, 509, 511, 513, 515, 517, 519, 521, 523, 525, 527, 529, 531, 533, 535, 537, 539, 541, 543, 545, 547, 549, 551, 553, 555, 557, 559, 561, 563, 565, 567, 569, 571, 573, 575, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, 627, 629, 631, 633, 635, 637, 639, 641, 643, 645, 647, 15 649, 651, 653, 655, 657, 659, 661, 663, 665, 667, 669, 671, 673, 687, 717, 719, 721, 723, 725, 727, 729 and 731.

In an even more preferred embodiment the invention relates to an isolated nucleic acid from mammal or human origin which nucleic acid corresponds to a mammal or human homologue of at least one of the sequences represented in SEQ ID NOs 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 20 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 25 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 30 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481, 483, 485, 487, 489, 491, 493, 495, 497, 499, 501, 503, 505, 507, 509, 511, 513, 515, 517, 519, 521, 523, 525, 527, 529, 531, 533, 535, 537, 539, 541, 543, 545, 547, 549, 551, 553, 555, 557, 559, 561, 563, 565, 567, 569, 571, 573, 575, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 35 621, 623, 625, 627, 629, 631, 633, 635, 637, 639, 641, 643, 645, 647, 649, 651, 653, 655, 657,

659, 661, 663, 665, 667, 669, 671, 673, 687, 691, 693, 695, 697, 699, 701, 703, 705, 707, 709, 711, 713, 715, 717, 719, 721, 723, 725, 727, 729 and 731.

Therefore, according to a further preferred embodiment, the invention relates to an isolated nucleic acid from mammal or human origin which nucleic acid sequence is selected from:

- 5 (a) a nucleic acid encoding a protein having an amino acid sequence as represented in any of SEQ ID NOs 676, 678, 680, 682, 684 and 686, or encoding a functional equivalent, derivative or bioprecursor of said protein;
- (b) a nucleic acid encoding a protein having an amino acid sequence which is more than 70% similar, preferably more than 75% or 80% similar, more preferably more than 85%, 90% or
10 95% similar and most preferably more than 97% similar to any of the amino acid sequences as represented by any of SEQ ID NOs 676, 678, 680, 682, 684 and 686;
- (c) a nucleic acid encoding a protein having an amino acid sequence which is more than 70% identical, preferably more than 75% or 80% identical, more preferably more than 85%, 90% or 95% identical and most preferably more than 97% identical to any of the amino acid
15 sequences as represented by any of SEQ ID NOs 676, 678, 680, 682, 684 and 686;
- (d) a nucleic acid comprising a sequence as represented in any of SEQ ID NOs 675, 677, 679, 681, 683 and 685;
- (e) a nucleic acid which is more than 70% identical, preferably more than 75 or 80% identical, more preferably more than 85%, or 90% or 95% identical and most preferably more than
20 97% identical to any of the nucleic acid sequences as represented by any of SEQ ID NOs 675, 677, 679, 681, 683 and 685;
- (f) a nucleic acid encoding a functional fragment of any of the nucleic acids as specified in a) to e); and
- (g) the complement of any of the nucleic acids as specified in a) to f),
- 25 for the preparation of a medicament for treating diseases associated with yeast or fungi.

The invention also relates to the use of said nucleic acids for treating and/or preventing and/or alleviating proliferative disorders or for the prevention of apoptosis in certain disorders or diseases.

- 30 The expression "proliferative disorders" or "proliferative diseases" refers to an abnormality within a patient or animal such as cancer. Normal cells start to proliferate due to a change in the coding or non-coding sequence of the DNA resulting in a swollen or distended tissue. Mutation may arise without obvious cause. An abnormal benign or malignant mass of tissue is formed that is not inflammatory. Cells of pre-existent tissue start to divide unexpectedly and resulting cell mass possesses no physiologic function.

The expression "apoptosis" or "apoptosis-related diseases" includes diseases such as autoimmunity diseases, ischemia, diseases related with viral infections or neurodegenerations.

It should be clear that the invention also relates to all nucleic acids according to the invention and which are specifically described above, and which can be DNA, cDNA, genomic DNA, synthetic DNA, or RNA wherein T is replaced by U. A nucleic acid according to the invention may also comprise any modified nucleotide known in the art.

The term "nucleic acid sequence" also includes the complementary sequence to any single stranded sequence given.

According to the invention, these sequences and their homologues in other yeast and fungi or in human or other mammals as well as the polypeptides which they encode represent novel molecular targets which can be incorporated into an assay to selectively identify compounds capable of inhibiting or activating expression of such polypeptides. Furthermore, the invention also relates to the potential use of said sequences in alleviating diseases or conditions associated with yeast or fungi infections, such as diseases caused by *Candida* spp., *Aspergillus* spp., *Microsporum* spp., *Trichophyton* spp., *Fusarium* spp., *Zygomycetes* spp., *Botritis* spp., *Cladosporium* spp., *Malassezia* spp., *Epidermophyton floccosum*, *Blastomyces dermatitidis*, *Coccidioides immitis*, *Histoplasma capsulatum*, *Paracoccidioides brasiliensis*, *Cryptococcus neoformans*, and *Sporothrix schenckii*, such as, but not limited to:

- Candidiasis, caused by *C. albicans* and other members of the genus *Candida*, which are primary or secondary mycotic infections, also named candidosis, moniliasis and thrush;
- Aspergilliosis, caused by members of the genus *Aspergillus*, form a spectrum of diseases;
- Histoplasmosis, caused by *Histoplasma capsulatum*, which is a pulmonary disease always seen in HIV positive or other immunocompromised individuals;
- Paracoccidioidomycosis, caused by *Paracoccidioides brasiliensis*, which is a granulomatous disease that originates as a pulmonary disease;
- Blastomycosis, caused by *Blastomyces dermatitidis*, which may be a benign and self-limiting infection or a chronic granulomatous and suppurative mycosis, also named Chicago disease or Gilchrist's disease;
- Coccidioidomycosis, caused by *Coccidioides immitis*, and which is a respiratory infection that typically resolves rapidly, but the mycosis can become acute, chronic, severe or fatal; also named San Joaquin Valley fever or Valley fever;
- Cryptococcosis, caused by *Cryptococcus neoformans*, which is a chronic, subacute to acute pulmonary, systemic or meningitic disease, also named Torulosis;

- Sporotrichosis, caused by *Sporothrix schenckii*, which is a chronic infection characterized by nodular lesions of cutaneous or subcutaneous tissues and adjacent lymphatics that suppurate, ulcerate and drain.

Some of the pathways leading to apoptosis are conserved between mammalian cells and yeast
5 or fungi. Therefore the invention also relates to the potential use of homologous sequences from human or mammalian origin for preventing and/or alleviating diseases or conditions where apoptosis or non-apoptosis of cells is impaired, for instance in proliferative disorders. In this respect also cancer can be seen as a proliferative disorder. Furthermore, targets which are part of such a conserved pathway may be used to stimulate or inhibit the apoptosis in mammalian
10 cells. E.g. stimulation of apoptosis is desirable in the treatment of tumor cells/tissues.

Human homologues according to the invention can be obtained by selective hybridisation of the yeast and candida nucleic acid molecules of the invention against human genome or cDNA libraries according to methods well known in the art (Sambrook *et al.*, 1989). Human polypeptide homologues are obtained from the corresponding human nucleic acid homologous
15 nucleotide sequences.

The present invention further relates to a nucleic acid capable of selectively hybridising to at least one of the nucleic acid molecules according to the invention, or the complement thereof.

The term "selectively hybridising" or "specifically hybridising" means hybridising under conditions wherein sequences can be detected which are homologues of the sequences of the
20 invention, but which are for instance derived from heterologous cells or organisms, and wherein said sequences do not hybridize with known sequences. In a preferred embodiment, mammalian homologues can be detected. It is well known to the person skilled in the art which methods for hybridisation can be used and which conditions are necessary for selectively or specifically hybridising. Preferably, hybridization under high stringency conditions can be
25 applied (Sambrook *et al.*, 1989).

As such, the present invention also relates to the use of the nucleic acid sequences of the invention for detecting homologues in heterologous organisms including but not limited to mammalian organisms.

The invention also relates to an isolated nucleic acid comprising a human homologue of at least
30 one of the yeast or candida nucleic acids described earlier. The invention also relates to a polypeptide encodable by said human homologue of said nucleic acid.

In a further embodiment the invention also relates to an expression vector comprising a human homologue of at least one of the yeast or candida nucleic acids described herein. Said expression vector according can be an expression vector wherein said nucleic acid sequence is
35 operably linked to one or more control sequences allowing the expression in prokaryotic and/or

eukaryotic host cells. According to a further embodiment, the expression vector comprises an inducible promoter and/or a reporter molecule.

The invention also relates to a host cell transformed, transfected or infected with any of the above described vectors.

- 5 According to a preferred embodiment, the invention relates to an antisense version of any of the nucleic acids of the invention and described above.

The present invention more particularly relates to an antisense molecule comprising a nucleic acid capable of selectively hybridising to at least one of the nucleic acids of the invention. In an interesting embodiment the invention relates to a nucleic acid capable of selectively hybridising
10 to a human homologue of at least one yeast or candida nucleic acid described herein.

Polynucleotides according to the invention may be inserted into vectors in an antisense orientation in order to provide for the production of antisense RNA. Antisense RNA or other antisense nucleic acids may also be produced by synthetic means.

The present invention also advantageously provides nucleic acid molecules of at least
15 approximately 10 contiguous nucleotides of a nucleic acid according to the invention and preferably from 10 to 50 nucleotides. These sequences may, advantageously be used as probes or primers to initiate replication, or the like. Such nucleic acid sequences may be produced according to techniques well known in the art, such as by recombinant or synthetic means. The probes will hybridise specifically with any of the nucleic acid molecules of the
20 invention. The primers will specifically amplify any of the nucleic acid molecules of the invention. The probes or primers according to the invention may also be used in diagnostic kits or the like for detecting the presence of a nucleic acid according to the invention. These tests generally comprise contacting the probe with the sample under hybridising conditions and detecting the presence of any duplex or triplex formation between the probe and any nucleic acid in the
25 sample.

According to the present invention these probes may be anchored to a solid support. Preferably, they are present on an array so that multiple probes can simultaneously hybridize to a single biological sample. The probes can be spotted onto the array or synthesized *in situ* on the array. (Lockhart *et al.*, 1996). A single array can contain more than 100, 500 or even 1,000 different
30 probes in discrete locations. Such arrays can be used to screen for compounds interacting with said probes.

Advantageously, the nucleic acid sequences, according to the invention may be produced using recombinant or synthetic means, such as for example using PCR cloning mechanisms which generally involve making a pair of primers, which may be from approximately 10 to 50
35 nucleotides to a region of the gene which is desired to be cloned, bringing the primers into

contact with mRNA, cDNA, or genomic DNA from the yeast or fungal cell, performing a polymerase chain reaction under conditions which bring about amplification of the desired region, isolating the amplified region or fragment and recovering the amplified DNA. Generally, such techniques as defined herein are well known in the art, such as described in Sambrook *et al.* (1989). These techniques can be used to clone homologues of the nucleic acid sequences of the invention in other organisms.

The nucleic acids or oligonucleotides according to the invention may carry a revealing label. Suitable labels include radioisotopes such as ^{32}P , ^{33}P or ^{35}S , enzyme labels or other protein labels such as biotin or fluorescent markers. Such labels may be added to the nucleic acids or oligonucleotides of the invention and may be detected using techniques known in the art.

According to another embodiment of the invention, the nucleic acid sequences according to the invention as defined above may, advantageously, be included in a suitable vector, preferably an expression vector which may be transformed, transfected or infected into a host cell. In such an expression vector the nucleic acid is operably linked to one or more control sequences allowing the expression in host cells, such as a suitable promoter, or the like, to ensure expression of the proteins according to the invention in a suitable prokaryotic or eukaryotic host cell. Said promoter may be either constitutive, inducible or cell- or tissue- or organ-specific. The expression vector may advantageously be a plasmid, cosmid, virus or other suitable vector which is known to those skilled in the art. The expression vector and the host cell defined herein also form part of the present invention. Said host cell can be from bacterial, yeast, fungal, insect, mammal or human origin, or any other host wherein said vector can be introduced by at least one of the methods known in the art. However, preferred host cells are lower eukaryotic cells such as a yeast cell or a fungal cell. Yeast and fungal cells are particularly advantageous because they provide the necessary post-translational modifications to the expressed proteins of the invention, similar to those of the natural proteins from which they are derived. These modifications confer optimal conformation of said proteins, which when isolated may advantageously be used in kits, methods or the like.

In a further embodiment, the expression vector may further comprise an inducible promoter, and/or further a reporter molecule.

The invention further relates to any one of the nucleic acids as defined above for use as a medicament.

Nucleotide sequences according to the invention are particularly advantageous for providing selective therapeutic targets for treating yeast or fungi-associated infections. For example, an antisense nucleic acid capable of binding to the nucleic acid sequences according to the invention may be used to selectively inhibit expression of the corresponding polypeptides,

leading to impaired growth or death of yeast and fungi with reductions of associated illnesses or diseases.

Also envisaged in the present invention are promoter or other control sequences that are comprised within the nucleic acids of the invention, said nucleic acid control sequences can also
5 serve as a target for the identification of compounds or proteins which interfere with the control of expression of downstream encoded polypeptides.

Furthermore, also the human homologues of the yeast and candida nucleic acids may be useful in diseases where apoptosis of cells plays a substantial role, both in situations where apoptosis of (particular) cells is wanted or unwanted.

10 The invention thus also relates to the use of any of the nucleic acids of the invention or to a human homologue thereof for treating proliferative disorders or for the prevention of apoptosis in certain disorders or diseases. As described above, the invention also relates to the use of antisense molecules of the nucleic acids of the invention or to an antisense of any of the human homologues for treating proliferative disorders or for the prevention of apoptosis in certain
15 disorders or diseases.

Said nucleic acids, human homologues and antisense molecules can also be used for the preparation of a medicament for treating or preventing the above-mentioned diseases.

According to yet another embodiment, the invention relates to at least one polypeptide encodable by a nucleic acid of the invention.

20 The invention also relates to the use of a polypeptide which is involved in a pathway eventually leading to programmed cell death of yeast or fungi, said polypeptide being selected from:

(a) a protein having an amino acid sequence as represented in any of SEQ ID NOs 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112,
25 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292,
30 294, 296, 298, 299, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 324, 326, 328, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462,
35 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498,

500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 692, 694, 696, 698, 700, 702, 704, 706, 708, 710, 712, 714, 716, 718, 720, 722, 724, 726, 728, 730 and 732, or encoding a functional equivalent, derivative or bioprecursor of said protein;

(b) a protein having an amino acid sequence which is more than 70% similar, preferably more than 75% or 80% similar, more preferably more than 85%, 90% or 95% similar and most preferably more than 97% similar to any of the amino acid sequences as represented by any of SEQ ID NOs 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 324, 326, 328, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 692, 694, 696, 698, 700, 702, 704, 706, 708, 710, 712, 714, 716, 718, 720, 722, 724, 726, 728, 730 and 732,

(c) a protein having an amino acid sequence which is more than 70% identical, preferably more than 75% or 80% identical, more preferably more than 85%, 90% or 95% identical and most preferably more than 97% identical to any of the amino acid sequences as represented by any of SEQ ID NOs 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54,

56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 299, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 324, 326, 328, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 569, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 692, 694, 696, 698, 700, 702, 704, 706, 708, 710, 712, 714, 716, 718, 720, 722, 724, 726, 728, 730 and 732, and,

(d) a functional fragment of any of said proteins as defined in a) to c),

for the preparation of a medicament for treating diseases associated with yeast or fungi.

The term "functional fragment" of a protein means a truncated version of the original protein or polypeptide referred to. The truncated protein sequence can vary widely in length; the minimum size being a sequence of sufficient size to provide a sequence with at least a comparable function and/or activity of the original sequence referred to, while the maximum size is not critical. In some applications, the maximum size usually is not substantially greater than that required to provide the desired activity and/or function(s) of the original sequence. A functional fragment can also relate to a subunit with similar function as said protein. Typically, the truncated amino acid sequence will range from about 5 to about 60 amino acids in length. More typically, however, the sequence will be a maximum of about 50 amino acids in length, preferably a maximum of about 60 amino acids. It is usually desirable to select sequences of at least about 10, 12 or 15 amino acids.

Functional fragments include those comprising an epitope which is specific or unique for the proteins according to the invention. Epitopes may be determined using, for example, peptide

scanning techniques as described in Geysen *et al.* (1986). Preferred functional fragments have a length of at least, for example, 5, 10, 25, 50, 75, 100, 125, 150, 175 or 200 amino acids.

The polypeptides to be used according to the invention from *Saccharomyces cerevisiae*, are represented by SEQ ID NOs 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50,

5 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 10 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 299, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 324, 326, 328, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 692, 694, 696, 698, 700, 702, 704, 706, 708, 710, 712, 714 and 716. Also according to the 15 invention is the use of the polypeptides from *Candida albicans* as represented by the SEQ ID NOs 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 20 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 569, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 718, 720, 722, 724, 726, 728, 730 and 732, and the use of human polypeptides as represented by SEQ ID NOs 676, 678, 25 680, 682, 684 and 686.

Thus, according to a preferred embodiment, the present invention relates to an isolated polypeptide which is involved in a pathway for programmed cell death of yeast or fungi, for instance a *Candida* spp., selected from:

(a) a polypeptide having an amino acid sequence as represented in any of SEQ ID NOs 30 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 35 568, 569, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590,

592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 718, 720, 722, 724, 726, 728, 730 and 732, or encoding a functional equivalent, derivative or bioprecursor of said protein;

- 5 (b) a polypeptide having an amino acid sequence which is more than 70% similar, preferably more than 75% or 80% similar, more preferably more than 85%, 90% or 95% similar and most preferably more than 97% similar to any of the amino acid sequences as represented by any of SEQ ID NOs 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 718, 720, 722, 724, 726, 728, 730 and 732,
- 10 (c) a polypeptide having an amino acid sequence which is more than 70% identical, preferably more than 75% or 80% identical, more preferably more than 85%, 90% or 95% identical and most preferably more than 97% identical to any of the amino acid sequences as represented by any of SEQ ID NOs 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 718, 720, 722, 724, 726, 728, 730 and 732, and
- 15 20 25 30

(d) a functional fragment of any of said polypeptides as defined in a) to c).

According to a further preferred embodiment, the present invention relates to an isolated polypeptide which is involved in a pathway for programmed cell death of mammalian cells selected from:

- (a) a polypeptide having an amino acid sequence as represented in any of SEQ ID NOs 676, 678, 680, 682, 684 and 686, or encoding a functional equivalent, derivative or bioprecursor of said protein;
- 5 (b) a polypeptide having an amino acid sequence which is more than 70% similar, preferably more than 75% or 80% similar, more preferably more than 85%, 90% or 95% similar and most preferably more than 97% similar to any of the amino acid sequences as represented by any of SEQ ID NOs human 676, 678, 680, 682, 684 and 686;
- 10 (c) a polypeptide having an amino acid sequence which is more than 70% identical, preferably more than 75% or 80% identical, more preferably more than 85%, 90% or 95% identical and most preferably more than 97% identical to any of the amino acid sequences as represented by any of SEQ ID NOs 676, 678, 680, 682, 684 and 686; and,
- (d) a functional fragment of any of said polypeptides as defined in a) to c).

The invention also relates to the polypeptides of the invention and described above for use as a
15 medicament.

Pharmaceutical or fungicidal compositions comprising at least one of the nucleic acids, antisense molecules, polypeptides of the invention optionally together with a pharmaceutically acceptable carrier, diluent or excipient therefor, are also part of the invention.

The polypeptides described above or the human or mammal homologues thereof can also be
20 used for treating proliferative disorders or for the prevention of apoptosis in certain diseases.

The invention furthermore relates to a pharmaceutical composition for use as a medicament for treating proliferative disorders or for the prevention of apoptosis in certain diseases comprising a nucleic acid molecule of the invention or a human homologue thereof, an antisense molecule to at least one of the nucleic acids of the invention or an antisense molecule to a mammalian
25 homologue of said nucleic acid or a polypeptide of the invention or a human homologue thereof together with a pharmaceutically acceptable carrier, diluent or excipient therefor.

The polypeptide or protein according to the invention may also include variants of any of the polypeptides of the invention as specified above having conservative amino acid changes.

The present invention also relates to a vaccine for immunizing a mammal comprising at least
30 one (recombinant) nucleic acid molecule or at least one (recombinant) polypeptide of the invention in a pharmaceutically acceptable carrier. Preferred vaccines are those that can be used for immunization against infections caused by yeast and fungi. Other preferred vaccines can be used for immunizing mammals against proliferative disorders or for preventing apoptosis in certain diseases.

Pharmaceutically acceptable carriers include any carrier that does not itself induce the production of antibodies harmful to the individual receiving the composition. Suitable carriers are typically large, slowly metabolizing macromolecules such as proteins, polysaccharides, polylactic acids, polyglycolic acids, polymeric amino acids, amino acid copolymers; and inactive virus particles. Such carriers are well known to those of ordinary skill in the art.

A "vaccine" is an immunogenic composition capable of eliciting protection against infections caused by yeast or fungi, whether partial or complete.

Said vaccine compositions may include prophylactic as well as therapeutic vaccine compositions. When a vaccine is used for protecting individuals against certain infections or diseases, it is called a prophylactic vaccine. A vaccine may also be useful for treatment of an individual, in which case it is called a therapeutic vaccine.

The term "therapeutic" refers to a composition capable of treating infections caused by yeast or fungi or capable of treating proliferative disorders.

Also encompassed within the present invention are antibodies, monoclonal or polyclonal, capable of specifically binding to one or more epitopes of the polypeptides or proteins of the invention. The polypeptides of the invention are represented in SEQ ID NOs 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 299, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 324, 326, 328, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 676, 678, 680, 682, 684, 686, 688, 692, 694, 696, 698, 700, 702, 704, 706, 708, 710, 712, 714, 716, 718, 720, 722, 724, 726, 728, 730 and 732.

The term "specific binding" implies that there is substantially no cross-reaction of the antibody with other proteins.

The antibodies according to the invention may be produced according to techniques which are known to those skilled in the art. Monoclonal antibodies may be prepared using conventional
5 hybridoma technology as described by Kohler and Milstein (1979). Polyclonal antibodies may also be prepared using conventional technology well known to those skilled in the art, and which comprises inoculating a host animal, such as a mouse, with a protein or epitope according to the invention and recovering the immune serum. The present invention also includes fragments of whole antibodies which maintain their binding activity, such as for example, Fv, F(ab') and
10 F(ab')₂ fragments as well as single chain antibodies.

The antibodies of the invention are capable of specifically binding to at least one of the yeast or candida polypeptides as defined earlier or to a human homologue thereof or to a specific epitope of said polypeptide or said human homologue. The invention also relates to the use of said antibodies in treating and/or preventing and/or alleviating proliferative disorders or for the
15 prevention of apoptosis in certain diseases. Said antibodies may also be used for the preparation of a medicament for and/or preventing and/or alleviating proliferative disorders or for the prevention of apoptosis in certain diseases.

Antibodies according to the invention may also be used in a method of detecting the presence of a polypeptide according to the invention, which method comprises reacting the antibody with
20 a sample and identifying any protein bound to said antibody. A kit may also be provided for performing said method which comprises an antibody according to the invention and means for reacting the antibody with said sample.

The antibodies according to the invention may be used as a medicament or may be comprised in a pharmaceutical composition. According to a more specific embodiment, the antibodies may
25 be used in the preparation of a medicament for treating diseases associated with yeast and fungi where the yeast or fungus is chosen from, but not restricted to *Candida* spp., *Aspergillus* spp., *Microsporum* spp., *Trichophyton* spp., *Fusarium* spp., *Zygomycetes* spp., *Botritis* spp., *Cladosporium* spp., *Malassezia* spp., *Epidermophyton floccosum*, *Blastomyces dermatitidis*, *Coccidioides immitis*, *Histoplasma capsulatum*, *Paracoccidioides brasiliensis*, *Cryptococcus neoformans*, and *Sporothrix schenckii*.
30

The invention also relates to a method of preventing infection with yeast or fungi, comprising administering a composition containing at least one polypeptide of the invention to a mammal in effective amount to stimulate the production of protective antibody or protective T-cell response. According to another embodiment, the present invention provides a method of identifying
35 compounds or polypeptides which selectively inhibit, induce or interfere with the

expression/production of the polypeptides encoded by the nucleotide sequences of the invention, or compounds which selectively inhibit, activate or interfere with the functionality of polypeptides expressed from the nucleotide sequences according to the invention, or which selectively inhibit, induce or interfere with the metabolic pathways in which these polypeptides are involved. Compounds (or polypeptides) may carry agonistic or antagonistic properties. The compounds (and polypeptides) to be screened may be of extracellular, intracellular, biologic or chemical origin.

Different alternative methods for identification of said compounds or polypeptides form part of the present invention.

10 According to a specific embodiment the invention relates to a method of identifying compounds which selectively modulate expression or functionality of polypeptides involved in a pathway eventually leading to programmed cell death of yeast and fungi or in metabolic pathways in which said polypeptides are involved, which method comprises (a) contacting a compound to be tested with yeast or fungal cells transformed, transfected or infected with an expression vector
15 comprising an antisense sequence of at least one of the nucleic acid sequences of the invention, which expression results in underexpression of said polypeptide, in addition to contacting one or more wild type cells with said compound, (b) monitoring the growth and/or death rate or activity of said transformed, transfected or infected cells compared to said wild type cells; wherein differential growth or activity of said transformed, transfected or infected yeast or fungal cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway, (c) alternatively monitoring the growth and/or death rate and/or activity of said transformed, transfected or infected cells compared to transformed, transfected or infected cells which were not contacted with the compound to be tested, wherein differential growth or activity of said mutated yeast or fungi cells is indicative of selective action of said
20 compound on a polypeptide in the same or a parallel pathway, (d) alternatively monitoring changes in morphologic and/or functional properties of components in said transformed, transfected or infected cells caused by the addition of the compound to be tested, and (e) optionally identifying the compound .

Alternative methods for identifying compounds which selectively modulate expression or
30 functionality of polypeptides involved in a pathway eventually leading to programmed cell death of yeast or fungi or in metabolic pathways in which said compounds are involved, may comprise the use of any other method known in the art resulting in gene activation, gene inactivation, gene modulation or gene silencing.

Another alternative to the above described method comprises (a) contacting a compound to be
35 tested with a genetically modified yeast or fungus in which modification results in the

overexpression or underexpression of at least one of the nucleic acids or the polypeptides of the invention, which overexpression or underexpression of said nucleic acid or polypeptide prevents, delays or sensitizes for apoptosis of said genetically modified yeast or fungus, in addition to contacting wild type cells with said compound, (b) monitoring the growth and/or death rate and/or activity of said genetically modified yeast or fungi cells compared to said wild type cells wherein differential growth or activity of said genetically modified yeast or fungi cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway, (c) alternatively monitoring the growth and/or death rate and/or activity of said genetically modified cells compared to genetically modified cells which were not contacted with the compound to be tested, wherein differential growth or activity of said genetically modified yeast or fungi cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway, (d) alternatively monitoring changes in morphologic and/or functional properties of components in said genetically modified cells caused by the addition of the compound to be tested, and, (e) optionally identifying the compound.

The invention also relates to a method of identifying compounds which selectively modulate expression of polypeptides which are involved in a pathway eventually leading to programmed cell death of yeast or fungi which method comprises (a) contacting host cells transformed, transfected or infected with an expression vector comprising a promoter sequence of a nucleic acid molecule of the invention joined in frame with a reporter gene and (b) monitoring increased or decreased expression of said reporter gene caused by the addition of the compound being tested. This enables to analyse the influence of the compound onto all/most aspects of transcriptional activation. Alternatively additional tests can routinely be performed to test the influence of the compound onto mRNA stability, translation and protein stability. All these aspects influence the concentration of corresponding proteins and consequently influence the effect of these on the metabolism of the cell.

The invention further relates to a method of identifying compounds or polypeptides which bind to or modulate the properties of polypeptides which are involved in a pathway eventually leading to programmed cell death of yeast or fungi, which method comprises (a) contacting a compound or polypeptide to be tested with at least one of the polypeptides of the invention, (b) detecting the complex formed between the compound or polypeptide to be tested and said polypeptide, (c) alternatively, examining the diminution/increase of complex formation between said polypeptide and a receptor/binding partner, caused by the addition of the compound or polypeptide being tested, (c) alternatively, examining the alteration in the functional activity of the polypeptide, caused by the addition of the compound or polypeptide being tested, and (d) optionally identifying the compound or polypeptide.

The invention also relates to a method for identifying compounds interacting with a polypeptide involved in a pathway eventually leading to programmed cell death of yeast and fungi comprising the steps of (a) providing a two-hybrid screening system wherein a polypeptide of the invention and a protein interacting with said polypeptide or an interacting polypeptide obtainable by a method as described above, are expressed, (b) interacting said compound with the complex formed by the expressed proteins as defined in a), (c) detecting a second complex, wherein the presence of said second complex identifies a compound which specifically binds to one of said polypeptide or to said second complex, and optionally (d) identifying the compound.

According to another embodiment the invention relates to a method for identifying compounds which selectively modulate expression of polypeptides which are involved in a pathway eventually leading to programmed cell death of yeast or fungi which method comprises: (a) contacting host cells transformed, transfected or infected with an expression vector comprising a promoter sequence of a nucleic acid of the invention joined in frame with a reporter gene, (b) monitoring increased or decreased expression of said reporter gene caused by the addition of the compound being tested, and, optionally (c) identifying the compound.

Yet another embodiment of the invention is a method for identifying polypeptides involved in a pathway eventually leading to programmed cell death comprising the steps of: (a) providing a two hybrid system wherein a polypeptide encoded by a nucleic acid or by any of the vectors of the invention as a bait and a *S. cerevisiae* cDNA library as a prey are used, (b) detecting an interaction between said polypeptide and a *S. cerevisiae* polypeptide encoded by said cDNA library, and, optionally (c) identifying said *S. cerevisiae* polypeptide.

The term "cells" as used in the above methods relates to any type of cells such as, but not limited to bacterial, yeast, fungal, plant or human cells.

Compounds found using this approach may additionally be tested on their efficiency in killing or inhibiting the growth of wild type cells in order to confirm their utility as medicament for treating wild type pathogenic strains/tumor cells.

According to the invention, the term "mutation" includes point mutations, deletions, insertions, duplications or any modification in the nucleic acid encoding said polypeptide, or at a different location in the genome of said cells, influencing the expression of said nucleic acid or polypeptide. In case point mutations occur, the number of nucleotides will be identical compared to the original sequence; only a change in nucleotide sequence can be observed. This stands in contrast with the other listed mutations where the number of the nucleotides will be different from the number observed in the wild type sequence and consequently will also reflect in a change of the nucleotide sequence.

Changes in morphologic and/or functional properties of cell components which can be monitored include for example morphological and molecular changes such as abnormal cell morphology, nuclear fragmentation, DNA breakage or changes in the expression of certain enzymes such as caspases, as well as monitoring changes in membrane potential or activity of mitochondria and release of cytochrome c from mitochondria. All these changes can be monitored on the whole cell which is contacted to the compound to be tested.

Detection of the complex formation can be performed using several approaches. First, binding of a compound onto a polypeptide can be studied using classical binding tests: one of the binding partners, compound or polypeptide is labeled and interaction of both is measured. Most of these tests comprise following steps: incubating both binding partners in conditions where binding is allowed, separation of free label from bound label present in the complex formed between both partners, and measuring the number of labeled complexes formed. Separation of free and bound label can be performed via filtration, centrifugation or other means as known by the person skilled in the art. Other techniques allow visualisation of complex formation without the need of such a separating step. For example, test systems using SPA (scintillation proximity assay) beads are based on the principle that radioactive ^3H can only be measured when present in scintillation fluid. SPA beads contain scintillation fluid and can be coated with one of the binding partners. When this bead is approached and binds the other binding partner which is radioactively labeled, a signal will be detected allowing the complex to be visualised. Binding of the radioactive compound onto the scintillation bead is needed in order to result in a detectable signal; non-bound radioactive partners that stay free into the solution will not result in a detectable signal.

The protein or peptide fragments according to the invention employed in such a method may be for example in solution or coated on suspended beads as described above. Alternatively, these can be affixed to a solid support, borne on a cell or phage surface or located intracellularly.

When protein or peptide fragments are coated on solid supports, they can be tested for their binding affinity for large numbers of compounds. These can be used in different kinds of high throughput screenings in order to identify compounds having suitable binding affinity to the polypeptides according to the invention. Platform technologies or technologies based on SPR (see below) can be applied.

One may measure for example, the formation of complexes between the proteins of the invention and the compound being tested. Alternatively, one may examine the diminution or increase of complex formation between the protein according to the invention and a receptor/binding partner caused by the compound being tested.

Proteins which interact with the polypeptide of the invention may be identified by investigating protein-protein interactions using the two-hybrid vector system first proposed by Chien *et al.* (1991).

This technique is based on functional reconstitution *in vivo* of a transcription factor which
5 activates a reporter gene. More particularly the technique comprises providing an appropriate host cell with a DNA construct comprising a reporter gene under the control of a promoter regulated by a transcription factor having a DNA binding domain and an activating domain, expressing in the host cell a first hybrid DNA sequence encoding a first fusion of a fragment or
10 all of a nucleic acid sequence according to the invention and either said DNA binding domain or said activating domain of the transcription factor, expressing in the host at least one second hybrid DNA sequence, such as a library or the like, encoding putative binding proteins to be investigated together with the DNA binding or activating domain of the transcription factor which is not incorporated in the first fusion; detecting any binding of the proteins to be investigated with a protein according to the invention by detecting for the presence of any reporter gene
15 product in the host cell; optionally isolating second hybrid DNA sequences encoding the binding protein.

An example of such a technique utilizes the *GAL4* protein in yeast. Gal4 is a transcriptional activator of galactose metabolism in yeast and has a separate domain for binding to activators upstream of the galactose metabolising genes as well as a protein-binding domain. Nucleotide
20 vectors may be constructed, one of which comprises the nucleotide residues encoding the DNA binding domain of Gal4. These binding domain residues may be fused to a known protein encoding sequence, such as for example the nucleic acids according to the invention. The other vector comprises the residues encoding the protein-binding domain of Gal4. These residues are fused to residues encoding a test protein. Any interaction between polypeptides encoded by the
25 nucleic acid according to the invention and the protein to be tested leads to transcriptional activation of a reporter molecule in a *GAL4* transcription deficient yeast cell into which the vectors have been transformed. Preferably, a reporter molecule such as β -galactosidase is activated upon restoration of transcription of the yeast galactose metabolism genes. Alternatively, other reporter proteins can be used such as EGFP (enhanced green fluorescent
30 protein), or hEGFP. This latter has a decreased lifetime enabling the system to screen for compounds improving the interaction of studied binding partners.

The two-hybrid approach was first developed for yeast, and is an ideal screening system when looking for compounds active in killing yeast or fungi. Indeed, proteins expressed in this system will most probably carry the correct modifications as found in the pathogenic yeast strains. In
35 addition, compounds active in this test system allow to screen and select compounds which are

able to enter the cell, this selection is not possible when using *in vitro* test systems. When compounds are needed to target mammalian cells, modification of the studied proteins can be different, changing the structure of corresponding proteins. Moreover working with yeast might block certain compounds to enter the cell, which are normally able to traverse the mammalian cell membrane. Consequently, working with mammalian two-hybrid system for this purpose will give already an immediate selection of the compounds that may enter mammalian cells.

Alternative *in vitro* methods can be used to investigate protein - protein interactions. Protein interaction analysis *in vitro* can shed light on their role in the intact cell by providing valuable information on specificity, affinity, and structure-function relation ship. Significant progress in this respect has become with the advent, in the last few years, of commercially available biosensor technology. This allows to study macromolecular interactions in real-time, providing a wealth of high-quality data that can be used for kinetic analysis, affinity measurements, competition studies, etc. A major advantage of biosensor analysis is that there is no requirement for labeling one of the interacting components and then separating bound from free molecules- a fact that simplifies experimental procedures and provides more accurate measurements. The principle of surface plasmon resonance (SPR) is based on the detection of a change of the refractive index of the medium when a compound or protein binds to an immobilised partner molecule. For the SPR technology, one needs to load one of the interacting partners to the chip surface, followed by the superfusion of the second binding partner or more molecules. The second partner can be available as purified product, but alternatively a complex suspension containing this partner can also be used. Interaction of two or more compounds can be analysed, alternatively, compounds can be identified interfering or increasing this binding affinity towards each other.

SPR is not restricted to protein-protein interactions; any macromolecule with a suitable size will change the refractive index of the medium in contact with the biosensor surface and therefore give a signal. Studies have been done with protein-DNA interactions, as well as protein-lipid interactions. Moreover intact viruses, and even cells, can also be injected over the biosensor surface, in order to analyse their binding to receptors, lectins, and so on.

Alternatively, NMR is also an excellent tool for a detailed study of protein-protein or DNA-protein interactions. Isotope edited or isotope filtered experiments whereby one compound is isotopically labeled with ^{15}N or ^{13}C are an ideal way to study these complexes. This method does not allow high throughput analysis of compounds interfering or enhancing molecular interactions. Nevertheless, medium or low throughput systems can be used to confirm results obtained by the high throughout assays or in cases where none of the binding partners are labeled. Other techniques which can be used to study interactions are: overlay, ligand blotting,

band-shift, co-immuno-precipitation, size exclusion chromatography and microcalorimetry (In. "Protein targeting Protocols" Ed. Clegg R.A. Humana Press, Totowa, New Jersey).

Compounds modulating pathways leading to apoptosis may change the activity of the polypeptide of the invention. Therefore screening tests may be setup looking for altered protein activity of the polypeptide of the invention. Based on the amino acid sequence a possible function of the polypeptide might be envisaged; activities can be confirmed and corresponding activity test can be started.

Alternatively additional tests can be performed to test the influence of the compound onto protein stability, post-translational modification, precursor processing and protein translocation.

10 All these aspects influence the concentration and/or activity of corresponding proteins and consequently influence the effect of these onto the metabolism of the cell. Also here, medium or low throughput systems can be used to confirm results obtained by the high throughput assays. In cases compounds need to be found to target tumor cells, screening assays will have to be used focused on the stimulation of the apoptotic pathway. This invention therefore also relates to *in vitro* and *in vivo* model systems comprising tumor tissue or cells expressing the polypeptides according to the invention which can be used to screen for therapeutic agents. *In vivo* modelsystems allow to test for compound efficacy but also the toxicity of these compounds can be tested. The compounds identified using any of the methods described in the invention not only include compounds which exert their effect in promoting cell death of yeast and fungi, but also include compounds which prevent or delay cell death. The latter compounds can be used to prevent or delay apoptosis of endogenic yeast or fungi in humans and other mammals which may be caused by pathogens or toxic environmental components.

According to a preferred aspect of the invention, the yeast or fungi according to any of the methods described, are chosen from *Candida* spp., *Aspergillus* spp., *Microsporum* spp., 25 *Trichophyton* spp., *Fusarium* spp., *Zygomycetes* spp., *Botritis*, spp., *Cladosporium* spp., *Malassezia* spp., *Epidermophyton floccosum*, *Blastomyces dermatitidis*, *Coccidioides immitis*, *Histoplasma capsulatum*, *Paracoccidioides brasiliensis*, *Cryptococcus neoformans*, and *Sporothrix schenckii*.

The invention also relates to a compound identified using any of the methods of the invention.

30 Compounds identifiable or identified using a method according to the invention, may advantageously be used as a medicament. The invention also relates to a method for treating diseases associated with yeast or fungi comprising admixing a compound obtainable by a method of the invention with a suitable pharmaceutically acceptable carrier.

The invention further relates to a method for preparing pharmaceutical composition for treating 35 diseases associated with yeast or fungi comprising admixing a compound as identified above

with a suitable pharmaceutically acceptable carrier. The invention also relates to said pharmaceutical composition.

The compounds or pharmaceutical compositions of the invention can be used for the preparation of a medicament to treat diseases or conditions associated with yeast and fungi infections, more preferably where the yeast or fungus is chosen from *Candida* spp., *Aspergillus* spp., *Microsporum* spp., *Trichophyton* spp., *Fusarium* spp., *Zygomycetes* spp., *Botritis*, spp., *Cladosporium* spp., *Malassezia* spp., *Epidermophyton floccosum*, *Blastomyces dermatitidis*, *Coccidioides immitis*, *Histoplasma capsulatum*, *Paracoccidioides brasiliensis*, *Cryptococcus neoformans*, and *Sporothrix schenckii*.

These compounds may also advantageously be included in a pharmaceutical composition together with a pharmaceutically acceptable carrier, diluent or excipient therefor.

A medicament according to the invention not only relates to fungicidal and fungistatic compounds for treating humans or mammals but also relates to fungicides for treating plants.

According to yet another embodiment, the invention relates to a genetically modified yeast or fungus in which modification results in the overexpression or underexpression of at least one of the nucleic acids or the polypeptides of the invention, which overexpression or underexpression of said nucleic acid or polypeptide prevents, delays or sensitizes for apoptosis of said genetically modified yeast or fungus. These genetically modified organisms may have a positive effect on the endogenic flora of humans and other mammals. The genetically modified yeast or fungi can be included in a pharmaceutical composition or can be used for the preparation of a medicament for prophylactic or therapeutic use.

Also according to the invention is the use of a compound obtainable by a method of the invention, a pharmaceutical composition or a genetically modified organism as described above for the preparation of a medicament for modifying the endogenic flora of humans and other mammals.

According to another embodiment, the invention relates to a genetically modified mammalian cell or non-human organism in which modification results in the overexpression or underexpression of at least one of the nucleic acids of the invention or a human homologue thereof or at least one of the polypeptides of the invention or a human homologue thereof, which overexpression or underexpression of said nucleic acid or polypeptide prevents or delays apoptosis of said genetically modified mammalian cell or in said genetically modified non-human organism.

According to a preferred embodiment, the invention relates to a genetically modified mammalian cell or non-human organism as described above wherein said modification comprises the

expression of an antisense molecule to at least one of the nucleic acids of the invention or an antisense molecule to a mammalian homologue of said nucleic acid.

The invention also relates to a method for identifying compounds for stimulating or inhibiting apoptosis comprising the use of at least one of the nucleic acid sequences of the invention or a
5 human homologue thereof and/or at least one of the polypeptides of the invention or a human homologue thereof and/or a genetically modified mammalian cell or non-human organism as described in the invention.

Some examples of preferred human homologues of yeast and/or *Candida* spp. sequences which can be used in the above methods are represented in SEQ ID NOs 675 to 686.

10 The invention further relates to the compounds identifiable according to the above-described method and their use as a medicament.

The invention further relates to a method for preparing a pharmaceutical composition for treating proliferative disorders or for preventing apoptosis in certain diseases comprising admixing a compound identifiable according to the above-described methods with a suitable
15 pharmaceutically acceptable carrier.

The invention also relates to the use of compounds obtainable by the above described methods for the preparation of a medicament for treating proliferative disorders or for preventing apoptosis in certain disorders.

Furthermore, the present inventors overexpressed the Bax protein in the pathogenic yeast
20 *Candida albicans* and found that this leads to a similar phenotype. However these results could only be received after having constructed a new synthetic *bax* gene which could be adequately expressed in this pathogenic organism.

Therefore, the present invention relates to an isolated nucleic acid representing a synthetic BAX-gene for expression in *Candida* spp. selected from the group of:

- 25
- a) a nucleic acid comprising a sequence as represented by SEQ ID NO 1,
 - b) a nucleic acid comprising a fragment of a sequence of SEQ ID NO 1 and encoding a functional fragment of the sequence represented by SEQ ID NO 2,
 - c) a nucleic acid comprising a sequence as represented in any of SEQ ID NOs 3 to 10,
 - d) a nucleic acid which is more than 75 % identical, preferably more than 80%, 85%, 90%
30 or 95% identical, most preferably more than 97% identical to the nucleic acid as represented by SEQ ID NO 1, or to a nucleic acid according to the nucleic acid as defined in b) or c), and
 - e) a nucleic acid as defined in any one of (a) to (d) interrupted by intervening DNA sequences,

or a nucleic acid representing the complement of any of said nucleic acids as defined in (a) to (d).

The synthetic *BAX* gene shows 73.7% identity with the gene coding for Bax- α . It should be clear that the present invention also relates to nucleic acids wherein other, also frequently used
5 *Candida* spp. codons, are used instead of the choice made for the sequence represented in SEQ ID NO 1. (Table 8)

It should be clear that all nucleic acids according to the invention and which are specifically described above, can be DNA, cDNA, genomic DNA, synthetic DNA, or RNA wherein T is replaced by U.

10 According to another embodiment of the invention, the nucleic acid sequences according to the invention as defined above may, advantageously, be included in a suitable vector, preferably an expression vector which may be transformed, transfected or infected into a host cell. In such an expression vector the nucleic acid is operably linked to one or more control sequences allowing the expression in host cells, such as a suitable promotor, or the like, to ensure expression of the
15 proteins according to the invention in a suitable prokaryotic or eukaryotic host cell. In this respect, a constitutive or an inducible promoter can be used.

As described in the examples, the invention also relates to nucleic acids and constructs comprising the synthetic *BAX*, or parts thereof, as a fusion with a carrier gene, such as, but not restricted to the yeast *GFP* gene. It is not necessary to include the complete gene of the fusion
20 partner in the expression construct, so the invention relates to various fusion products which can result from the synthetic *BAX* gene and its fusion partner.

The expression vectors comprising the synthetic construct or fusion protein and the host cell defined herein also form part of the present invention. Said host cell can be from bacterial, yeast, fungal, insect, mammal or human origin. An interesting host cell according to the
25 invention is a *Candida* spp. cell.

In another embodiment, the expression vector may further comprise an inducible promoter, and/or further a reporter molecule.

The invention also relates to a vector as described above for inducing programmed cell death in *Candida* spp.

30 The invention further also relates a genetically modified yeast or fungal cell as described above wherein said modification results in the onset of at least one pathway eventually leading to programmed cell death.

The invention also relates to a genetically modified *Candida* spp. cell wherein said modification results in the onset of at least one pathway eventually leading to programmed cell death

According to a further embodiment, the invention relates to a method for identifying genes in *Candida* spp. which are differentially expressed in a pathway eventually leading to programmed cell death using a synthetic *BAX* gene, as described above, or a vector comprising said gene as described herein, or a genetically modified yeast or fungal cell as described above.

- 5 In this respect different model systems are envisaged. It has been shown in the present invention that expression of the synthetic *BAX* gene as a fusion protein more rapidly kills the host cells than when expressed without a fusion partner. Accordingly there will be a difference in which *Candida* spp. genes will be differentially expressed in each system. The invention thus relates to methods for identifying genes in *Candida* spp. which are differentially expressed in a
10 pathway eventually leading to programmed cell death, wherein in said methods the host cells will need a longer or shorter time period for starving. Said time period is dependent on the expression construct or system used.

The invention further relates to a method for obtaining and identifying *Candida* spp. sequences (genes or polypeptides) involved in a pathway eventually leading to programmed cell death
15 comprising the steps of:

- a) providing a two hybrid system wherein a polypeptide encoded by a nucleic acid as described above or a vector as described above as a bait and a *Candida* spp. cDNA library as a prey are expressed,
- b) detecting an interaction between said polypeptide and a *Candida* spp. polypeptide
20 encoded by said cDNA library, and,
- c) identifying said *Candida* spp. polypeptide.

The invention also relates to a method for identifying inhibitors (or inhibitor sequences) of Bax-induced cell death comprising the steps of:

- a) providing a genetically modified organism as described above,
- 25 b) expressing a cDNA library in said genetically modified organism, and,
- c) identifying a polypeptide or a cDNA which expression has a beneficial effect on the survival and/or growth of said genetically modified organism.

The invention further relates to a method for identifying Bax-resistant yeast or fungi comprising the steps of:

- 30 a) providing (a) genetically modified yeast or fungi as described above,
- b) treating said genetically modified yeast or fungi with a mutagen,
- c) isolating resistant yeast or fungal cells, and,
- d) optionally identifying and/or characterizing mutated genes in said resistant yeast or fungal cells.

The invention further relates to any of the methods described above wherein said genetically modified organism is a *Candida* spp.

The invention also relates to an isolated *Candida* spp. nucleic acid identifiable by any of the methods described above.

5

The invention, now being generally described, may be more clearly understood by reference to the following examples, which are included merely for purposes of illustration of certain aspects and embodiments of the present invention and are not intended to limit the invention. The contents of all references referred to in this text are hereby incorporated by reference.

FIGURE AND TABLE LEGENDS

Figure 1. *Saccharomyces cerevisiae* sequences based on information obtained from the Saccharomyces Genome Database (SGD) (SEQ ID NOs 17 to 396 and SEQ ID NOs 691 to 716)

Figure 2. *Candida albicans* (SEQ ID NOs 397 to 674, 687, 688 and 717 to 732) and human homologues (SEQ ID NOs 675 to 686).

Human homologues were confirmed via forward and reverse BLAST using BLOSUM62 as a scoring matrix.

YGL080W (SEQ ID NO 161) codes for a yeast protein with an unknown cellular role and an unknown biochemical function. The human homologue (330 bp (SEQ ID NO 675), 109 aa (SEQ ID NO 676)) LOC51660/g7706369 has no reported cellular role or biochemical function.

YGR243W (SEQ ID NO 189) codes for a yeast protein with an unknown cellular role and an unknown biochemical function. The human homologue (384 bp (SEQ ID NO 677), 127 aa (SEQ ID NO 678)) DKFZP564B167/g5817257 has no reported cellular role or biochemical function.

YGR183C (QCR9) (Table 3) codes for a yeast protein with a known cellular role and a known biochemical function. QCR9 codes for subunit 9 of ubiquinol cytochrome-c reductase (7.3 kDa protein) which is a component of the ubiquinol cytochrome-c reductase complex. Cellular role: energy generation. Biochemical function: oxidoreductase and active transporter. The human homologue (132aa (SEQ ID NO 679), 399bp (SEQ ID NO 680)) AF161536 was predicted to have an analogous cellular role and biochemical function.

YBR009C (SEQ ID NO 37), **YGR209C** (SEQ ID NO 187) and **YPR028W** (SEQ ID NO 393) correspond to known yeast ORFs. Their human homologues have a reported cellular role or biochemical function.

Figure 3. Yeast genome macroarray containing a total of 6144 gene ORFs spotted on 2 nylon membrane filters (I and II). Each filter contains 2 fields and each field is divided into 8 grids, organised in 24 rows and 8 columns.

The spots represent the genome wide expression profile without (Minus BAX) and with (Plus BAX) induction of Bax expression for 30 min, 1 hour, 2 hours, 3 hours and 6 hours.

Figure 4 Yeast cells with a disrupted **YGR183C** gene are fully resistant to Bax-induced cell death. Resistance is observed in both the low-copy (A) and the high-copy (B) Bax

expression system. Clonogenic survival was determined by recovering cells at various times from galactose-containing medium and plating of 1000 cells on glucose-based semisolid medium. Data are representative of three experiments (mean \pm SD, n=3). SD bars are obscured by symbols.

- 5 **Figure 5.** Scheme for the synthesis of the synthetic *BAX* gene using *C. albicans* optimal codons.
- Figure 6.** DNA (SEQ ID NO 1) and protein (SEQ ID NO 2) sequence of the synthetic *C. albicans BAX* gene.
- Figure 7.** Representation of the expression constructs of the synthetic *CaBAX* gene (A) and the *yEGFP-synth CaBAX* fusion (B).
- 10 **Figure 8.** Growth of the *Candida Albicans* transformants: the individual transformants of pGAL1P:synth*CaBAX* and pGAL1P:*GFP-synthCaBAX* were streaked onto plates containing either 2% glucose or 2% galactose as sole carbon source. Growth was monitored 4 days later.
- 15 **Figure 9.** Growth kinetics of GAL1P:synth*CaBAX* (A) and GAL1P:*GFP-synthCaBAX* (B) on galactose containing minimal medium.
- Figure 10.** Immunoblot analysis of two independent transformants of GAL1P:synth*CaBAX* after 15 hours *Bax* induction on minimal galactose containing media. The arrow at 20kDa indicates the position of the *Bax* protein. The band seen at 50kDa probably represents a cell wall mannan. Not all of the contamination of the polyclonal *Bax* antibody could be removed by the treatment with *S. cerevisiae* mannan.
- 20 **Figure 11.** Immunoblot analysis of the GAL1P:*GFP-synthCaBAX* strain on galactose containing minimal medium. The band appearing at 45kDa represents the *Gfp-Bax* fusion protein, while the band at 20kDa represents the *Gfp* protein alone.
- 25 **Figure 12.** FACS analysis of two independent GAL1P:*GFP-synthCaBAX* transformants grown on galactose containing media: the light grey peak indicates the autofluorescence of the wt strain, the *GFP-fluorescence* peak is not shaded.
- Figure 13.** Viability test synth*CaBAX* (A) and *GFP-synthCaBAX* transformants (B): Cells were pregrown in minimal dextrose medium and then switched to fresh minimal medium containing galactose. At the time points indicated, samples were taken and equal cell amounts were spread on minimal dextrose plates. The appearing colonies represented the viable fraction of the total pool.
- 30 **Figure 13.** Viability test synth*CaBAX* (A) and *GFP-synthCaBAX* transformants (B): Cells were pregrown in minimal dextrose medium and then switched to fresh minimal medium containing galactose. At the time points indicated, samples were taken and equal cell amounts were spread on minimal dextrose plates. The appearing colonies represented the viable fraction of the total pool.
- 35 **Table 1.** Oligonucleotides used for construction of the synthetic *CaBAXx* gene: start and stop codon are in bold, restriction sites used for cloning are in bold and italic.

Tables 2- 6. Genes modulated by Bax expression in *S. cerevisiae*.

This list includes the genes for which mRNA levels changed significantly after a 30 min (Table 2), 1 hour (Table 3), 2 hours (Table 4), 3 hours (Table 5) or 6 hours (Table 6) induction of Bax protein expression. The Qt values were calculated using the PathwaysTM software (Research Genetics).

5

Table 7. Genes modulated by *Bax* expression in *S. cerevisiae*. This list includes all the genes for which mRNA levels changed significantly after induction of Bax protein expression. The Qt values were calculated using the Pathways software (Research Genetics). Positive values correspond with upregulated genes. Negative values correspond with downregulated genes. (Comparable with ↑ and ↓ respectively in Tables 2-6).

10

Table 8. Codon usage for the synthetic *BAX* gene.

Table 9. Regulation of 23 selected "Bax-specific" functions.

EXAMPLES

Example 1. Differential gene expression analysis upon Bax-induced cell death

Materials and media

5 Bacterial strain *Escherichia coli* MC1061 (Casadaban and Cohen, 1980) was used for the construction and the amplification of plasmids. Yeast strains were grown under normal conditions on standard media (Sherman *et al.*, 1979). The *Saccharomyces cerevisiae* strain INVSc1 (Invitrogen®, San Diego, CA, USA) was transformed by means of the lithium acetate method (Schiestl and Gietz, 1989) with YIpUTyL or YIpUTyLMuBax, after linearisation in the Ty
10 δ element (Zhu, 1986).

Cloning of mouse BAX cDNA

Mouse *bax* cDNA, encoding the mouse Bax- α protein, was cloned by Pfu DNA polymerase (Stratagene®, La Jolla, CA, USA) chain reaction amplification (PCR) from an EL4/13.18
15 thymoma cDNA library (BCCM™/LMBP-LIB15) by making use of the primers:

5'-ATGGACGGGTCCGGGAGCAG-3' (SEQ ID NO 689) and

5'-TCAGCCCATCTTCTTCCAGATGGTGAG-3' (SEQ ID NO 690).

The resulting PCR product was cloned in a *HincII*-openend pUC19 according to standard procedures (Sambrook J. *et al.*, 1989).
20

Plasmid constructions

The 2 μ ori and the *URA3* marker gene were removed from pUT332 (Gatignol *et al.*, 1990) by successive digestions with *Clal* and *BglII*. A *BamHI-HindIII GAL1* promoter fragment was ligated into the *BglII-HindIII*-opened plasmid. A *XbaI-Fspl FLP* terminator fragment was inserted into
25 this *XbaI-HindIII*(blunted)-opened plasmid so that the plasmid YIpUT was obtained. Insertion of a blunted *EcoRI-BsaAI* Ty δ element in the *KpnI-AatII*-opened and blunted YIpUT resulted in the plasmid YIpUTy. Subsequent insertion of the *LEU2* marker gene, as a blunted *BsaAI-BsrGI* fragment, in the *BamHI*-openend and blunted YIpUTy resulted in the plasmid YIpUTyL.

Mouse *bax* cDNA was excised from pUC19 by digestion with *XbaI* and *HindIII* and subcloned
30 into the *XbaI-HindIII*-opened plasmid YIpUTyL, obtaining the final expression plasmid YIpUTyLMuBax.

The plasmid YIpUTyLMuBax has been deposited in the BCCM™/LMBP culture collection as pSCTyGALmBax with accession number 3871 under restricted use.

GeneFilters

The Yeast GeneFilters™ were purchased from Research Genetics Inc. (Huntsville, AL, USA).

5 The Yeast GeneFilters™ are hybridization ready nylon membranes containing a total of 6144 gene ORFs (Open Reading Frames) individually amplified by PCR and spotted on 2 nylon membrane filters (Filter I and II). The filters are cut in the upper right corner and the DNA is on the labeled side of the filter.

Filter I contains 3072 ORFs organized into two fields (fields 1 and 2). Each field contains 1536 ORFs divided into 8 grids (A, B, C, D, E, F, G and H). The grids are organized in 24 rows and 8 columns.

10 Filter II contains 3072 ORFs organized in two fields (field 3 and 4). Fields 3 and 4 are organized in the same way as fields 1 and 2.

The Yeast ORF target

15 The yeast filters consist of over 6144 PCR products corresponding to 6144 yeast ORFs derived from the SGD. The PCR reactions used ORF specific primer pairs designed to amplify the entire open reading frame. The primers were generated from unique sequences containing the start codon ATG and termination codon (kindly provided by M. Cherry at Stanford Genome Center). Thus the PCR product contains the complete open reading frame including the start and stop codons. These products were purified and resuspended at 50 nanograms per microliter in a colored solution to allow the printing to be monitored. A robotic device was used to spot
20 approximately 1/10 of a microliter of the denatured PCR product solution on a positively charged nylon membrane. The DNA was then UV cross-linked to the membrane.

Results**25 Induction of Bax-expression in yeast cells**

A preculture of yeast strain INVSc1 containing YlpUTyLMuBax, wherein 5 Bax cassettes under the control of the *GAL1* promotor are integrated in the genome near Ty δ elements, was grown overnight in minimal glucose-containing medium in parallel with the yeast strain INVSc1 containing YlpUTyL as a control. The precultures were diluted in 100-ml minimal glucose-
30 containing medium and grown until an OD₆₀₀ of 1 was reached. Subsequently, the yeast cells were transferred into 100-ml galactose-containing medium and incubated for an additional period of 30 min, 1 hour, 2 hours, 3 hours or 6 hours.

RNA isolation

Total RNA was isolated using RNApure™ Reagent (GenHunter Corporation Nashville, TN, USA) according to the GenHunter protocol. 1.5 10⁹ cells were concentrated in a microcentrifuge tube and 1ml RNApure™ Reagent was added together with 1 g of glass pearls. The yeast cells
5 were broken by thorough mixing during five 2-minutes periods, and placed on ice in-between to avoid RNA degradation. Chloroform (150 µl) was added to the lysate and centrifuged for 10 min at 4°C and at 15000 rpm. The supernatant was transferred to a new tube and the RNA was precipitated with an equal volume of isopropanol. After 10 min incubation on ice, the RNA was pelleted by centrifugation and the pellet was washed with 70% ice-cold ethanol. The dried RNA
10 pellet was resuspended in 50 µl RNase free dH₂O.

First strand cDNA synthesis in the presence of α -³³P dCTP

Probes with high specific activity were prepared by first strand cDNA synthesis using total RNA isolated from INVSc1 YIpUTyLMuBax or INVSc1 YIpUTyL yeast cells and incorporation of α -³³P
15 dCTP as follows: 2 µl (1 µg/ml) of Oligo dT was added to 20 µg of total RNA in a maximal volume of 8 µl RNase-free dH₂O and incubated at 70°C for 10 min. After cooling down on ice for 1 min, the following components were added:

6 µl 5x concentrated First Strand Buffer (GIBCO-BRL, Paisley, UK)
1 µl 0,1 M DTT
20 1 µl RNase Block (40 units/µl) (Stratagene)
1,5 µl 20 mM dXTP-solution (X = A, G and T) (Amersham Pharmacia biotech Uppsala, Sweden)
1,5 µl SuperScript™ Reverse Transcriptase (200 units/µl) (GIBCO-BRL)
10 µl α -³³P dCTP (10mCi/ml, 3000 Ci/mmol) (Amersham Pharmacia biotech Uppsala,
25 Sweden),

and incubated for 2 h at 37°C during which first strand cDNA synthesis took place.

Unincorporated label was separated from the probe on a Sephadex G-50 column (Amersham Pharmacia biotech Uppsala, Sweden). The radioactivity incorporated in the probe was measured by liquid scintillation. The specific activity of the probes was 5.10⁸ cpm/µg for both
30 the INVSc1YIpUTyL and the INVSc1 YIpUTyLMuBax probes.

Additionally, the length of first strand cDNA probes was controlled on an alkaline 2% agarose gel using standard electrophoresis techniques, and resulted in the detection, via stimulated phosphorescence autoradiography, of the bulk of the fragments around 500 bp.

Hybridisation with the *S. cerevisiae* Yeast GeneFilters™ and signal detection

The Yeast GeneFilters™ were successively hybridised with the α -³³P dCTP labelled cDNA probes using the MicroHyb™ solution provided by the manufacturer (Research Genetics Inc., Huntsville, AL, USA). This solution was applied as well in the prehybridisation step as during
5 hybridisation. The MicroHyb™ solution contains formamide to allow hybridisation to occur at lower temperatures.

The hybridisation experiment was performed essentially as follows: during prehybridisation, the Yeast GeneFilters™ were placed in a hybridisation flask (35x250 mm) filled with 5 ml MicroHyb™ solution (42°C) containing 5 µl polydA (1 µg/ml) and incubated for 24 hours at 42°C
10 whilst rotating (10 rpm). After disposal of the prehybridisation solution, the denatured (3 min at 100°C) cDNA was added in 5 ml prewarmed MicroHyb solution and again incubated overnight at 42°C whilst rotating. Following two wash steps of 20 min in wash buffer (2x SSC, 1% SDS) at 50°C, a third wash step was performed in a second wash buffer (0,5x SSC, 1% SDS) for an additional 15 min at room temperature. The Yeast GeneFilters™ were placed in a
15 PhosphorImager™ cassette (Molecular Dynamics, Sunnyvale, CA, USA) with storage phosphor screen. After 4 days of development the screen was scanned at a resolution of 50 µm using the (BioRad, Richmond, CA, USA) Personal FX. The results of these can be seen in Figure 3.

Example 2. Quantification of Hybridisation Signals

20 Quantification of the hybridisation signals was done using the Pathways™ software (Research Genetics, Huntsville, AL, USA) and these signals were normalised against all data points. Comparison of these normalised data revealed differentially expressed candidate genes. Visual inspection of the hybridisation spots confirmed their selection. The genes as well as the factors with which they are up- or down- regulated are listed in the Tables 2 to 6 for each individual time
25 point. An overview of the up and down regulated genes modulated in function of induction of Bax expression for several time points is shown in Table 7. The sequences of these genes and amino acid sequences that they encode are shown in Figure 1.

Example 3. Comparative gene expression analysis upon Bax-induced cell death and H₂O₂-induced cell death**The oxidative H₂O₂-challenge**

A preculture of yeast strain INVSc1 containing YlpUTyL was grown overnight in minimal glucose-containing medium. The preculture was diluted in 100-ml minimal glucose-containing medium and grown until an OD₆₀₀ of 1 was reached. Subsequently, the yeast cells were
35 transferred into 100-ml galactose-containing medium supplemented with 0.1 mM H₂O₂, and

incubated for an additional period of 1 hour. This oxidative challenge resulted in the same final toxicity as a 1-hour induction of Bax expression in the same growth conditions.

First strand cDNA synthesis in the presence of α -³²P dCTP

- 5 RNA was isolated as mentioned in Example 1. Probes with high specific activity were prepared (detailed in Example 1) by first strand cDNA synthesis using total RNA isolated from INVSc1 YIpUTyLMuBax or INVSc1 YIpUTyL (growth conditions as described in Example 1) or oxidatively stressed INVSc1 YIpUTyL yeast cells.

The specific activity of all probes was $5 \cdot 10^8$ cpm/ μ g.

10

Quantification of Hybridisation Signals

Hybridisation and signal detection as described in Example 1. Conversion of the digital images to a 16 bit TIFF format using the Quantity One program (BioRad, Hercules, CA, USA) preserved image data and was necessary for file import into the Pathways® software (Research Genetics,

- 15 Huntsville, AL, USA). Pathways® was used for the quantification of hybridisation signals and these signals were normalised against all data points.

Identification of Bax-responsive genes

Pairwise comparisons of the normalised data obtained from INVSc1 YIpUTyLMuBax (B) and
20 INVSc1 YIpUTyL (C) revealed differentially expressed genes. To determine the -fold induction or repression, the normalised signal intensity after Bax induction (B) was divided by that before the shock (C). Visual inspection of the hybridisation spots confirmed their selection (*replacement*).

25 ***Identification of Bax-specific genes within the Bax-responsive pool***

Pairwise comparisons of the normalised data obtained from INVSc1 YIpUTyLMuBax (B) and INVSc1 YIpUTyL (C) at the 1-hour time point revealed differentially expressed genes. Linear ratios (B vs C) were estimated significant when changes were at least two-fold and the normalised signal intensity of one spot was at least tenfold above the average background
30 value. The normalised data of the Bax-responsive genes were compared with data obtained from the H₂O₂-stressed INVSc1 YIpUTyL (H). A Bax-responsive (up-regulated/down-regulated) gene was considered to be Bax-specific when the normalised signal intensity after Bax induction was at least twice as high/low as the corresponding intensity after oxidative stress. Visual inspection of the hybridisation spots confirmed their selection. An overview of the Bax-

specific genes for the 1-hour time point is shown in Table 9. The sequences of these genes and amino acid sequences that they encode are shown in Figure 2.

Example 4. Search for homologues in *Candida albicans* and human

- 5 Sequence similarity searches against public and commercial sequence databases were performed with the BLAST software package (Altschul *et al.*, 1990) version 2. Both the original nucleotide sequence and the six-frame conceptual translations were used as query sequences. The used public databases were the EMBL nucleotide sequence database (Stoesser *et al.*, 1998), the SWISS-PROT protein sequence database and its supplement TrEMBL (Bairoch and
- 10 Apweiler, 1998), and the ALCES *Candida albicans* sequence database (Stanford University, University of Minesota). The commercial sequence database used was the PathoSeq™ microbial genomic database (Incyte Pharmaceuticals Inc., Palo Alto, CA, USA).
- Sequence similarity searches were performed using the BLAST software package version 2. The identity between 2 sequences was calculated as percentage identical residues, the
- 15 similarity percentage between two sequences was calculated using BLOSUM62 as a scoring matrix.
- The sequences of homologues *Candida* spp. and human genes and the corresponding amino acid sequences are shown in Figure 2.

20 **Example 5. Screening for compounds modulating expression of polypeptides involved in induction of cell death of *C. albicans***

- The method proposed is based on observations (Sandbaken *et al.*, 1990; Hinnebusch and Liebman 1991; Ribogene PCT WO 95/11969, 1995) suggesting that underexpression or overexpression of any component of a process (e.g. translation) could lead to altered sensitivity
- 25 to an inhibitor of a relevant step in that process. Such an inhibitor should be more potent against a cell limited by a deficiency in the macromolecule catalyzing that step and/or less potent macromolecule, as compared to the wild type (WT) cell.
- Mutant yeast strains, for example, have shown that some steps of translation are sensitive to the stoichiometry of macromolecules involved. (Sandbaken *et al.*, 1990). Such strains are more
- 30 sensitive to compounds which specifically perturb translation (by acting on a component that participates in translation) but are equally sensitive to compounds with other mechanisms of action.
- This method thus not only provides a means to identify whether a test compound perturbs a certain process but also an indication of the site at which it exerts its effect. The component

which is present in altered form or amount in a cell whose growth is affected by a test compound is potentially the site of action of the test compound.

The assay to be set up involves measurement of growth and/or death rate of an isogenic strain which has been modified only in a certain specific allele, relative to a wild type (WT) *Candida albicans* strain, in the presence of R-compounds. Strains can be ones in which the expression of a specific protein is impaired upon induction of anti-sense or strains which carry disruptions in an essential gene. An *in silico* approach to find novel genes in *Candida albicans* will be performed. A number of essential genes identified in this way will be disrupted (in one allele) and the resulting strains can be used for comparative growth and/or death rate screening.

Example 6. Assay for High Throughput screening for drugs

35 µl minimal medium (S medium + 2% galactose + 2% maltose) is transferred in a transparent flat-bottomed 96 well plate (MW96) using an automated pipetting system (Multidrop, Labsystems, Helsinki, Finland). A 96-channel pipettor transfers 2.5 µl of R-compound at 10^{-3} M in DMSO from a stock plate into the assay plate.

The selected *Candida albicans* strains (mutant and parent (CAI-4) strain) are stored as glycerol stocks (15%) at -70°C . The strains are streaked out on selective plates (SD medium) and incubated for two days at 30°C . For the parent strain, CAI-4, the medium is always supplemented with 20 µg/ml uridine. A single colony is scooped up and resuspended in 1 ml minimal medium (S medium + 2% galactose + 2% maltose). Cells are incubated at 30°C for 8 hours while shaking at 250 rpm. A 10 ml culture is inoculated at 250.000 cells/ml. Cultures are incubated at 30°C for 24 hours while shaking at 250 rpm. Cells are counted in Coulter counter and the final culture (S medium + 2% galactose + 2% maltose) is inoculated at 20.000 to 50.000 cells/ml. Cultures are grown at 30°C while shaking at 250 rpm until a final OD_{600} of 0.24 (+/- 0.04) is reached.

200 µl of this yeast suspension is added to all wells of MW96 plates containing R-compounds in a 450 µl total volume. MW96 plates are incubated (static) at 30°C for 48 hours.

Optical densities are measured after 48 hours.

Test growth is expressed as a percentage of positive control growth for both mutant (x) and wild type (y) strains. The ratio (x/y) of these derived variables is calculated.

Example 7. Yeast cell viability assay upon induction of Bax expression

Materials and media

Yeast strains were grown under normal conditions on standard media (Sherman *et al.*, 1979). The *Saccharomyces cerevisiae* BY4742 wild type strain and BY4742 with the *YGR183C* gene disruption (EUROSCARF collection) were transformed by means of the lithium acetate method (Schiestl and Gietz, 1989) with the low-copy centromeric pRS415Bax plasmid or pRS415 as a control, or with the high-copy episomal pRS425Bax plasmid or pRS425 as a control.

Plasmid constructions

The Bax expression cassette, a *BsgI*(blunted)-*SapI*(blunted) fragment excised from YlpUTyLMuBax containing the *GAL1* promoter, the *bax* cDNA and the *FLP* terminator, was ligated into the *Eco*136II-opened pRS415 (ATCC 87520) and pRS425 (ATCC 77106) plasmids, obtaining the low-copy centromeric pRS415Bax and the high-copy episomal pRS425Bax expression plasmids.

Results

Single colonies of yeast cells transformed with pRS415 or pRS415Bax or pRS425 or pRS425Bax were grown in 10 ml minimal glucose-containing medium with vigorous aeration at 30°C to an optical density of 1 OD₆₀₀. Cells were pelleted by centrifugation and washed two times with sterile dH₂O before resuspending in 10 ml minimal galactose-containing medium. After culturing for various times at 30°C, the total cell density of the cultures was determined, and 1000 cells were spread on minimal glucose-based semisolid medium, followed by incubation at 30°C for 3 days. The number of colonies on plates from the 0 hr cultures was designated as 100% (Fig. 4).

Example 8. Bax Expression in *Candida* cells

Strains

The *Candida albicans* strain CAI4 (*ura3 Δ*) was used to perform the experiments (Fonzi and Irwin 1993).

E. coli transformations were done using the Top10 strain from Invitrogen (San Diego, CA, USA) (F' *mcrA* Δ (*mrr-hsdRMS-mcrBC*) Δ 80/*lacZ* Δ M15 Δ *lacX74 deoR recA1 araD139* Δ (*ara-leu*)7697 *galU galK rpsL* (Str^R) *endA1 nupG*).

Media

Synthetic dextrose media (SD), containing 2% glucose, 1.34% Yeast Nitrogen Base without amino acids and 0.77g/l CSM-ura (Bio 101, Vista, CA, USA) was used to grow the *Candida albicans* transformants. In case of the wild type (CAI4), the media was supplemented with

50µg/ml uridine. To prepare plates the media was solidified with 2% agar. Expression of the synthetic *BAX* gene was performed using 2% galactose as carbon source.

Construction of the codon-optimised *BAX* gene

- 5 Construction of the synthetic *BAX* gene followed the nomenclature described for *Candida albicans* (Lloyd and Sharp 1992; Brown, *et al.* 1991; <http://alces.med.umn.edu/candida/codons.html>; <http://www.kazusa.or.jp/codon>). To ensure a high expression of the synthetic gene, the subset of 'optimal' codons of highly expressed genes was used to design the synthetic *BAX* gene.
- 10 The synthCa*BAX* gene was constructed in three parts using eight oligonucleotides (Fig. 5). The sequences of the oligonucleotides are given in Table 7. Primer A1 introduced upstream of the ATG codon a *Pst* I site and a *Bgl* II site. The *Pst* I site was used later on for direct cloning into the *Candida albicans* expression vector, while the *Bgl* II site served as a linker for a *yEGFP* fusion. Primer C2 introduced a *Sma* I site, suitable for cloning into the expression vector.
- 15 Fragment A and B were synthesised in two steps: in a first PCR round primer X1 and X2 (X represents A or B, respectively) were used together. The resulting fragment served as a template in a second PCR round together with primers X1 and X3. Fragment C was synthesised in a single PCR round using the primers C1 and C2. Fragment A and B were cloned into the pCR-BluntII-TOPO vector (Stratagene), while fragment C was cloned into the pCR2.1-TOPO
- 20 vector (Stratagene). All three fragments were sequenced to ensure that no mutation was introduced by the PCR.
- Subsequently, fragment A was digested with *Pst* I and *Taq* I, fragment B with *Taq* I and *Bam* HI and fragment C with *Bam* HI and *Sma* I. The three products were cloned in a quadruple ligation into pUC21 digested with *Pst* I and *Sma* I resulting in the plasmid pUC21:synthCandidaBAX.
- 25 The sequence of the synthetic *BAX* gene is shown in Figure 6.

Construction of synthetic *BAX*- and *GFP*-synthetic *BAX* expression plasmids

- A *Pst* I-*Sma* I fragment containing the ORF of the synthetic *BAX* gene was cloned into the *Pst* I-*Stu* I digested vector pGAL1ACT1LUC (W. Martinet, EP application nr 99204557.5) resulting in
- 30 the expression construct pGAL1P:synthCa*BAX* (Fig. 7A). To facilitate recognition of the AUG codon during formation of initiation complexes a purine base (A) was introduced at position -3 from the AUG codon (Kozak 1981) using the Quick change site directed mutagenesis kit from Stratagene.
- The yeast enhanced *GFP* gene *yEGFP*; (Cormack *et al.* 1997) was amplified by PCR using
- 35 primer 5'-AACTGCAGATGTCTAAAGGTGAAGAATTATTC-3' (SEQ ID NO 11) as upstream primer and primer 5'-GGAAGATCTTCCTTTGTACAATTCATCC ATACC-3' (SEQ ID NO 12) as

downstream primer. The sense primer introduced a *Pst* I site (shown in bold and italic), while the anti-sense primer contained a *Bgl* II linker (shown in bold and italic) for fusion with the synthetic *BAX* gene. After cloning of the *yEGFP* gene into the pCR2.1-TOPO vector (Stratagene), the gene was sequenced to ensure that no mutation was introduced by PCR.

- 5 The *yEGFP*-synth *Candida BAX* fusion was created by cloning a *Pst*I-*Bgl*II *yEGFP* fragment together with a *Bgl* II-*Sma* I synthetic *Candida BAX* fragment into the *Pst* I-*Stu* I digested expression vector pGAL1ACT1LUC. The obtained pGAL1P:*yEGFP*-synthCa*BAX* fusion construct (Fig.7B) was sequenced to ensure that no frameshift had occurred.

10 **Creation of the synthetic *BAX* expression strains**

- Transformation of the expression plasmids was performed using a modified procedure (Logghe, unpublished) of the spheroblasting protocol (Herreros *et al.* 1992). The plasmids were linearised with *Bpu*1102 I to allow directed integration into the genome at the GAL1 promoter site. Correct integration was analysed by Southern blotting. Therefore genomic DNA from different
- 15 transformants was prepared using the Nucleon[®] extraction and purification kit (Amersham Pharmacia Biotech) and digested with *Xba* I. The *BAX* probe used in the Southern blot was prepared by PCR. The PCR was performed using the pGAL1P:synthCa*BAX* plasmid as template, together with the sense primer 5'-ATGGATGGTTCTGGTGAAC-3' (SEQ ID NO 13) and the anti-sense primer 5'-TTAACCCATTTTTTCCAGATG-3' (SEQ ID NO 14). Standard
- 20 PCR conditions were used. For detection of the *yEGFP* a probe was synthesised by PCR using primer 5'-AGAGATCTCGAGGGATCC-3' (SEQ ID NO 15) as sense primer and primer 5'-GCATTATTTGTACAATTCATCC-3' (SEQ ID NO 16) as anti-sense primer. Southern blot hybridisation and detection were performed using the AlkPhos DIRECT labelling and detection system (Amersham Pharmacia Biotech) following the instructions of the manufacturer.

25

Western blot analysis

- For Western blot analysis cells were pre-grown over night in SD-ura media till late log phase. The cells were harvested by centrifugation, washed twice with water and inoculated in SG-ura to induce *Bax* expression. Induction was performed for 15 hours. Yeast crude extracts were
- 30 prepared as described before (Sambook, Fritsch *et al.* 1989). Detection of the *Bax* protein was performed using a polyclonal rabbit anti-mouse /rat *Bax* antibody (Pharmingen). Due to contamination of this antibody with yeast cell wall mannan antibodies, a very high background occurred. This problem could be avoided by pre-incubation of the antibody with 0.5mg/ml purified yeast mannan (Rossanese *et al.* 1999). Detection of the *Gfp* protein was done using an
- 35 anti-*Gfp* monoclonal antibody (Molecular Probes, Eugene, OR, USA).

Growth curves

For growth curves, yeast cells were grown for 24 h in SD-ura medium (supplemented with uridine for the wild type). These cultures were harvested, washed twice with water and inoculated to an OD₆₀₀ of 0.1 into fresh SD-ura or SG-ura media. Growth was monitored in
5 microtitre plates using the Bioscreen C system (Labsystems).

Viability tests

Cells were pregrown in minimal dextrose medium to an OD₆₀₀ of 1. After washing the cells twice with water they were switched to minimal medium containing galactose as carbon source. At the
10 time points indicated, samples were taken and equal cell amounts were spread on minimal dextrose plates. The appearing colonies represent the viable fraction of the pool.

Results : Conditional expression of the synthetic *BAX* gene in *Candida albicans*

A cDNA encoding the full-length mouse Bax protein was placed under control of the *Candida albicans* GAL1 promoter allowing for conditional expression when cells are grown in galactose
15 containing media. Initial experiments were performed using the wild type mouse *bax* gene. Expression of this gene did not result in any detectable phenotype, no difference in growth compared to the wild type was observed when cells were grown on galactose containing media (data not shown). This could be due to the non-traditional codon strategy adopted by *Candida*
20 *albicans* and related species. Analysis of the codons used in the mouse *BAX* gene revealed a for *Candida albicans* not optimal codon usage as found for highly expressed genes in this yeast. To ensure a high expression of the *BAX* gene a codon-adapted, synthetic version of the gene was created using the strategy described above. The synthetic *BAX* gene was fused to the *yEGFP* to allow screening for transformants with a high *yEGFP-synthCaBAX* expression level
25 using FACS technology. The newly obtained plasmids pGAL1P:synthCaBAX and pGAL1:*GFP-synthCaBAX* were transformed into the *C. albicans* CAI4 strain. Transformants were selected on uridine-free minimal medium. About 25 transformants of each expression construct were chosen and streaked onto minimal dextrose medium (non-inducing conditions) as well as on minimal galactose medium (inducing conditions). After two days incubation at 30°C all
30 transformants did grow on the glucose containing media. When galactose was used as a sole carbon source, most of the transformants did not grow (Fig. 8). Southern blot analysis of the galactose negative transformants revealed that a copy of the synthCaBAX gene had been integrated into the endogenous copy of the GAL1 promoter. To study differences in growth, the transformants were grown over night in synthetic glucose containing medium. Subsequently,
35 cells were washed with water and switched to fresh medium containing galactose as carbon source. While the wild type strain did grow well on galactose containing media no growth was

observed for the Bax expressing transformants (Fig. 9A and B). Western blot analysis of the synthCaBAX transformants showed accumulation of the Bax protein (15 hours Bax induction, Fig. 10). A similar result was observed when immunoblotting was performed with the GFP-synthCaBAX expressing strains. Here the fusion protein was detected at the expected
5 molecular weight of about 45K under inducing conditions (galactose as carbon source). In addition to the fusion protein a band appeared at the molecular weight of about 20K. This corresponds to the molecular weight of the Gfp protein alone. Addition of a Gfp-expressing strain as a positive control to the western blot did confirm these results. Here the Gfp protein was detected at the same molecular weight as the unexpected band in the GFP-synthCaBAX
10 expressing strain (Fig. 11). This is most probably due to a partly proteolytic degradation of the fusion protein. Analysis of the Gfp-fluorescence using FACS technology showed a high Gfp-fluorescence signal for the transformants expressing the fusion protein (Fig. 12). When cell viability was analysed, different results were obtained for the synthCaBAX strain and the GFP-synthCaBAX strain. The synthCaBAX strain showed quite a rapid decrease in the amount of
15 colony forming units during the first 6 hours of incubation on galactose containing media. Afterwards the process slowed down significantly. This is in contrast to the results obtained for the strain expressing the gfp-synthCabax fusion protein. Here almost all the cells died at a very rapid rate during the first 3 hours of incubation in media containing galactose as sole carbon source. It is possible that the Bax trigger in the synthCabax expressing cells is not strong
20 enough to kill all cells. The cell has enough time to activate a sort of defence mechanism, possibly by proteolytic degradation of the Bax protein. The situation is different for the fusion protein. Gfp is a very stable protein itself. Fusion of the Gfp to another protein could result in a stabilisation of this protein. It would be more resistant to proteolytic degradation. This would explain the situation for the Gfp-Bax fusion. The Gfp-Bax protein is more protected from
25 proteolytic degradation. Like that it is for a longer period present in the cell. The death trigger is herewith stronger, so the cells die faster. The time that the cells have to activate the proteolytic machinery is not sufficient for them to survive.

Table 1:

Oligo	Sequence 5' → 3'
A1	AACTGCGAGGAAGATCTCCATGGATGGTCTGGTGAACAATGGGTTCTGGTGG TCCAACCTCTTCTGAACAAATCATGAAACCGGTGCTTCTTGTTG (SEQ ID NO 3) TAGAAGCATCTTGTGGTGGTTCGAAGGTCAATTCTGGGTTTCACCCAGCC ATTCTACCAGCTCTATCTTGGATGAACCTTGCAACAAGAAAGCACC (SEQ ID NO 4) GGAATTCTCGACATCAGCGATCATCTTTGCAATTCATGTAGAAATCCAATTC ATCACCGATTCTTCTCAAAACATTCAGACAATTTTGGTAGAGCATCTTGTTG (SEQ ID NO 5) GGAATTGCGCTGATGTCGATACCGATTCTCCAAGAGAAGTCTTCTTCAGAGTCG CTGCTGATATGTCGCTGATGGTAACCTCAACTG (SEQ ID NO 6) AATTCTGGGACTTTGGTACACAAAGCTTTCAGACCCTTTCAGAAAGCGAAGTA GAACAAGCGACGACTCTACCCAGTTGAAGTTACCA (SEQ ID NO 7) CCACCTTGATCTTGGATCCAGACCAACAATCTTCTCTCAAGAAATCCAAGGTC CAACCCATGATGGTTCGATCAATCTGGGACTTTG (SEQ ID NO 8) ATTGTTGGTCTGGATCCAAGATCAAGTGGTGGGAAGGTTGTGTCTTACTT CGGTACCCCAACCTGGCAACCGTCA (SEQ ID NO 9) TCCCCCGGGGATTAAACCCATTTTTCAGATGGTCAAAAGAAGCGGTCAAGAC ACCAGCGACGAAGATGGTGACGGTTTGCCAGGTTGGG (SEQ ID NO 10)
A2	
A3	
B1	
B2	
B3	
C1	
C2	

Table 2: Overview of the differentially expressed genes after 30 min Bax expression**Comparison: INVSc1 YlpUTL versus INVSc1 YlpUTyLB**

Gene	Gene	Normalised intensities		Up/down	Cr value
YER	YEB	YEB	YEB		
<i>Cellular role : Cell cycle control</i>					
YBR133C	HSL7	18932.54	37877.20	↑	2.00
<i>Cellular role : Polymerase II transcription</i>					
YDR253C	MET32	17661.13	45567.17	↑	2.58
YBR112C	SSN6	26698.87	65315.83	↑	2.45
YDR145W	TAF61	38697.96	73117.62	↑	1.89
YBR289W	SNF5	33111.77	72328.70	↑	2.18
YDR216W	ADR1	30127.45	8815.87	↓	3.42
YEL009C	GCN4	16533.76	3030.44	↓	5.46
YBR089C-A	NHP6B	22698.63	6297.49	↓	3.60
YMR043W	MCM1	39141.64	84180.45	↑	2.15
YKR092C	SRP40	5965.63	16105.82	↑	2.70
YMR273C	ZDS1	14699.61	35508.04	↑	2.42
YPL089C	RLM1	34922.91	67856.88	↑	1.94
YOR372C	NDD1	20285.12	44445.20	↑	2.19
YPL037C	EGD1	30633.33	5250.70	↓	5.83
<i>Cellular role : Cell polarity</i>					
YBL085W	BOI1	7693.29	18614.99	↑	2.42
<i>Cellular role : Chromatine structure</i>					
YBR009C	HHF1	16668.00	4178.80	↓	3.99
YNL030W	HHF2	49878.04	12566.96	↓	3.97
YDR224C	HTB1	67355.40	23156.82	↓	2.91
YBL002W	HTB2	25269.02	5383.97	↓	4.69
<i>Cellular role: RNA processing</i>					
YER112W	USS1	12776.74	31470.70	↑	2.46
YPL190C	NAB3	6381.36	17892.11	↑	2.80
YNL112W	DBP2	9958.84	28036.48	↑	2.82
<i>Cellular role: Energy generation</i>					
YPL078C	ATP4	26902.69	5980.38	↓	4.50
YDL004W	ATP16	36525.08	3004.34	↓	12.16
YDR377W	ATP17	14419.41	756.86	↓	19.05
YDR529C	QCR7	35346.95	5394.65	↓	6.55
YGR008C	STF2	13275.51	2276.27	↓	5.83
YEL039C	CYC7	13604.38	2689.66	↓	5.06
YKL150W	MCR1	105337.67	30743.75	↓	3.43
YLR038C	COX12	52687.73	5455.83	↓	9.66
YLR327C		113.966.77	54.014.65	↓	2.11
<i>Cellular role: Carbohydrate metabolism</i>					
YBR149W	ARA1	15149.55	4095.17	↓	3.70
YHR094C	HXT1	12526.90	785.73	↓	15.94
YDR345C	HXT3	36643.13	1632.48	↓	22.45
YDR343C	HXT6	77064.71	32060.05	↓	2.40
YDR342C	HXT7	76349.13	27615.15	↓	2.76
<i>Cellular role: Signal transduction</i>					
YER177W	BMH1	22856.29	44771.71	↑	1.96
YDR099W	BMH2	40127.38	74572.38	↑	1.86

YGR070W	ROM1	12055.28	28169.57	↑	2.34
YGR023W	MTL1	7354.78	19648.06	↑	2.67
<i>Cellular role: Protein synthesis</i>					
YGR034W	RPL26B	71942.48	74625.22	↑	1.04
<i>Cellular role: Protein folding</i>					
YLR216C	CPR6	9616.80	31126.02	↑	3.24
<i>Cellular role: Protein modification/degradation</i>					
YFR052W	RPN12	5583.57	14855.67	↑	2.66
YDL147W	RPN5	31932.20	52939.11	↑	1.66
YGR132C	PHB1	15429.56	5591.19	↓	2.76
YGR135W	PRE9	39921.63	5517.17	↓	7.24
YFR010W	UBP6	1892.76	828.94	↓	2.28
<i>Cellular role: Cell stress</i>					
YIR037W	GPX3	7869.22	21789.00	↑	2.77
YDR513W	TTR1	55986.32	33263.12	↓	1.68
YCL035C	GRX1	70248.30	10969.97	↓	6.40
YFL014W	HSP12	41689.29	18658.48	↓	2.23
YHR053C	CUP1A	72852.07	43488.52	↓	1.68
YHR055C	CUP1B	71934.03	56799.80	↓	2.77
YMR173W	DDR48	16870.70	5022.40	↓	3.32
YMR251W-A	HOR7	26879.95	417.36	↓	64.41
YLR043C	TRX1	58251.39	4435.79	↓	13.13
YBL064C	PRX1	21525.00	40969.00	↑	1.90
YOL151W	GRE2	2624.55	24152.03	↑	9.20
<i>Cellular role: Unknown</i>					
YBL081W		73834.11	74612.35	↑	1.01
YDR366C		39998.46	57428.80	↑	1.44
YCR004C	YCP4	6869.06	28115.73	↑	4.09
YCR013C		3988.55	15144.34	↑	3.80
YBR050C	REG2	4687.91	14408.20	↑	3.07
YBL109W		18744.60	35440.24	↑	1.89
YDR154C		19565.23	69428.03	↑	3.55
YEL071W	DLD3	22235.73	68790.83	↑	3.09
YHR095W		14426.76	34896.68	↑	2.42
YGR069W		43413.57	72420.39	↑	1.67
YDR544C		13587.00	27004.37	↑	1.99
YGR236C		24927.59	8032.35	↓	3.10
YIL057C		24246.39	773.56	↓	31.34
YGL080W		23425.00	3217.81	↓	7.28
YGL072C		16437.52	2652.80	↓	6.20
YHR056C	RSC30	72072.88	57446.85	↓	1.25
YKL054C	VID31	17990.49	38258.80	↑	2.13
YLR311C		7992.40	24164.87	↑	3.02
YJR115W		64690.69	102066.34	↑	1.58
YJL188C	BUD19	7580.28	22325.70	↑	2.95
YKR040C		50934.78	100733.41	↑	1.98
YLR053C		8117.66	20317.34	↑	2.50
YOR121C		59950.94	92470.43	↑	1.54
YNL143C		98911.28	110534.34	↑	1.12
YOR131C		7941.55	22353.72	↑	2.81
YNL338W		21800.45	38777.28	↑	1.78
YNL179C		13729.36	39516.53	↑	2.88
YOL150C		3408.74	60298.39	↑	17.69

YMR107W		65118.70	10042.46	↓	6.48
YKL065C	YET1	69556.19	12804.88	↓	5.43
YJR096W		21780.37	10655.13	↓	2.04
YJL161W		16468.73	2618.26	↓	6.29
YML128C	MSC1	80130.20	13795.84	↓	5.81
YMR251W		26879.95	417.36	↓	64.41
YMR173W-A		110104.98	61951.23	↓	1.78
YPL201C		17913.32	5018.97	↓	3.57
YOR285W		64074.73	29749.43	↓	2.15
YOR286W		13458.08	733.06	↓	18.36
<i>Cellular role: Cell wall maintenance</i>					
YKR076W	ECM4	2674.15	13040.04	↑	4.88
YLR390W	ECM19	5472.05	15145.85	↑	2.77
<i>Cellular role: Membrane fusion</i>					
YHR138C		19921.35	3707.57	↓	5.37
<i>Cellular role: Vesicular transport</i>					
YHR161C	YAP180A	13086.35	30160.90	↑	2.30
YPL085W	SEC16	6668.57	15206.49	↑	2.28
YKL196C	YKT6	18933.84	2890.07	↓	6.55
YPR028W	YIP2	25434.34	2049.47	↓	12.41
<i>Cellular role: DNA repair/recombination</i>					
YDL059C	RAD59	1948.61	13089.13	↑	6.72
<i>Cellular role: DNA synthesis</i>					
YEL032W	MCM3	23422.85	44327.48	↑	1.89
<i>Cellular role: Amino acid metabolism</i>					
YIL074C	SER33	3978.42	16702.66	↑	4.20
YGR155W	CYS4	4184.59	19270.89	↑	4.61
<i>Cellular role: Fatty acid metabolism</i>					
YHR179W	OYE2	2291.36	40274.02	↑	17.58
<i>Cellular role: Protein translocation</i>					
YNL131W	TOM22	16287.21	1679.78	↓	9.70
<i>Cellular role: Small molecule transport</i>					
YDR276C	SNA1	21148.46	1580.68	↓	13.38
YOR267C	HRK1	62689.30	110516.24	↑	1.76
YHR039-C	VMA10	60107.90	8490.93	↓	7.08
YOR382W	FIT2	6780.82	27236.15	↑	4.02

Table 3: Overview of the differentially expressed genes after 1h Bax expression**Comparison: INVSc1 YlpUTL versus INVSc1 YlpUTyLB**

ORF	Gene	Normalised intensities		Up/down	Q-value
		UTL	UTyLB		
Cellular role : Polymerase II transcription					
YDR145W	TAF61	20729.58	57376.27	↑	2.77
YDR216W	ADR1	5925.91	18459.00	↑	3.11
YBR112C	CYC8	50186.77	64511.50	↑	1.29
YMR043W	MCM1	21011.54	53700.49	↑	2.56
YPL089C	RLM1	23440.54	64284.32	↑	2.74
YOR372C	NDD1	26412.58	50804.99	↑	1.92
Cellular role : Cell cycle control					
YBR133C	HSL7	18761.64	53238.86	↑	2.84
Cellular role : Cell polarity					
YBL085W	BOI1	37895.40	57761.52	↑	1.52
Cellular role : Chromatine structure					
YDR224C	HTB1	13661.40	55656.34	↑	4.07
Cellular role: Energy generation					
YGR183C	QCR9	23181.54	81865.40	↑	3.53
YLR294C		5054.57	28994.72	↑	5.74
YKL150W	MCR1	43663.07	60593.16	↑	1.39
YMR256C	COX7	7606.58	28801.54	↑	3.79
YOL126C	MDH2	34144.61	65326.97	↑	1.91
YLR327C		97415.94	101651.17	↑	1.04
Cellular role: Vesicular transport					
YHR161C	YAP180A	11602.81	34695.20	↑	2.99
YLR206W	ENT2	14439.24	34621.70	↑	2.40
Cellular role: Carbohydrate metabolism					
YDR342C	HXT7	65273.56	22231.06	↓	2.94
YDR343C	HXT6	43572.28	6075.38	↓	7.17
YDR345C	HXT3	76352.52	40296.00	↓	1.89
YGR192C	TDH3	38472.30	14145.84	↓	2.72
YKR097W	PCK1	22919.81	38225.98	↑	1.67
YOR374W	ALD4	33711.37	2607.43	↓	12.93
Cellular role: Signal transduction					
YER177W	BMH1	16298.14	31748.91	↑	1.95
YDR099W	BMH2	50572.45	65123.58	↑	1.29
Cellular role: Cell wall maintenance					
YLR110C	CCW12	102525.29	11230.41	↓	9.13
Cellular role: Protein modification/degradation					
YOR261C	RPN8	12575.49	32568.47	↑	2.59
Cellular role: Cell stress					
YHR053C	CUP1A	32531.53	63579.94	↑	1.95
YHR055C	CUP1B	27939.92	65142.82	↑	2.33
YMR173W	DDR48	38338.83	60514.70	↑	1.58
YOR031W	CRS5	2922.32	23848.60	↑	8.16

YLR109W	AHP1	43067.08	6302.46	↓	6.83
Cellular role: Unknown					
YBL081W		82476.13	44279.86	↑	1.86
YBL109W		22998.63	63428.23	↑	2.76
YDR366C		14599.17	46494.73	↑	3.18
YDR154C		21296.57	56534.93	↑	2.65
YGR236C	SPG1	17717.80	64439.96	↑	3.64
YHR056C	RSC30	27020.16	65110.42	↑	2.41
YGR182C		8171.02	34669.96	↑	4.24
YDR544C		14797.70	37704.91	↑	2.55
YHR162W		13836.79	33381.64	↑	2.41
YGR243W		30829.66	59765.39	↑	1.94
YBR050C	REG2	14008.24	29603.16	↑	2.11
YEL071W	DLD3	19487.41	35273.39	↑	1.81
YDR133C		83074.54	62986.96	↓	1.32
YDR134C		83111.03	16839.53	↓	4.94
YHL021C		46028.06	8577.00	↓	5.37
YKL054C	VID31	28018.46	66537.91	↑	2.37
YLR311C		7803.52	31160.73	↑	3.99
YMR107W		13453.15	78850.98	↑	5.86
YKL066W		8751.84	24129.32	↑	2.76
YMR173W-A		38338.83	60514.70	↑	1.58
YML053C		23670.86	66254.48	↑	2.80
YOR121C		17039.58	58016.58	↑	3.40
YOL106W		19917.67	69853.66	↑	3.51
YNL338W		17864.90	49911.08	↑	2.79
YJR115W		84858.02	98161.71	↑	1.16
Cellular role: Small molecule transport					
YOR267C	HRK1	90123.84	96824.51	↑	1.07

Table 4: Overview of the differentially expressed genes after 2h Bax expression**Comparison: INVSc1 YlpUTL versus INVSc1 YlpUTyLB**

ORF	Gene	Normalised Intensities		Up/Down	Q1 value
		YLB	YLB		
<i>Cellular role: Protein modification/degradation</i>					
YCL052C	PBN1	5264.22	8175.70	↑	1.55
YDL147W	RPN5	22386.40	47857.67	↑	2.14
YOR261C	RPN8	27349.25	42198.05	↑	1.54
YGR132C	PHB1	5252.03	8459.53	↑	1.61
YBR139W		9458.26	3611.21	↓	2.62
<i>Cellular role : Unknown</i>					
YDR202C	RAV2	7483.71	10089.19	↑	1.35
YBR062C		4893.97	9894.82	↑	2.02
YDR366C		25468.2	59682.92	↑	2.34
YBL109W		24803.62	37444.64	↑	1.51
YDR154C		21166.26	33434.35	↑	1.58
YEL071W	DLD3	34153.85	44083.39	↑	1.29
YGR236C	SPG1	16978.52	31419.12	↑	1.85
YGR182C		30569.31	58805.05	↑	1.92
YDR544C		15937.14	24421.99	↑	1.53
YHR162W		26610.34	33794.73	↑	1.27
YHR056C	RSC30	33372.66	68425.24	↑	2.05
YDR133C		75520.99	62984.59	↓	1.20
YCR010C	ADY2	17240.59	11835.82	↓	1.46
YDR134C		72723.66	9776.23	↓	7.44
YGR069W		65418.73	53767.35	↓	1.22
YIL057C		16510.16	2198.04	↓	7.51
YGL072C		12209.68	6509.91	↓	1.88
YGL080W		22550.76	11525.24	↓	1.96
YLR311C		11095.31	24660.47	↑	2.22
YJR115W		74757.79	103422.48	↑	1.38
YMR099C		7057.15	11477.42	↑	1.63
YMR173W-A		31901.05	48886.91	↑	1.47
YML132W	COS3	24648.97	34895.33	↑	1.42
YKL066W		13581.94	25433.97	↑	1.87
YJL142C		7205.86	11920.21	↑	1.65
YLR346C		6447.57	11569.63	↑	1.79
YLR053C		41161.10	78636.82	↑	1.91
YMR110C		19410.64	29661.23	↑	1.53
YKR075C		19104.57	29948.72	↑	1.57
YOR121C		36492.56	59452.09	↑	1.63

Cellular role : Unknown					
YOL108W		31382.10	76664.72	↑	2.44
YNL338W		24117.93	38981.22	↑	1.62
YNL134C		9617.33	14613.60	↑	1.52
YKL065C	YET1	52422.65	33794.03	↓	1.55
YMR009W		20666.22	9519.29	↓	2.17
YJL144W		10316.92	3122.77	↓	3.30
YML128C	MSC1	584128.13	25434.11	↓	2.29
YNL179C		21938.96	10883.98	↓	2.02
YOL109W	ZEO1	22711.98	6581.11	↓	3.45
YNR002C	FUN34	18241.25	9752.25	↓	1.87
Cellular role: Chromatine structure					
YDR224C	HTB1	25356.73	30827.54	↑	1.22
YBL002W	HTB2	9241.68	14261.54	↑	1.54
YBL003C	HTA2	3453.55	6553.49	↑	1.90
YNL031C	HHT2	13376.02	2348.84	↓	5.69
Cellular role: Polymerase II transcription					
YBR289W	SNF5	59542.27	65885.13	↑	1.11
YDR073W	SNF11	12190.01	23088.03	↑	1.89
YMR043W	MCM1	66457.16	77022.05	↑	1.16
YPL089C	RLM1	49844.99	60624.28	↑	1.22
Cellular role : Signal transduction					
YDR099W	BMH2	55902.13	73874.51	↑	1.32
Cellular role: Cell stress					
YBL064C	PRX1	11203.87	14815.42	↑	1.32
YBR101C		25016.27	35781.64	↑	1.43
YLR043C	TRX1	10864.53	3912.03	↓	2.78
YGR209C	TRX2	30492.33	37829.20	↑	1.24
YER103W	SSA4	8763.38	15799.18	↑	1.80
YHR055C	CUP1B	18824.43	77613.05	↑	4.12
YHR053C	CUP1A	32726.62	63536.72	↑	1.94
YDR256C	CTA1	9614.29	4232.17	↓	2.27
YCR021C	HSP30	8090.05	3604.78	↓	2.24
YCL035C	GRX1	28437.57	12843.99	↓	2.21
YGR086C		36796.12	24272.57	↓	1.52
YFL014W	HSP12	61868.64	23288.19	↓	2.66
YOR031W	CRS5	6015.69	14519.12	↑	2.41
YMR251W-A	HOR7	17731.14	4231.39	↓	4.19
YOR120W	GCY1	114252.98	78052.05	↓	1.46
Cellular role: Protein synthesis					
YAL003W	EFB1	3044.80	5772.68	↑	1.90
YOL127W	RPL25	6266.96	12055.41	↑	1.92
YHR010W	RPL27	4057.16	10856.34	↑	2.68
YLR325C	RPL38	5401.85	12955.89	↑	2.40
YJL189W	RPL39	2044.64	8010.67	↑	3.92
YIL148W	RPL40A	5052.35	11595.54	↑	2.30
YKR094C	RPL40B	3994.57	10011.13	↑	2.54
YOL139C	CDC33	4132.18	8956.14	↑	2.17

Cellular role : Protein folding					
YLR216C	CPR6	20353.43	32713.37	↑	1.61
YKL117W	SBA1	11144.25	1500.56	↓	7.43
Cellular role: Vesicular transport					
YCR009C	RVS161	5350.32	9780.92	↑	1.83
YHR161C	YAP180A	25136.63	32461.67	↑	1.29
YBL078C	AUT7	16528.91	9843.25	↓	1.68
Cellular role : Carbohydrate metabolism					
YBL058W	SHP1	4626.50	8179.94	↑	1.77
YBR149W	ARA1	30706.41	9637.76	↓	3.19
YDR178W	SDH4	14880.91	6237.35	↓	2.39
YHR094C	HXT1	30389.99	18383.00	↓	1.65
YMR011W	HXT2	39524.90	21221.96	↓	1.86
YDR345C	HXT3	77025.40	56749.40	↓	1.36
YDR343C	HXT6	73149.70	8676.17	↓	8.43
YDR342C	HXT7	75331.76	27052.43	↓	2.78
YKL060C	FBA1	16273.54	21323.23	↑	1.31
Cellular role : Cell cycle control					
YBR133C	HSL7	32903	41964.32	↑	1.28
Cellular role : Energy generation					
YMR256C	COX7	18558.01	40422.91	↑	2.18
YML129C	COX14	11418.54	21798.88	↑	1.91
YFR033C	QCR6	9159.48	13398.67	↑	1.46
YDR529C	QCR7	24821.75	16558.87	↓	1.50
YJL166W	QCR8	15554.30	24509.26	↑	1.58
YHR001W-A	QCR10	12416.35	23465.31	↑	1.89
YBR039W	ATP3	11709.79	3088.19	↓	3.79
YPL078C	ATP4	11325.64	13769.72	↑	1.22
YPL271W	ATP15	3261.75	7839.05	↑	2.40
YLR327C		51742.90	128511.27	↑	2.48
YLR294C		15832.61	38544.44	↑	2.43
YAL060W	FUN49	11792.72	5778.91	↓	2.04
Cellular role: Small molecule transport					
YDR276C	SNA1	19337.39	12392.29	↓	1.56
YGR197C	SNG1	4768.18	10484.09	↑	2.20
YHR039C-B	VMA10	21190.93	10592.98	↓	2.00
YOR267C	HRK1	111849.17	101339.10	↓	1.10
Cellular role: RNA processing					
YGR250C		8709.92	17358.43	↑	1.99
Cellular role : Cell wall maintenance					
YER150W	SPI1	55592.73	22403.59	↓	2.48
YLR110C	CCW12	35147.41	5786.88	↓	6.07
Cellular role : Cell polarity					
YOR122C	PFY1	14459.45	20176.41	↑	1.40
Cellular role : Amino acid metabolism					
YPR035W	GLN1	20894.14	7522.05	↓	2.78

Table 5: Overview of the differentially expressed genes after 3h Bax expression**Comparison: INVSc1 YlpUTL versus INVSc1 YlpUTyLB**

ORF	Gene	Normalised intensities YTL	Normalised intensities YLB	Up/down	Q value
<i>Cellular role : Cell cycle control</i>					
YBR133C	HSL7	63562.10	43191.28	↓	1.47
<i>Cellular role : Cell polarity</i>					
YBL085W	BOI1	32734.79	23497.41	↓	1.39
<i>Cellular role : Chromatine structure</i>					
YDR545W	YRF1-1	20111.51	11479.67	↓	1.75
<i>Cellular role: Energy generation</i>					
YCR005C	CIT2	11882.42	25632.94	↑	2.16
YGR183C	QCR9	74474.20	11510.99	↓	6.47
YOL126C	MDH2	55984.88	17978.10	↓	3.11
<i>Cellular role: Carbohydrate metabolism</i>					
YBR019C	GAL10	3092.50	15697.54	↑	5.08
YDR345C	HXT3	14086.41	25657.66	↑	1.82
YKR097W	PCK1	50736.44	20858.02	↓	2.43
<i>Cellular role: Signal transduction</i>					
YDR099W	BMH2	63285.16	56028.91	↓	1.13
<i>Cellular role: Protein synthesis</i>					
YHR010W	RPL27A	23254.90	7217.14	↓	3.22
YLR325C	RPL38	26725.96	9121.29	↓	2.93
<i>Cellular role: Cell stress</i>					
YFL014W	HSP12	40848.44	69781.91	↑	1.71
YHR053C	CUP1A	20399.10	65037.14	↑	3.19
YHR055C	CUP1B	21763.09	64594.58	↑	2.97
YMR173W	DDR48	75407.16	36354.37	↓	2.07
YOL052C-A	DDR2	20479.72	33702.23	↑	1.65
<i>Cellular role: Unknown</i>					
YIL057C		7602.78	24104.02	↑	3.17
YHR056C	RSC30	41473.41	64809.08	↑	1.56
YDR544C		55075.67	29731.72	↓	1.85
YKR040C		48049.71	59649.47	↑	1.24
YNL338W		86107.91	30045.62	↓	2.87
YJR115W		74889.58	81238.98	↓	1.08
YBL109W		64754.79	57185.99	↓	1.13
YMR173W-A		75407.16	36354.37	↓	2.07

Table 6: Overview of the differentially expressed genes after 6h Bax expression**Comparison: INVSc1 YlpUTL versus INVSc1 YlpUTyLB**

Gene	Gene	Normalised intensities INVSc1 YlpUTL	Normalised intensities INVSc1 YlpUTyLB	Up/Down	Q value
<i>Cellular role: Cell stress</i>					
YDR171W	HSP42	13484.04	27183.07	↑	2.02
YFL014W	HSP12	41197.12	29081.08	↓	1.42
YDR513W	TTR1	19985.22	12935.62	↓	1.54
YCL035C	GRX1	31735.39	12930.71	↓	2.45
YGR209C	TRX2	54455.65	47569.21	↓	1.14
YHR053C	CUP1A	81488.84	15289.39	↓	5.33
YHR055C	CUP1B	81278.95	20031.69	↓	4.06
YMR251W-A	HOR7	18824.54	5914.28	↓	3.18
<i>Cellular role: Signal transduction</i>					
YDR099W	BMH2	29412.99	58598.42	↑	1.99
<i>Cellular role: Protein synthesis</i>					
YGL147C	RPL9A	13655.66	1585.97	↓	8.61
YGR085C	RPL11B	27465.15	3791.35	↓	7.24
YDR418W	RPL12B	14417.77	1555.24	↓	9.27
YLR029C	RPL15A	37122.11	9321.81	↓	3.98
YOR312C	RPL20B	50334.94	5706.59	↓	8.82
YBR191W	RPL21A	21740.90	2571.30	↓	8.46
YPL079W	RPL21B	31059.43	5023.61	↓	6.18
YOL127W	RPL25	75971.72	11749.17	↓	6.47
YHR010W	RPL27A	45716.64	8096.40	↓	5.65
YDR471W	RPL27B	14636.79	2613.40	↓	5.60
YDL075W	RPL31A	11969.47	2611.53	↓	4.58
YBL092W	RPL32	7872.80	857.85	↓	9.18
YDL191W	RPL35A	28582.59	6046.25	↓	4.73
YDL136W	RPL35B	25433.49	5064.51	↓	5.02
YLR325C	RPL38	48051.23	8217.18	↓	5.85
YIL148W	RPL40A	47028.95	9543.85	↓	4.93
YKR094C	RPL40B	39900.50	5957.78	↓	6.70
YHR141C	RPL42B	10163.88	937.21	↓	10.84
YML063W	RPS1B	15916.48	1144.54	↓	13.91
YGL123W	RPS2	12505.56	2243.26	↓	5.57
YOR096W	RPS7A	24164.37	3223.60	↓	7.50
YBL072C	RPS8A	17198.50	3233.30	↓	5.32
YER102W	RPS8B	16234.83	1791.18	↓	9.06
YBR189W	RPS9B	10075.22	2150.89	↓	4.68
YOR293W	RPS10A	51787.23	12110.74	↓	4.28
YDR064W	RPS13	9736.57	1587.67	↓	6.13
YDR450W	RPS18A	37913.71	5674.60	↓	6.68
YML026C	RPS18B	14458.01	2027.28	↓	7.13
YKL156W	RPS27A	23725.18	11117.26	↓	2.13
YLR167W	RPS31	38648.54	2611.97	↓	14.80
YJL138C	TIF2	20154.61	7264.66	↓	2.77
<i>Cellular role: Energy metabolism</i>					
YGR183C	QCR9	57357.59	80447.53	↑	1.40
YDL004W	ATP16	25047.95	10988.85	↓	2.28
YKL150W	MCR1	50931.46	37076.83	↓	1.37

YLR038C	COX12	39506.06	29534.70	↓	1.34
Cellular role: Unknown					
YDR442W		14654.61	2242.42	↓	6.54
YDR134C		17025.59	10561.72	↓	1.61
YHR056C	RSC30	81350.52	31447.10	↓	2.59
YKR040C		48390.21	90125.88	↑	1.86
YLR414C		13463.40	8085.92	↓	1.67
YLR312C		25589.67	16184.57	↓	1.58
YJL188C	BUD19	22074.09	4526.39	↓	4.88
YOR285W		75099.98	61896.00	↓	1.21
YOL109W	ZEO1	66287.15	35502.43	↓	1.87
Cellular role: Chromatine structure					
YBR009C	HHF1	11173.15	5416.74	↓	2.06
YNL030W	HHF2	31366.74	20132.23	↓	1.56
Cellular role: Nucleotide metabolism					
YDR399W	HPT1	13339.03	5333.81	↓	2.50
Cellular role: Polymerase II transcription					
YEL009C	GCN4	34617.98	20798.63	↓	1.66
YPL037C	EGD1	17862.37	8229.01	↓	2.17
Cellular role: Vesicular transport					
YBL078C	AUT7	42661.70	32333.01	↓	1.32
YOR327C	SNC2	22716.56	13704.48	↓	1.66
Cellular role : Small molecule transport					
YHR039C-B	VMA10	44429.30	23826.51	↓	1.86
Cellular role : Cell wall maintenance					
YKL097W-A	CWP2	13529.93	1617.20	↓	8.37
Cellular role: Carbohydrate metabolism					
YKL060C	FBA1	33329.74	10367.82	↓	3.21

Table 7:

Sequence ID NO	ORF	GENE	30 min	1h	2h	3h	6h
SEQ ID NO 17	YAL003W	EFB1			1.90		
SEQ ID NO 19	YAL060W	FUN49			-2.00		
SEQ ID NO 21	YBL002W	HTB2	-4.69		1.54		
SEQ ID NO 23	YBL058W	SHP1			1.77		
SEQ ID NO 25	YBL064C	PRX1	1.90		1.32		
SEQ ID NO 27	YBL072C	RPS8A					-5.32
SEQ ID NO 29	YBL081W		1.01	1.86			
SEQ ID NO 31	YBL085W	BOI1	2.42	1.52		-1.39	
SEQ ID NO 33	YBL092W	RPL32			2.76		-9.18
SEQ ID NO 35	YBL109W		1.89	2.76	1.51	-1.13	
SEQ ID NO 37	YBR009C	HHF1	-3.99				-2.06
SEQ ID NO 39	YBR019C	GAL10				5.08	
SEQ ID NO 41	YBR039W	ATP3			-3.70		
SEQ ID NO 43	YBR050C	REG2	3.07	2.11			
SEQ ID NO 45	YBR062C				2.02		
SEQ ID NO 47	YBR089C-A	NHP6B	-3.60				
SEQ ID NO 49	YBR101C				1.43		
SEQ ID NO 51	YBR112C	SSN6	2.45	1.29			
SEQ ID NO 53	YBR133C	HSL7	2.00	2.84	1.28	-1.47	
SEQ ID NO 55	YBR139W				-2.60		
SEQ ID NO 57	YBR149W	ARA1	-3.70		-3.11		
SEQ ID NO 59	YBR189W	RPS9B					-4.68
SEQ ID NO 61	YBR191W	RPL21A					-8.46
SEQ ID NO 63	YBR289W	SNF5	2.18		1.11		
SEQ ID NO 65	YCL035C	GRX1	-6.40		-2.20		-2.45
SEQ ID NO 67	YCL052C	PBN1			1.55		
SEQ ID NO 69	YCR004C	YCP4	4.09				
SEQ ID NO 71	YCR005C	CIT2				2.16	
SEQ ID NO 73	YCR009C	RVS161			1.83		
SEQ ID NO 75	YCR010C				-1.40		
SEQ ID NO 77	YCR013C		3.80				
SEQ ID NO 79	YCR021C	HSP30			-2.20		
SEQ ID NO 81	YDL004W	ATP16	-12.16				-2.28
SEQ ID NO 83	YDL059C	RAD59	6.72				
SEQ ID NO 85	YDL075W	RPL31A					-4.58
SEQ ID NO 87	YDL147W	RPN5	1.66		2.14		
SEQ ID NO 89	YDR064W	RPS13					-6.13
SEQ ID NO 91	YDR073W	SNF11			1.89		
SEQ ID NO 93	YDR099W	BMH2	1.86	1.29	1.32	-1.13	1.99
SEQ ID NO 95	YDR133C			-1.32	-1.20		
SEQ ID NO 97	YDR134C			-4.94	-7.40		-1.61
SEQ ID NO 99	YDR145W	TAF61	1.89	2.77			
SEQ ID NO 101	YDR154C		3.55	2.65	1.58		
SEQ ID NO 103	YDR171W	HSP42					2.02
SEQ ID NO 105	YDR178W	SDH4			-2.30		
SEQ ID NO 107	YDR202C	RAV2			1.35		
SEQ ID NO 109	YDR216W	ADR1	-3.42	3.11			
SEQ ID NO 111	YDR224C	HTB1	-2.91	4.07	1.22		
SEQ ID NO 113	YDR253C	MET32	2.58				
SEQ ID NO 115	YDR256C	CTA1			-2.20		
SEQ ID NO 117	YDR276C	SNA1	-13.38		-1.50		

Sequence ID NO	ORF	GENE	30 min	1h	2h	3h	6h
SEQ ID NO 119	YDR342C	HXT7	-2.76	-2.94	-2.70		
SEQ ID NO 121	YDR343C	HXT6	-2.40	-7.17	-8.40		
SEQ ID NO 123	YDR345C	HXT3	-22.45	-1.89	-1.30	1.82	
SEQ ID NO 125	YDR366C		1.44	3.18	2.34		
SEQ ID NO 127	YDR377W	ATP17	-19.05				
SEQ ID NO 129	YDR399W	HPT1					-2.50
SEQ ID NO 131	YDR418W	RPL12B					-9.27
SEQ ID NO 133	YDR513W	TTR1	-1.68				-1.54
SEQ ID NO 135	YDR544C		1.99	2.55	1.53	-1.85	
SEQ ID NO 137	YDR545W	YRF1-1				-1.75	
SEQ ID NO 139	YEL009C	GCN4	-5.46				-1.66
SEQ ID NO 697	YEL032W	MCM3	1.89				
SEQ ID NO 141	YEL039C	CYC7	-5.06				
SEQ ID NO 143	YEL071W	DLD3	3.09	1.81	1.29		
SEQ ID NO 145	YER103W	SSA4			1.80		
SEQ ID NO 147	YER112W	USS1	2.46				
SEQ ID NO 149	YER150W	SPI1			-2.40		
SEQ ID NO 151	YER177W	BMH1	1.96	1.95			
SEQ ID NO 153	YFR010W	UBP6	-2.28				
SEQ ID NO 155	YFR033C	QCR6			1.46		
SEQ ID NO 157	YFR052W	RPN12	2.66				
SEQ ID NO 159	YGL072C		-6.20		-1.80		
SEQ ID NO 161	YGL080W		-7.28		-1.90		
SEQ ID NO 163	YGL123W	RPS2					-5.57
SEQ ID NO 165	YGR008C	STF2	-5.83				
SEQ ID NO 167	YGR023W	MTL1	2.67				
SEQ ID NO 169	YGR034W	RPL26B	1.04				
SEQ ID NO 171	YGR069W		1.67		-1.20		
SEQ ID NO 173	YGR070W	ROM1	-2.34				
SEQ ID NO 175	YGR086C				-1.50		
SEQ ID NO 177	YGR132C	PHB1	-2.76		1.61		
SEQ ID NO 179	YGR135W	PRE9	-7.24				
SEQ ID NO 181	YGR155W	CYS4	4.61				
SEQ ID NO 183	YGR192C	TDH3		-2.72			
SEQ ID NO 185	YGR197C	SNG1			2.20		
SEQ ID NO 187	YGR209C	TRX2			1.24		-1.14
SEQ ID NO 189	YGR243W			1.94			
SEQ ID NO 191	YGR250C				1.99		
SEQ ID NO 193	YHL021C			-5.37			
SEQ ID NO 195	YHR001W-A	QCR10			1.89		
SEQ ID NO 197	YHR039C-B	VMA10	-7.08		-2.00		-1.86
SEQ ID NO 199	YHR053C	CUP1A	-1.68	1.95	1.94	3.19	-5.33
SEQ ID NO 201	YHR055C	CUP1B	-2.77	2.33	4.12	2.97	-4.06
SEQ ID NO 203	YHR056C		-1.25	2.41	2.05	1.56	-2.59
SEQ ID NO 205	YHR094C	HXT1	-15.94		-1.60		
SEQ ID NO 207	YHR095W		2.42				
SEQ ID NO 209	YHR138C		-5.37				
SEQ ID NO 211	YHR161C	YAP180A	2.30	2.99	1.29		
SEQ ID NO 213	YHR162W			2.41	1.27		
SEQ ID NO 215	YHR179W	OYE2	17.58				
SEQ ID NO 217	YIL057C		-31.34		-7.50	3.17	
SEQ ID NO 219	YIL074C	SER33	4.20				
SEQ ID NO 221	YIR037W	GPX3	2.77				

Sequence ID NO	ORF	GENE	30 min	1h	2h	3h	6h
SEQ ID NO 223	YJL138C	TIF2					-2.77
SEQ ID NO 225	YJL142C				1.65		
SEQ ID NO 227	YJL144W				-3.30		
SEQ ID NO 229	YJL161W		-6.29				
SEQ ID NO 231	YJL166W	QCR8			1.58		
SEQ ID NO 233	YJR096W		-2.04				
SEQ ID NO 235	YJR115W		1.58	1.16	1.38	-1.08	
SEQ ID NO 237	YKL054C	VID31	2.13	2.37			
SEQ ID NO 239	YKL060C	FBA1			1.31		-3.21
SEQ ID NO 241	YKL065C	YET1	-5.43		-1.55		
SEQ ID NO 243	YKL066W			2.76	1.87		
SEQ ID NO 245	YKL097W-A	CWP2					-8.37
SEQ ID NO 247	YKL117W	SBA1			-7.43		
SEQ ID NO 249	YKL150W	MCR1	-3.43	1.39			-1.37
SEQ ID NO 251	YKL156W	RPS27A					-2.13
SEQ ID NO 253	YKL196C	YKT6	-6.55				
SEQ ID NO 255	YKR040C		1.98			1.24	1.86
SEQ ID NO 257	YKR075C				1.57		
SEQ ID NO 259	YKR076W	ECM4	4.88				
SEQ ID NO 261	YKR092C	SRP40	2.70				
SEQ ID NO 263	YKR097W	PCK1		1.67		-2.43	
SEQ ID NO 265	YLR029C	RPL15A					-3.98
SEQ ID NO 267	YLR038C	COX12	-9.66				-1.34
SEQ ID NO 269	YLR043C	TRX1	-13.13		-2.78		
SEQ ID NO 271	YLR053C		2.50		1.91		
SEQ ID NO 273	YLR109W	AHP1		-6.83			
SEQ ID NO 275	YLR110C			-9.13	-6.07		
SEQ ID NO 277	YLR206W	ENT2		2.40			
SEQ ID NO 279	YLR216C	CPR6	3.24		1.61		
SEQ ID NO 281	YLR294C			5.74	2.43		
SEQ ID NO 283	YLR311C		3.02	3.99	2.22		
SEQ ID NO 285	YLR312C						-1.58
SEQ ID NO 287	YLR327C		-2.10	1.04	2.48		
SEQ ID NO 289	YLR346C				1.79		
SEQ ID NO 291	YLR390W	ECM19	2.77				
SEQ ID NO 293	YLR414C						-1.67
SEQ ID NO 295	YML053C			2.80			
SEQ ID NO 297	YML129C	COX14			1.91		
SEQ ID NO 299	YML132W	COS3			1.42		
SEQ ID NO 301	YMR009W				-2.17		
SEQ ID NO 303	YMR011W	HXT2			-1.86		
SEQ ID NO 305	YMR043W	MCM1	2.15	2.56	1.16		
SEQ ID NO 307	YMR099C				1.63		
SEQ ID NO 309	YMR107W		-6.48	5.86			
SEQ ID NO 311	YMR110C				1.53		
SEQ ID NO 313	YMR173W	DDR48	-3.32	1.58		-2.07	
SEQ ID NO 691	YMR173W-A		-1.78	1.58	1.47	-2.07	
SEQ ID NO 315	YMR251W		-64.41				
SEQ ID NO 317	YMR251W-A	HOR7	-64.41		-4.19		-3.18
SEQ ID NO 319	YMR256C	COX7		3.79	2.18		
SEQ ID NO 321	YMR273C	ZDS1	2.42				
SEQ ID NO 323	YNL030W	HHF2	-3.97				-1.56
SEQ ID NO 325	YNL031C	HHT2			-5.69		

Sequence ID NO	ORF	GENE	30 min	1h	2h	3h	6h
SEQ ID NO 327	YNL112W	DBP2	2.82				
SEQ ID NO 329	YNL131W	TOM22	-9.70				
SEQ ID NO 331	YNL134C				1.52		
SEQ ID NO 333	YNL143C		1.12				
SEQ ID NO 335	YNL179C		2.88		-2.02		
SEQ ID NO 337	YNL338W		1.78	2.79	1.62	-2.87	
SEQ ID NO 339	YNR002C	FUN34			-1.87		
SEQ ID NO 709	YOL052C-A	DDR2				1.65	
SEQ ID NO 341	YOL106W			3.51	2.44		
SEQ ID NO 343	YOL109W	ZEO1			-3.45		-1.87
SEQ ID NO 345	YOL126C	MDH2		1.91		-3.11	
SEQ ID NO 347	YOL139C	CDC33			2.17		
SEQ ID NO 349	YOL150C		17.69				
SEQ ID NO 351	YOL151W	GRE2	9.20				
SEQ ID NO 353	YOR120W	GCY1			-1.46		
SEQ ID NO 355	YOR121C		1.54	3.40	1.63		
SEQ ID NO 357	YOR122C	PFY1			1.40		
SEQ ID NO 359	YOR131C		2.81				
SEQ ID NO 361	YOR261C	RPN8		2.59	1.54		
SEQ ID NO 363	YOR267C		1.76	1.07	-1.10		
SEQ ID NO 365	YOR285W		-2.15				-1.21
SEQ ID NO 367	YOR286W		-18.36				
SEQ ID NO 369	YOR327C	SNC2					-1.66
SEQ ID NO 371	YOR372C	NDD1	2.19	1.92			
SEQ ID NO 373	YOR374W	ALD4		-12.93			
SEQ ID NO 375	YOR382W		4.02				
SEQ ID NO 377	YPL037C	EGD1	-5.83				-2.17
SEQ ID NO 379	YPL078C	ATP4	-4.50		1.22		
SEQ ID NO 381	YPL079W	RPL21B					-6.18
SEQ ID NO 383	YPL085W	SEC16	2.28				
SEQ ID NO 385	YPL089C	RLM1	1.94	2.74	1.22		
SEQ ID NO 387	YPL190C	NAB3	2.80				
SEQ ID NO 389	YPL201C		-3.57				
SEQ ID NO 391	YPL271W	ATP15			2.40		
SEQ ID NO 393	YPR028W	YIP2	-12.41				
SEQ ID NO 395	YPR035W	GLN1			-2.78		

TABLE 8

C. albicans 522 CDS's										S. cerevisiae 11645 CDS's		
aa	codons	frequency: per thousand	total number	codon chosen for		codons used in		frequency: per thousand		total number		
				synthCaBAX gene		wt muBAX gene						
Ala	GCU	30.7	8686	x		6		21.1		118595		
	GCC	12.7	3582			4		12.6		70785		
	GCA	15.4	4357			2		16.2		91018		
	GCG	2	578			1		6.1		34546		
Arg	CGU	5.9	1682			1		6.5		36518		
	CGC	0.7	204			1		2.6		14571		
	CGA	3.5	989			3		3		16957		
	CGG	0.8	220			3		1.7		9801		
	AGA	23.6	6673	x		1		21.3		119672		
	AGG	2.7	769			2		9.3		52057		
Asn	AAU	37.9	10731	x		1		36		202351		
	AAC	18.7	5293			2		24.9		140194		
Asp	GAU	43.6	12323	x		5		37.8		212658		
	GAC	14.7	4152			7		20.4		114451		
Cys	UGU	9.7	2757	x		1		8		44797		
	UGC	1.7	493			1		4.7		26357		
Gln	CAA	35.2	9964	x		1		27.5		154529		
	CAG	6.9	1948			8		12.2		68463		
Glu	GAA	49.5	14001	x		3		45.9		257930		
	GAG	11.5	3252			10		19.1		107568		

TABLE 8 - continued

aa	codons	C. albicans 522 CDS's				S. cerevisiae 11645 CDS's		
		frequency: per thousand	total number	codon chosen for synthCaBAX gene	codons used in wt muBAX gene	frequency: per thousand	total number	
Gly	GGU	33.5	9492	x	2	23.9	134515	
	GGC	4.5	1281		7	9.7	54629	
	GGA	13.7	3874		2	10.9	61481	
His	GGG	7.7	2182		8	6	33627	
	CAU	14	3964			13.7	77260	
	CAC	5.8	1642			7.8	43878	
Ile	AUU	39.9	11281	x	3	30.2	169795	
	AUC	14.2	4005		7	17.1	96126	
	AUA	12.3	3478			17.8	100027	
Leu	UUA	1	295	x		26.3	148133	
	UUG	36.1	10204			27.1	152590	
	CUU	9.8	2777			12.2	68479	
	CUC	2.5	694			5.4	30218	
	CUA	4	1133			13.4	75414	
Lys	AAA	48.6	13760	x	2	42.1	236746	
	AAG	19.4	5477		6	30.8	173174	
Met	AUG	18.4	5219	x	8	20.9	117410	
Phe	UUU	28.6	8100	x	4	26	146355	
	UUC	15.9	4486		7	18.2	102389	

TABLE 8 - continued

C. albicans 522 CDS's					S. cerevisiae 11645 CDS's		
aa	codons	frequency: per thousand	total number	codon chosen for synthCaBAX gene	codons used in wt muBAX gene	frequency: per thousand	total number
Pro	CCU	13.2	3722		1	13.6	76366
	CCC	3.6	1027		5	6.8	38247
	CCA	26.6	7531	x		18.2	102277
	CCG	2.4	686		1	5.3	29758
Ser	CUG	3.1	875		9	10.4	58583
	UCU	23.3	6595	x	1	23.6	132608
	UCC	10.3	2928		4	14.2	79928
	UCA	24.6	6955			18.8	105570
	UCG	6.5	1836		1	8.6	48186
	AGU	23.6	6673			14.2	79649
	AGC	4.5	1269		5	9.7	54330
Thr	ACU	30.7	8689		1	20.2	113634
	ACC	13.9	3928	x	8	12.6	70777
	ACA	17.4	4928		5	17.7	99759
	ACG	3.6	1019		1	8	44817
Trp	UGG	11	3115	x	6	10.3	58092
Tyr	UAU	24	6782			18.8	105489
	UAC	11.6	3280	x	2	14.7	82483
Val	GUU	33.2	9391		1	22	123726
	GUC	10.3	2927	x	3	11.6	65203
	GUA	8	2265			11.8	66100
	GUG	10	2842		7	10.7	60033

TABLE 9: Regulation of 23 selected "Bax-specific" functions

<i>Cellular role: Amino-acid metabolism</i>					
ORF	Gene	Control	Bax	H2O2	B vs C
YOR302W	YOR302W	11541.92	26806.35	8895.74	2.32
<i>Cellular role: Cell stress</i>					
ORF	Gene	Control	Bax	H2O2	B vs C
YML028W	TSA1	12889.91	2166.45	11327.36	0.17
<i>Cellular role: Chromatin/chromosome structure</i>					
ORF	Gene	Control	Bax	H2O2	B vs C
YBR009C	HHF1	2149.69	8655.43	2909.14	4.03
YDR224C	HTB1	13661.40	55656.34	18829.27	4.07
YNL030W	HHF2	8676.99	19603.93	4732.39	2.26
<i>Cellular role: Energy generation</i>					
ORF	Gene	Control	Bax	H2O2	B vs C
YBL099W	ATP1	2728.21	8786.71	1644.48	3.22
YGR183C	QCR9	23181.54	81865.40	24053.00	3.53
YJL166W	QCR8	5296.71	18093.93	5001.65	3.42
YLR038C	COX12	7336.65	19935.69	5118.43	2.72
<i>Cellular role: Signal transduction</i>					
ORF	Gene	Control	Bax	H2O2	B vs C
YHR135C	YCK1	3939.64	8358.11	3707.17	2.12
YOL100W	PKH2	2218.45	6088.96	2619.31	2.74
<i>Cellular role: Transcription factor</i>					
ORF	Gene	Control	Bax	H2O2	B vs C
YDR216W	ADR1	5925.91	18459.00	6434.43	3.11
<i>Cellular role: Unknown</i>					
ORF	Gene	Control	Bax	H2O2	B vs C
YDR504C	YDR504C	2741.47	6908.49	2839.62	2.52
YGR146C	YGR146C	2099.74	5616.94	1303.89	2.68
YGR236C	SPG1	17717.80	64439.96	24134.29	3.64
YHR138C	YHR138C	6218.30	14817.41	5220.50	2.38
YJL142C	YJL142C	6988.27	16006.02	6740.46	2.29
YKL123W	YKL123W	2826.82	5952.34	2766.04	2.11
YLR414C	YLR414C	4510.80	11867.69	3531.27	2.63
YMR107W	YMR107W	13453.15	78850.98	17417.00	5.86
YOL099C	YOL099C	3690.45	11604.72	5454.15	3.14
YPL201C	YPL201C	15960.14	33633.74	7449.66	2.11
YJL060W	YJL060W	8798.50	2406.39	6356.11	0.27

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CLAIMS

1. An isolated nucleic acid representing a synthetic *BAX*-gene selected from the group consisting of:
 - 5 a) a nucleic acid comprising a sequence as represented by SEQ ID NO 1,
 - b) a nucleic acid comprising a fragment of a sequence of SEQ ID NO 1 and encoding a functional fragment of the sequence represented by SEQ ID NO 2,
 - c) a nucleic acid comprising a sequence as represented in any of SEQ ID NOs 3 to 10,
 - 10 d) a nucleic acid which is more than 75 % identical to the nucleic acid as represented by SEQ ID NO 1, or to a nucleic acid according to the nucleic acid as defined in b) or c), and,
 - e) a nucleic acid as defined in any one of (a) to (i) interrupted by intervening DNA sequences,or a nucleic acid representing the complement of any of said nucleic acids as defined in (a) to (d).
- 15 2. An isolated nucleic acid according to claim 1 which is DNA, cDNA, genomic DNA, synthetic DNA, or RNA wherein T is replaced by U.
3. A vector comprising a nucleic acid as defined in claim 1 or 2.
4. A vector according to claim 3 which is an expression vector wherein said nucleic acid sequence is operably linked to one or more control sequences allowing the expression in
- 20 5. An expression vector according to claim 4 which comprises an inducible promoter
6. An expression vector according to claim 4 or 5 which comprises a sequence encoding a reporter molecule.
- 25 7. A vector according to any of claims 3 to 6 for inducing programmed cell death in *Candida* spp.
8. A host cell transformed, transfected or infected with a vector according to any of claims 3 to 7.
9. A host cell of claim 8 which is a bacterial, yeast or fungal cell.
- 30 10. A host cell according to claim 8 or 9 wherein said cell is a *Candida* spp. cell.
11. A genetically modified yeast or fungal cell according to claim 9 wherein said modification results in the onset of at least one pathway eventually leading to programmed cell death.

12. A genetically modified *Candida* spp. cell according to claim 10 wherein said modification results in the onset of at least one pathway eventually leading to programmed cell death.
13. A method for identifying Bax-resistant yeast or fungi comprising the steps of:
- a) providing (a) genetically modified yeast or fungi according to claim 11,
 - 5 b) treating said genetically modified yeast or fungi with a mutagen,
 - c) isolating resistant yeast or fungal cells, and,
 - d) optionally identifying and/or characterizing mutated genes in said resistant yeast or fungal cells.
14. A method for identifying *Candida* spp. sequences which are differentially expressed in a pathway eventually leading to programmed cell death using a nucleic acid as defined in claim 1 or 2, a vector according to any of claims 3 to 7 or a genetically modified host cell according to claim 10.
15. A method for obtaining and identifying *Candida* spp. sequences involved in a pathway eventually leading to programmed cell death comprising the steps of:
- 15 a) providing a two hybrid system wherein a polypeptide encoded by a nucleic acid according to claim 1 or a vector according to any of claims 3 to 7 as a bait and a *Candida* spp. cDNA library as a prey are expressed,
 - b) detecting an interaction between said polypeptide and a *Candida* spp. polypeptide encoded by said cDNA library, and,
 - 20 c) identifying said *Candida* spp. polypeptide or cDNA.
16. A method for identifying inhibitors (or inhibitor sequences) of Bax-induced cell death comprising the steps of:
- a) providing a genetically modified organism according to claim 10,
 - b) expressing a cDNA library in said genetically modified organism, and,
 - 25 c) identifying a polypeptide or a cDNA which expression has a beneficial effect on the survival and/or growth of said genetically modified organism.
17. A method according to claim 16 wherein said genetically modified organism is a *Candida* spp.
- 30 18. An isolated *Candida* spp. nucleic acid identifiable by any of the methods of any of claims 12 to 17.
19. An isolated *Candida* spp. nucleic acid according to claim 18 selected from:

- (a) a nucleic acid encoding a protein having an amino acid sequence as represented in any of SEQ ID NOs 434, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 718, 720, 722, 724, 726, 728, 730 and 732, or encoding a functional equivalent, derivative or bioprecursor of said protein,
- b) a nucleic acid encoding a protein having an amino acid sequence which is more than 70 % similar to any of the amino acid sequences represented in SEQ ID NOs 434, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 718, 720, 722, 724, 726, 728, 730 and 732,
- c) a nucleic acid encoding a protein having an amino acid sequence which is more than 70 % identical to any of the amino acid sequences represented in SEQ ID NOs 434, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 718, 720, 722, 724, 726, 728, 730 and 732,

- 5 d) a nucleic acid comprising a sequence as represented in any of SEQ ID NOs 433, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481, 483, 485, 487, 489, 491, 493, 495, 497, 499, 501, 503, 505, 507, 509, 511, 513, 515, 517, 519, 521, 523, 525, 527, 529, 531, 533, 535, 537, 539, 541, 543, 545, 547, 549, 551, 553, 555, 557, 559, 561, 563, 565, 567, 569, 571, 573, 575, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, 627, 629, 631, 633, 635, 637, 639, 641, 643, 645, 647, 649, 651, 653, 655, 657, 659, 661, 663, 665, 667, 669, 671, 673, 687, 717, 719, 721, 723, 725, 727, 729 and 731,
- 10 e) a nucleic acid which is more than 70 % identical to any of the nucleic acid sequences as represented by any of SEQ ID NOs 433, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481, 483, 485, 487, 489, 491, 493, 495, 497, 499, 501, 503, 505, 507, 509, 511, 513, 515, 517, 519, 521, 523, 525, 527, 529, 531, 533, 535, 537, 539, 541, 543, 545, 547, 549, 551, 553, 555, 557, 559, 561, 563, 565, 567, 569, 571, 573, 575, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, 627, 629, 631, 633, 635, 637, 639, 641, 643, 645, 647, 649, 651, 653, 655, 657, 659, 661, 663, 665, 667, 669, 671, 673, 687, 717, 719, 721, 723, 725, 727, 729 and 731, and
- 15 f) a nucleic acid encoding a functional fragment of any of the nucleic acid sequences as specified in any of a) to d),
- 20 20. An isolated nucleic acid as defined in according to claim 19 which is DNA, cDNA, genomic DNA, synthetic DNA, or RNA wherein T is replaced by U.
- 25 21. An isolated nucleic acid capable of selectively hybridizing to a nucleic acid as defined in any of claims 18 to 20 or the complement thereof.
22. An antisense molecule comprising a nucleic acid capable of selectively hybridizing to a nucleic acid as defined in any of claims 18 to 21.
- 30 23. A nucleic acid probe which selectively hybridises with any of the nucleic acid molecules as defined in claim 18 or 19.
24. A nucleic acid primer which selectively amplifies any of the nucleic acid molecules defined in claim 18 or 19.

25. An expression vector comprising a nucleic acid according to any of claims 18 to 22.
26. An expression vector according to claim 25 which is an expression vector wherein said nucleic acid is operably linked to one or more control sequences allowing the expression in prokaryotic and/or eukaryotic host cells.
- 5 27. An expression vector according to claim 25 or 26 which comprises an inducible promoter.
28. An expression vector according to any of claims 25 to 27 which comprises a sequence encoding a reporter molecule.
29. A host cell transformed, transfected or infected with the vector of any of claims 25 to 28.
30. An isolated nucleic acid according to any of claims 18 to 22 for use as a medicament.
- 10 31. An isolated polypeptide which is involved in a pathway for programmed cell death of *Candida* spp. and encoded by a nucleic acid as defined in claim 18 or 19, wherein said polypeptide is selected from:
- (a) a polypeptide having an amino acid sequence as represented in any of SEQ ID NOs
- 15 434, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590,
- 20 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 718, 720, 722, 724, 726, 728, 730 and 732, or encoding a functional equivalent, derivative or bioprecursor of said protein;
- (b) a polypeptide having an amino acid sequence which is more than 70% similar to any of
- 25 the amino acid sequences as represented by any of SEQ ID NOs 434, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540,
- 30 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632,

634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 718, 720, 722, 724, 726, 728, 730 and 732,

- 5 (c) a polypeptide having an amino acid sequence which is more than 70% identical to any of the amino acid sequences as represented by any of SEQ ID NOs 434, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 560, 562, 564, 10 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 718, 720, 722, 724, 726, 728, 730 and 732, and
- (d) a functional fragment of any of said polypeptides as defined in a) to c).

- 15 32. A polypeptide according to claim 31 for use as a medicament.
33. An antibody capable of specifically binding to a polypeptide of claim 30 or to a specific epitope of said polypeptide.
34. An antibody according to claim 33 for use as a medicament.
35. A pharmaceutical composition comprising an antibody of claim 33 or 34.
- 20 36. Use of an isolated nucleic acid encoding a polypeptide which is involved in a pathway eventually leading to programmed cell death of yeast or fungi and which nucleic acid is selected from:
- (a) a nucleic acid encoding a protein having an amino acid sequence as represented in any of SEQ ID NOs 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 25 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 30 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 324, 326, 328, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396,

398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 692, 694, 696, 698, 700, 702, 704, 706, 708, 710, 712, 714, 716, 718, 720, 722, 724, 726, 728, 730 and 732, or encoding a functional equivalent, derivative or bioprecursor of said protein;

(b) a nucleic acid encoding a protein having an amino acid sequence which is more than 70% similar to any of the amino acid sequences as represented by any of SEQ ID NOs 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 299, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 324, 326, 328, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 692, 694, 696, 698, 700, 702, 704, 706, 708, 710, 712, 714, 716, 718, 720, 722, 724, 726, 728, 730 and 732,

- (c) a nucleic acid encoding a protein having an amino acid sequence which is more than 70% identical to any of the amino acid sequences as represented by any of SEQ ID NOs 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 299, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 324, 326, 328, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 692, 694, 696, 698, 700, 702, 704, 706, 708, 710, 712, 714, 716, 718, 720, 722, 724, 726, 728, 730 and 732,
- (d) a nucleic acid comprising a sequence as represented in any of SEQ ID NOs 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415,

- 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481, 483, 485, 487, 489, 491, 493, 495, 497, 499, 501, 503, 505, 507, 509, 511, 513, 515, 517, 519, 521, 523, 525, 527, 529, 531, 533, 535, 537, 539, 541, 543, 545, 547, 549, 551, 553, 555, 557, 559, 561, 563, 565, 567, 569, 571, 573, 575, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, 627, 629, 631, 633, 635, 637, 639, 641, 643, 645, 647, 649, 651, 653, 655, 657, 659, 661, 663, 665, 667, 669, 671, 673, 687, 691, 693, 695, 697, 699, 701, 703, 705, 707, 709, 711, 713, 715, 717, 719, 721, 723, 725, 727, 729 and 731,
- 5 (e) a nucleic acid which is more than 70% identical to any of the nucleic acid sequences as represented by any of SEQ ID NOs 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481, 483, 485, 487, 489, 491, 493, 495, 497, 499, 501, 503, 505, 507, 509, 511, 513, 515, 517, 519, 521, 523, 525, 527, 529, 531, 533, 535, 537, 539, 541, 543, 545, 547, 549, 551, 553, 555, 557, 559, 561, 563, 565, 567, 569, 571, 573, 575, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, 627, 629, 631, 633, 635, 637, 639, 641, 643, 645, 647, 649, 651, 653, 655, 657, 659, 661, 663, 665, 667, 669, 671, 673, 687, 691, 693, 695, 697, 699, 701, 703, 705, 707, 709, 711, 713, 715, 717, 719, 721, 723, 725, 727, 729 and 731,
- 10 (f) a nucleic acid encoding a functional fragment of any of the nucleic acid sequences as specified in a) to e), and
- 15 (g) the complement of any of the nucleic acid molecule as specified in a) to f),
- 20 for the preparation of a medicament for treating diseases associated with yeast or fungi.
- 25
- 30
- 35

37. Use of an isolated polypeptide which is involved in a pathway eventually leading to programmed cell death of yeast or fungi, said polypeptide being selected from:

- (a) a polypeptide having an amino acid sequence as represented in any of SEQ ID NOs
- 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60,
5 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102,
104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136,
138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170,
172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204,
206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238,
10 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272,
274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 299, 292, 294, 296,
298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330,
332, 324, 326, 328, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364,
366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398,
15 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432,
434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466,
468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500,
502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534,
536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568,
20 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592,
594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626,
628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660,
662, 664, 666, 668, 670, 672, 674, 688, 692, 694, 696, 698, 700, 702, 704, 706, 708,
710, 712, 714, 716, 718, 720, 722, 724, 726, 728, 730 and 732, or encoding a
25 functional equivalent, derivative or bioprecursor of said protein,
- (b) a polypeptide having an amino acid sequence which is more than 70% similar o any
of the amino acid sequences as represented by any of SEQ ID NOs 18, 20, 22, 24,
26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68,
70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108,
30 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142,
144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176,
178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210,
212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244,
246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278,
35 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 299, 292, 294, 296, 298, 300, 302,

- 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 324, 326, 328, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 692, 694, 696, 698, 700, 702, 704, 706, 708, 710, 712, 714, 716, 718, 720, 722, 724, 726, 728, 730 and 732,
- (c) a polypeptide having an amino acid sequence which is more than 70% identical to any of the amino acid sequences as represented by any of SEQ ID 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 324, 326, 328, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666,

668, 670, 672, 674, 688, 692, 694, 696, 698, 700, 702, 704, 706, 708, 710, 712, 714, 716, 718, 720, 722, 724, 726, 728, 730 and 732, and,

(d) a functional fragment of any of said polypeptides as defined in a) to c),

for the preparation of a medicament for treating diseases associated with yeast or fungi.

- 5 38. A pharmaceutical or fungicidal composition comprising a nucleic acid as defined in claim 36 or a polypeptide as defined in claim 37 together with a pharmaceutically acceptable carrier diluent or excipient therefor.
39. A vaccine for immunizing a mammal against yeast or fungal infections comprising at least one nucleic acid as defined in claim 36 or at least one polypeptide as defined in claim 37 in
10 a pharmaceutically acceptable carrier.
40. A genetically modified yeast or fungus in which modification results in the overexpression or underexpression of at least one of the nucleic acids as defined in claim 36 or the polypeptides as defined in claim 36, which overexpression or underexpression of said nucleic acid or polypeptide prevents, delays or sensitizes for apoptosis of said genetically
15 modified yeast or fungus.
41. A method of identifying compounds which selectively modulate expression or functionality of polypeptides involved in a pathway eventually leading to programmed cell death of yeast or fungi or in metabolic pathways in which said polypeptides are involved, which method comprises:
- 20 (a) contacting a compound to be tested with a genetically modified yeast or fungus according to claim 40, in addition to contacting wild type cells with said compound,
- (b) monitoring the growth and/or death rate and/or activity of said genetically modified cells compared to said wild type cells; wherein differential growth or activity of said genetically modified yeast or fungi cells is indicative of selective action of said
25 compound on a polypeptide in the same or a parallel pathway,
- (c) alternatively monitoring the growth and/or death rate and/or activity of said genetically modified cells compared to genetically modified cells which were not contacted with the compound to be tested, wherein differential growth or activity of said genetically modified yeast or fungi cells is indicative of selective action of said
30 compound on a polypeptide in the same or a parallel pathway,
- (d) alternatively monitoring changes in morphologic and/or functional properties of components in said genetically modified cells caused by the addition of the compound to be tested, and,
- (e) identifying the compound.

42. A method of identifying compounds which selectively modulate expression or functionality of polypeptides involved in a pathway eventually leading to programmed cell death of yeast and fungi or in metabolic pathways in which said polypeptides are involved, which method comprises:

- 5 (a) contacting a compound to be tested with yeast or fungal cells transformed, transfected or infected with an expression vector comprising an antisense sequence of at least one of the nucleic acid as defined in claim 36, which expression results in underexpression of said polypeptide, in addition to contacting one or more wild type cells with said compound,
- 10 (b) monitoring the growth and/or death rate and/or activity of said transformed, transfected or infected cells compared to said wild type cells; wherein differential growth or activity of said transformed, transfected or infected yeast or fungal cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway,
- 15 (c) alternatively monitoring the growth and/or death rate and/or activity of said transformed, transfected or infected cells compared to transformed, transfected or infected cells which were not contacted with the compound to be tested, wherein differential growth or activity of said mutated yeast or fungi cells is indicative of selective action of said compound on a polypeptide in the same or a parallel
- 20 pathway,
- (d) alternatively monitoring changes in morphologic and/or functional properties of components in said transformed, transfected or infected cells caused by the addition of the compound to be tested, and,
- (e) identifying the compound.

25 43. A method of identifying compounds or polypeptides which bind to or modulate the properties of polypeptides which are involved in a pathway eventually leading to programmed cell death of yeast or fungi, which method comprises:

- (a) contacting a compound or polypeptides to be tested with at least one of the polypeptides as defined in claim 37,
- 30 (b) detecting the complex formed between the compound or polypeptide to be tested and said polypeptide,
- (c) alternatively, examining the diminution of complex formation between said polypeptide and a binding partner, caused by the addition of the compound or polypeptide being tested,

- (d) alternatively, examining the alteration in the functional activity of the polypeptide, caused by the addition of the compound or polypeptide being tested, and,
- (e) identifying the compound or protein.

5 44. A method for identifying compounds interacting with a polypeptide involved in a pathway eventually leading to programmed cell death of yeast and fungi comprising the steps of:

- (a) providing a two-hybrid screening system wherein a polypeptide of claim 37 and a protein interacting with said polypeptide or an interacting polypeptide obtainable by a method of claim 41, are expressed,
- 10 (b) interacting said compound with the complex formed by the expressed proteins as defined in a),
- (c) detecting a second complex, wherein the presence of said second complex identifies a compound which specifically binds to one of said polypeptide or to said second complex, and,
- (d) identifying the compound.

15 45. A method of identifying compounds which selectively modulate expression of polypeptides which are involved in a pathway eventually leading to programmed cell death of yeast or fungi which method comprises:

- (a) contacting host cells transformed, transfected or infected with an expression vector comprising a promoter sequence of a nucleic acid as defined in claim 36 joined in
20 frame with a reporter gene,
- (b) monitoring increased or decreased expression of said reporter gene caused by the addition of the compound being tested, and,
- (c) identifying the compound.

25 46. A method for identifying polypeptides involved in a pathway eventually leading to programmed cell death comprising the steps of:

- (a) providing a two-hybrid system wherein a polypeptide encoded by a nucleic acid according to claim 36 or a vector according to any of claims 3 to 7 as a bait and a yeast or fungal cDNA library as a prey are used,
- (b) detecting an interaction between said polypeptide and a yeast or fungal polypeptide
30 encoded by said cDNA library, and,
- (c) identifying said yeast or fungal polypeptide.

47. A method according to any of claims 41 to 46 wherein said yeast or fungus is chosen from *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Candida albicans*, or *Aspergillus fumigatus*.

48. A compound or polypeptide identifiable according to the method of any of claims 41 to 47.
49. A compound or polypeptide according to claim 48 for use as a medicament.
50. A method for preparing a pharmaceutical composition for treating diseases associated with yeast or fungi comprising admixing a compound or polypeptide according to claim 49 with a suitable pharmaceutically acceptable carrier.
51. A pharmaceutical composition comprising a compound or polypeptide according to claim 49 together with a suitable pharmaceutically acceptable carrier.
52. Use of a compound or polypeptide according to claim 48 or 49 or a pharmaceutical composition according to claim 51 or obtainable by the method of claim 50 for the preparation of a medicament for treating diseases associated with yeast and fungi.
53. A method for preventing infection with yeast or fungi comprising administering a composition according to claim 51 or obtainable by the method of claim 50 to a mammal in an effective amount to stimulate the production of protective antibody or protective T-cell response.
54. Use of an antibody capable of specifically binding to at least one of the polypeptides as defined in claim 37 or to a specific epitope of said polypeptide, for the preparation of a medicament for treating diseases associated with yeast and fungi.
55. Use according to any of claims 52 to 54 wherein said disease is associated with yeast or fungi, where the yeast or fungus is chosen from *Candida* spp., *Aspergillus* spp., *Microsporum* spp., *Trichophyton* spp., *Fusarium* spp., *Zygomycetes* spp., *Botritis*, spp., *Cladosporium* spp., *Malassezia* spp., *Epidermophyton floccosum*, *Blastomyces dermatitidis*, *Coccidioides immitis*, *Histoplasma capsulatum*, *Paracoccidioides brasiliensis*, *Cryptococcus neoformans*, and *Sporothrix schenckii*.
56. Use of a compound or polypeptide according to claim 48 or 49 or a pharmaceutical composition according to claim 51 or a genetically modified organism as defined in claim 40 for the preparation of a medicament for modifying the endogenic flora of humans and other mammals.
57. A genetically modified mammalian cell or non-human organism in which modification results in the overexpression or underexpression of at least one of the nucleic acids as defined in claim 36 or a human homologue thereof or at least one of the polypeptides as defined in claim 37 or a human homologue thereof, which overexpression or underexpression of said nucleic acid or polypeptide prevents, delays or sensitizes for apoptosis of said genetically modified mammalian cell or in said genetically modified non-human organism.

58. A genetically modified mammalian cell or non-human organism according to claim 57 wherein said modification comprises the expression of an antisense molecule to at least one of the nucleic acids as defined in claim 36 or an antisense molecule to a mammalian homologue of said nucleic acid.
- 5 59. A method for identifying compounds for stimulating or inhibiting apoptosis comprising the use of at least one of the nucleic acids as defined in claim 36 or a human homologue thereof and/or at least one of the polypeptides as defined in claim 37 or a human homologue thereof and/or a genetically modified mammalian cell or non-human organism according to claim 57 or 58.
- 10 60. A compound identifiable according to the method of claim 59.
61. A compound according to claim 60 for use as a medicament.
62. A method for preparing a pharmaceutical composition for treating proliferative disorders or for preventing apoptosis in certain diseases comprising admixing a compound according to claim 60 or 61 with a suitable pharmaceutically acceptable carrier.
- 15 63. Use of a compound according to claim 60 or 61 for the preparation of a medicament for treating proliferative disorders or for preventing apoptosis in certain disorders.
64. Use of a nucleic acid selected from any of the nucleic acids as defined in claim 36 or a human homologue thereof for treating and/or preventing and/or alleviating proliferative disorders or for the prevention of apoptosis in certain diseases.
- 20 65. Use of a nucleic acid selected from any of the nucleic acids as defined in claim 36 or a human homologue thereof for the preparation of a medicament for treating and/or preventing and/or alleviating proliferative disorders or for the prevention of apoptosis in certain diseases.
- 25 66. Use of an antisense molecule to at least one of the nucleic acids as defined in claim 36 or an antisense molecule to a mammalian homologue of said nucleic acid for treating and/or preventing and/or alleviating proliferative disorders or for preventing apoptosis in certain disorders.
- 30 67. Use of an antisense molecule to at least one of the nucleic acids as defined in claim 36 or an antisense molecule to a mammalian homologue of said nucleic acid for the preparation of a medicament for treating and/or preventing and/or alleviating proliferative disorders or for preventing apoptosis in certain disorders.

68. Use of a polypeptide selected from any of the polypeptides as defined in claim 37 or a human homologue thereof for treating and/or preventing and/or alleviating proliferative disorders or for the prevention of apoptosis in certain diseases.
69. A pharmaceutical composition for use as a medicament for treating proliferative disorders or
5 for the prevention of apoptosis in certain diseases comprising a nucleic acid molecule as defined in claim 36 or a human homologue thereof or an antisense molecule to at least one of the nucleic acids as defined in claim 36 or an antisense molecule to a mammalian homologue of said nucleic acid or a polypeptide as defined in claim 37 or a human homologue thereof together with a pharmaceutically acceptable carrier diluent or excipient
10 therefor.
70. A vaccine for immunizing mammals against proliferative disorders or for preventing apoptosis in certain diseases comprising least one nucleic acid as defined in claim 36 or a human homologue thereof or at least one polypeptide as defined in claim 37 or a human analogue thereof in a pharmaceutically acceptable carrier.
- 15 71. Use of an antibody capable of specifically binding to at least one of the polypeptides as defined in claim 37 or to a human homologue thereof or to a specific epitope of said polypeptide or said human homologue, for the preparation of a medicament for treating proliferative disorders or for the prevention of apoptosis in certain diseases.
- 20 72. An expression vector comprising a human homologue of a nucleic acid as defined in claim 36.
73. An expression vector according to claim 72 which is an expression vector wherein said nucleic acid sequence is operably linked to one or more control sequences allowing the expression in prokaryotic and/or eukaryotic host cells.
74. An expression vector according to claim 72 or 73 which comprises an inducible promoter.
- 25 75. An expression vector according to any of claims 72 to 74 which comprises a sequence encoding a reporter molecule.
76. A host cell transformed, transfected or infected with the vector of any of claims 72 to 75.
77. An isolated nucleic acid comprising a human homologue of at least one of the nucleic acids as defined in claim 36.
- 30 78. An antisense molecule comprising a nucleic acid sequence capable of selectively hybridising to the nucleic acid molecule of claim 77.
79. A polypeptide encoded by a nucleic acid of claim 77.

Figure 1:

YBL002W, 896 bp, CDS: 501-896 (SEQ ID NO 21)

TGTTTGATATTAGTAGTCATGTTGTAATCTCTGGCCTAAGTATACGTAACGAAAAATGGTA
GCACGTCGCGTTTATGGCCCCCAGGTTAATGTGTTCTCTGAAATTCGCATCACTTTGAGA
AATAATGGGAACACCTTACGCGTGAGCTGTGCCACCCTTCGCCATAATAAGCGGTGTT
CTCAAAATTTCTCCCCGTTTTCAGGATCACGAGCGCCATCTAGTTCTGGTAAAATCGCGC
TTACAAGAACAAAGAAAAGAAACATCGCGTAATGCAACAGTGAGACACTTGCCGTCATAT
ATAAGGTTTGGATCAGTAACCGTTATTTGAGCATAACACAGGTTTTTAAATATATTATT
ATATATCATGGTATATGTGTAAAATTTTTTTGCTGACTGGTTTTGTTTATTTATTAGCT
TTTTAAAAATTTTACTTTCTTCTTGTAAATTTTTTCTGATTGCTCTATACTCAAACCAAC
AACAACTTACTCTACAACTAATGTCCCTCTGCCGCCGAAAAGAAACCAGCTTCCAAAGCTC
CAGCTGAAAAGGAGACCTATTCCCTCTTATATTTACAAAGTTTGAAGCAAACATCACC
CTAAGGTTAGAAAAGGAGACCTATTCCCTCTTATATTTACAAAGTTTGAAGCAAACATCACC
CAGACACTGGTATTTCCCAGAAGTCTATGTCTATTTTGAAGTTTTCGTTAACGATATCT
TTGAAAGAATTGCTACTGAAGCTTCTAAATTTGGCCGCTTATAACAAGAAATCCACTATTT
CTGCTAGAGAAATCCAAACAGCCGTTAGATTGATCTTACCTGGTGAATTGGCTAAACATG
CCGTCTCCGAAGGTACTAGGGCTGTTACCAAATACTCCTCCTCTACTCAAGCCTAA

YBL002W, 131 aa (SEQ ID NO 22)

MSSAAEKKPASKAPAEEKKPAKKTSTSVGKKRSKVRKETYSYIYKVLKQTHPDTGISQ
KSMILNSFVNDIFERATEASKLAAYNKKSTISAREIQTAVRLILPGELAKHAVSEGTR
AVTKYSSSTQA

YBL064C, 1286 bp, CDS: 501-1286 (SEQ ID NO 25)

TTGCCAACCTCAAAGAAGAAGATTATGGGCATATTGACCTTCTCCGGTTTTCCCTCCCGC
GCTCTCGTATCCGTCTGCATTTGACCTCGAGCAAGCGCTCCACTATGTCTATATGTTTAC
CAGTAAACTTCTTAACGTTTGTGATATTTTTTGAAGTTCAACCACATTCAGTATGCGTG
TGTATATAAGATATTCCTGATAGCACTATGTTTATCTTTATACAATATACAAAAGGTCA
CCCAGGACGAGCAGCGCGCTATTTTTCTATCATTCGGTGAATAGCGACCAACGGTCGGC
GGCTATTTTTTTTTTTTGCAATTTTTTTCGGGATGGGTTCCTCCCGCAAAAGCTAGCCCCGGA
GATTTTTTAATTACGTAAAGAAACAAGGGGCCGATGTTGCTGCTATTGGTATATAAAGAG
AGAAGGAGAGATATAGAAAATTGTGCTTCTAGATTCTCGCAGTAGGATGAGATAAATTTTC
AAAGAAGCAGGAAGCAAAGGATGTTTAGTAGAATTTGTAGCGCTCAATTAAAGAGGACGG
CATGGACCTTCTTAAGCAGGCTCACTTGCAATCACAGACGATTAAAACATTTGCCACAG
CACCTATTTCTGTGCAACAATTCAAACAAGTGATCAACCAAGACTAAGAATAAACTCTG
ATGCTCCTAACTTTGATGCTGACACAACGGTTGGTAAAATCAATTTTTACGACTACTTGG
GCGACTCTTGGGGGGTCTTGTTTTCTCACCACGAGATTTCACCCCCTGTCTGCACCACCG
AAGTCAGCGCATTCGCCAAATTGAAGCCGGAATTCGACAAGAGAAATGTTAAATTGATCG
GGCTTTCAGTGGAAGATGTTGAGTCCCACGAAAAATGGATTCAAGACATCAAGGAAATAG
CAAAGGTTAAAAATGTTGGTTTCCCAATAATTGGTGACACTTTTAGAAAACGTGGCATTTCC
TATATGATATGGTAGATGCCGAAGGATTCAAAAATATCAATGATGGGTCACTGAAGACCG
TGAGGTCTGTTTTCTGTCATCGATCCCAAGAAGAAGATTAGACTGATTTTTACCTACCTTT
CCACCGTCGGAAGAAACACTTCTGAAGTGTTAAGGGTAATCGACGCTTGCAATTGACTG
ACAAGGAGGGCGTAGTAACCTCAATTAATTGGCAGCCAGCTGACGATGTCATTATTCCTC
CCTCTGTCTCAATGATGAGGCGAAGCTAAATTTGGTCAATTTAATGAAATTAAACCTT
ATTTAAGATTACCAAGTCGAAATAA

YBL064C, 261 aa (SEQ ID NO 26)

MFSRICSAQLKRTAWTLPKQAHLSQTIKTFATAPILCKQFKQSDQPRRLRNSDAPNFDA
DTTVGKINFYDYLGDWSGVLFSPADFTPVCTTEVSFAFLKPEFDKRNKVLIGLSVEDV
ESHEKWIQDIKEIAKVKNVGFPIIGDTFRNVAFLYDMVDAEGFKNINDGSLKTVRSVFVI
DPKKKIRLIFTYPSTVGRNTSEVLRVIDALQLTDEGVVTFINWQPADDVLIIPPSVSNDE
AKAKFGQFNEIKPYLRFTKSK

2/251

YBR089C-A, 800 bp, CDS: 501-800 (SEQ ID NO 47)

TTTTTTAGGTGGCGCGCAACTATAAAGTACAGCAAGTGAGGTTGAGGCAATACTGGGAG
TTTACACTATGGGAGACAGCTCCTAACACCAAGCAGAAAAACGACTTTTTTCGCAAAGTAT
GTAAGGCGCTGGGTGAGCCCAGCGGACGAGGATGGGCTTAATAAGAACGTACAGTTTAGC
ACAGCTAGAACAGGATACAGCTAAGGGCAACTCTGCTTTTCGGGAGAAGTTAAAGAGGGG
TAGACAATGATGGTAATCTTATAAACCGGCTACAATGAAGGTTGTAGCAGCAAGGAAGAT
GATATTTTAATACGGTTCAGGTGAAATGAAATAGCCGCCCATACCGGCATGCTCAAGTTG
TAAGTCAGGACTCTAGCTTTCTACTGTAGTATCCTCTAAAGGACTGCTGTTCTGTGCACC
CCCTTCCTTTGTTTATCATAGCGCACGACAAGAGTACTAACTAATTAACCTTAGAACATTA
ACATATATAAACTAGCGCTATGGCCGCAACTAAAGAAGCAAAGCAACCAAAGGAACCAA
AGAAGAGGACCACCAGGAGAAAGAAGGATCCTAACGCCCCCTAAGAGGCGGTTGTCTAGCTT
ATATGTTCTTTGCTAATGAAAACAGAGACATTGTCCGTTCCGAGAATCCTGACGTAACCTT
TTGGCCAAGTAGGCAGAATATTGGGTGAGAGGTGGAAGGCCTTAAGTCTGAAGAAAAGC
AACCCCTATGAATCTAAGGCTCAAGCAGACAAGAAGAGATACGAATCTGAAAAGGAATTGT
ACAATGCTACACGTGCTTGA

YBR089C-A, 99 aa (SEQ ID NO 48)

MAATKEAKQPKPKKRTTRRKDPNAPKRRLSAYMFFANENRDIVRSENPDVTFGQVGRI
LGERWKALTAEEKQPYESKAQADKKRYESEKELYNATRA

YBR149W, 1535 bp, CDS: 501-1535 (SEQ ID NO 57)

TTCGCAACATCAACTTCTCCTTAATCGACCAACTGACAATGAACTTCAGGTTCTACGAG
AGATCTGCCAATTTCCAGAAGGAAACAATAGGTGGGTAAAGAATGATGCTACAAGATAAG
GATAACTATATCAAAACACTGATGCAACATTTGAAGAAAAAGAGAGTACAAAGTTGATA
AAAGACAGCAAGAATGGCGCCTCCACCTTAACATCTTAACAATTTTCGTTTACTGAAAATG
CTACTAGTATATAATCATTAAGTATCTAACTATCACTCAATAAAAAATATTATAGATCGCT
TAAAAACTCGTTTATTGCCGATTATAAATCCACCAAAAGCCGCTCTACCCTTACCTCCGC
CTGGA AAAAATTATAATATATAAAGTGAGCCTCGTAATACAGGGGTAAAAAGGAAAGAGGG
GGATATCAAGCATCTGGACTTATTTGCACTATCTCCGCCTTCAATTGATAAAAGCGTCTT
GATTTTAATCAACTGCTATCATGTCTTCTTCAGTAGCCTCAACCGAAAACATAGTCGAAA
ATATGTTGCATCCAAAGACTACAGAAATATACTTTTCACTCAACAATGGTGTTCGTATCC
CAGCACTGGGTTTGGGGACAGCAAATCCTCACGAAAAGTTAGCTGAAACAAAACAAGCCG
TAAAAGCTGCAATCAAAGCTGGATACAGGCACATTGATACTGCTTGGGCCTACGAGACAG
AGCCATTTCGTAGGTGAAGCCATCAAGGAGTTATTAGAAGATGGATCTATCAAAAGGGAGG
ATCTTTTTCATAACCACAAAAGTGTGGCCGGTTCTATGGGACGAAGTGGACAGATCATTGA
ATGAATCTTTGAAAAGCTTTAGGCTTGGGAATACGTCGACTTGCTCTTGCAACATTGGCCGC
TATGTTTTGAAAAGATTAAGGACCCTAAGGGGATCAGCGGACTGGTGAAGACTCCGGTTG
ATGATTTCTGGA AAAAACAATGTATGCTGCCGACGGTGACTATTTAGAACTTACAAGCAAT
TGGAAAAAATTTACCTTGATCCTAACGATCATCGTGTGAGAGCCATTGGTGTCTCAAATT
TTTCCATTGAGTATTTGGAACGTCTCATTAAAGGAATGCAGAGTTAAGCCAACGGTGAACC
AAGTGGAACTCACCTCACTTACCACAAATGGAAGTAAAGAAAGTTCTGCTTTATGCACG
ACATTCTGTTAACAGCATACTCACCATTAGGTTCCCATGGCGCACCAAACTTGAAAATCC
CACTAGTGAAAAAGCTTGCCGAAAAGTACAATGTACAGGAAATGACTTGCTAATTTCTT
ACCATATTAGACAAGGCACTATCGTAATTCGAGATCCTTGAATCCAGTTAGGATTTCTT
CGAGTATTGAATTCGCATCTTTGACAAAGGATGAATTACAAGAGTTGAACGACTTCGGTG
AAAAATACCCAGTGAGATTCATCGATGAGCCATTTGCAGCCATCCTTCCAGAGTTTACTG
GTAACGGACCAAACTTGGACAATTTAAAGTATTAA

YBR149W, 344 aa (SEQ ID NO 58)

MSSSVASTENIVENMLHPKTTEIYFSLNNGVRIPALGLGTANPHEKLAETKQAVKAAIKA
GYRHIDTAWAYETEPFVGEAIKELLEDSIKREDLFITTKVWPVLWDEVDRSLNESLKAL
GLEYYDLLLLQHWPLCFEKIKDPKGISGLVKTPVDDSGKTMYAADGDYLETYKQLEKIYLD
PNDHRVRAIGVSNFSEYLERLIKECRVKPTVNQVETHPHLPQMELRKFCFMHDILLTAY
SPLGSHGAPNLKIPLVKKLAEKYNVTGNDLLISYHIRQGTIVIPRSLNPVRISSSIEFAS
LTKDELQELNDFGEKYPVRFIDEPFAAILPEFTGNGPNLDNLKY

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YBR289W, 3218 bp, CDS: 501-3218 (SEQ ID NO 63)

GATACGATCTATAGTCTCTAAAAAGGTAAAAACAATCAAGCGGGCCTTTTGACTTCGAAGT
GGAGGCTAAGCACCATAATTGAGCTTATTTATAACTGAGAAATACTTATAGACCTCTAA
ATCTCTTCCAACCATTGAATGGTCTAAATAATCATCACTACTGCTATCTTCGAGCAATTG
AGGACATGTGGTACGAACGCGGGTCCACAGGTGCTTGAAGGAGGGAGCTGTTGCACCTAA
AAGATACTGGAAAATAAGTTTGTCTTTGTATCAGTGATATAGAATGACAAATACATCTA
TTTTGGTTGGGTTGGTAAGGTTTACAGCCTCTGTTGTTGCCCAAGTCCTGTTATCGCCAA
CTTTAAATAAATCTCTTCTTGTCTTTGACCAAAAATTTTCAATTTTCGTTCGATTAAAA
GAAACTGAAATTTCAAACATAAACACCAAAACAAAGCATCATCAAGGGAACATATAGTAA
AGAATAACACAAAAGCAACAATGAATAATCAGCCGCGAGGGTACCAACAGCGTTCCAAATA
GTATTGGAAATATATTTAGCAACATTGGAATCCATCTTTTAACATGGCGCAAATTCGCG
AACAGCTGTATCAGAGCCTCACACCACAACAATTGCAGATGATTAGCAACGACACCAAC
AGTTACTGAGGAGTCGTCTACAACAACAACAACAACAACAACAACAACAACTTCACCGCCAC
CGCAAACGCATCAATCTCCACCCCTCCTCCGCAACAATCTCAACCCATTGCTAATCAAT
CAGCGACTTCTACCCCTCCTCCTCCTCCAGCACCAACAACCTTACATCCCCAAATTGGT
AAGTGCCCTTAGCTCCAGCGCCTATTAATTTGCCTCCACAAATTGCTCAGTTACCTTTGG
CTACACAGCAACAAGTTTGAACAAGTTGAGGCAGCAGGCCATAGCAAAAAATAATCCAC
AGGTTGTGAATGCAATTACTGTTGCACAACAACAAGTGCAACGCCAAATTGAGCAGCAAA
AGGGACAGCAACCGGCACAACTCAGCTAGAACAGCAGAGGCAATTGCTGGTTTCAGCAGC
AACAGCAGCAGCAACTTAGAAACCAATACAGCGACAACAGCAACAACAGTTTAGGCATC
ATGTGCAAAATACAACAGCAGCAACAAAAGCAACAACAACAGCAGCAGCAGCATCAGCAAC
AACAACAACAACAACAGCAACAGCAGCAACAGCAACAGCAACAGCAGCAGCAACAACAAC
AGCAACAACAACAACAACAGCAGCAGCAGCAGCAGCAGCAGCAAGGACAAATACCGCAAT
CTCAGCAAGTTTCTCAAGTTAGATCCATGAGTGGACAACCTCCCACCAATGTTTCAGCCCA
CTATTGGCCAACTTCTCAACTTCCAAAATTAAACTTACCCAAGTACCAAACTATTCAAT
ACGATCCACCAGAAACCAAGCTACCATATCCAACCTATTGGTCAGACAAAAAAGCAGATA
CGGATACTTTGTTGTACGAACAAATTATCCAGCGTGATAAAATTAAACAAATATTCGCTAA
TAAGAGAAACCAATGGTTACGATCCGTTTAGCATTTATGGATTAGTAATAAAGAGTATA
TTAGTAGACTGTGGCATACTGAAGTATTATCAAGATTTGAAGAACACTAGAATGAAAT
CTATCACAAGCACTTCTCAGAAGATTCTTCGGCAAGTATTTGGGGAAATGGTTACTCAG
GGTATGGTAATGGGATTACGAATACAACCTACCAGAGTTATTCCACAAGTAGAAGTTGGAA
ATAGGAAGCATTACCTAGAGGATAAATTAAAGTCTATAAACAGGCCATGAATGAGACAT
CGGAACAGTTAGTTCCCATAGATTGGAGTTTCGATCAAGATCGTGACAGATTCTTCTCTCA
GGGACACTTTGTTATGGAACAAAATGACAAGCTTATTAAAAATTGAAGACTTTGTGGACG
ACATGTTGCGAGATTACCGATTTGAGGACGCTACGAGAGAGCAACACATTGATACTATTT
GTCAATCTATACAAGAGCAGATTTCAGGAGTTTCAAGGAAATCCATATATAGAGTTGAATC
AGGACCGTCTAGGCGGTGATGACTTGAGAATTAGAATCAAGCTGGATATTGTTCGTGGGAC
AAAACCAAGTTAATCGATCAATTTGAGTGGGAGATCTCTAATAGTGATAACTGTCCAGAAG
AGTTTGCAGAGTCCATGTGTCAAGAATTAGAATACCAGGTGAGTTTGTGACTGCCATTG
CTCACTCCATAAGAGAGCAAGTTCATATGTATCATAAATCACTGGCACTGTTAGGTTACA
ATTTTGATGGATCAGCGATAGAAGATGATGACATTAGAAGCAGAATGCTCCCAACGATTA
CTCTTGATGATGTTTATAGGCCTGCAGCGGAAAGCAAAATTTTACTCCAAACCTATTAC
AGATTTTCAGCTGCAGAGTTAGAGAGATTGGATAAAGATAAGGACAGAGACACAAGAAGGA
AAAGAAGACAAGGTAGATCTAATAGACGTGGTATGCTCGCATTGTCCGGCACATCTGCAA
GTAATACATCTATGAACGGCGTTCACAACACAGTAGCAGCAGGAAATGCTTCATCGTTGC
CACCAGGAGAGATTTTACTGCCAGATATTGCAGATATTCCAAGAACTTTCAGGACTCCAG
TACCTAGCACTTTAATGCCTGGTGGTGTGACGTAGGCCCTTCTGTGGAATCGTACGAAT
TGAGAAACACAACCACTTATAAAAGCAGGCCAGATAGACCTAAGCCAGTTTACCTCCTT
GTTATATTATTGACCATATTCGGGTCATTTCGCTACTACTTTCTATTAACTGCCTGGGA
AAGTTAATACAAAAGAAGAGTTTCGAGCAGCGCCCAATGACACAAGTAGTGGCACCAATG
CAATGCTTCCGAGTCCAGAATCGCTGAAAACCTAAGCTGAATAGTAACATTTCGCGCTGGTG
TGACGATACCTTCAATCCCAAACCCGATTGCCAATCACACTGTTACTAATTCACCCAATC
CCACACTGCAGCCAGTAATCCCAGGTGGGGCAGCTAGTAAATCGGTACCTACACCTAGTC
TTCTTATAGCACCTCCAGTAGCACCATGATAGCGAAGCGACATTGTTGACTAATAGCA
ATAATGGTAGCAGTAACAATAACACACAGAATACATAG

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YBR289W, 905 aa (SEQ ID NO 64)

MNNQPQGTNSVPNSIGNIFSNIQTSPFNMAQIPQQLYQSLTPQQQLQMIQQRHQQLLSRL
QQQQQQQQQTSPPPQTHQSPPPPPQSQPIANQSATSTPPPPFAPHNLHPQIGQVPLAPA
PINLPPQIAQLPLATQQQVLNKLRRQAIKNNPQVVNAITVAQQQVQRQIEQQKQQTAAQ
TQLEQQRQLLVQQQQQQQLRNQIQRRQQQQQFRHHVQIQQQQQKQQQQQQQHQQQQQQQQQ
QQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQIQPSQQVPQVRMSGQPPTNVQPTIGQLPQ
LPKLNLPKYQTIQYDPPETKLPYPTYWSDKKADTDLLYEQIIQRDKINKYSLIRETNGY
DPFSIYGFSNKEYISRLWHTLKYYQDLKNTRMKSITSTSQKIPASASIWGNNGYSGYNGGIT
NTTTRVIFPQVEVGNRKHYLEDKLVYKQAMNETSEQLVPIRLEFDQDRDRFFLRDTLLWN
KNDKLIKIEDFVDDMLRDYRFEDATREQHIDTICQSIQEQIQEFQGNPYIELNQDRLGGD
DLRIRIKLDIVVGQNLIDQFEWEISNSDNCPEEFAESMCQELELPGEFVTAIAHSIREQ
VHMYHKSALLGYNFDGSAIEDDDIRSRMLPTITLDDVYRPAAESKIFTNLLQISAAEL
ERLDKDKDRDTRRKRRQGRSNRRGMLALSGTSASNTSMNGVHNTVAAGNASSLPPEGILL
PDIADIPRTFRTVPVSTLMPGGVDVGPSVESYELRNTTTYKSRPDRPKPVSPPCYIIDHI
PGHSLLLSIKLPKGVNTKEEFAAAPNDTSSGTNAMLSPESLKTCLNSNIRAGVTIPISIP
NPIANHTVTNSPNPTLQPVIPGGAASKSVPTPSLPIAPPVAPHDSEATLLTNSNNGSSNN
NTQNT

YCR004C, 1244 bp, CDS: 501-1244 (SEQ ID NO 69)

TTAAGAAAATGAACGTTACTATTTCTTCTCGTTTTAGTTACATAAAAATTTACTAATGG
TTGGAATAATTGCGGAAGCTATCACGCGATAACTAGGTACACACGCATTATTTTTATAATC
CCATTATTAATAAATCCGTTATGACCCTTTTAGTAATAACTTATTAAGAACCTCCGGGTA
AAATACTGTACTGCGGGGAAAGAAGGCGCTTCCCCTTCTTGGAACCTAATATAAATAATA
AATTTGCCTAAGGGCATTAGGCCTTACTGCCTTGGCTAGCGTACTTATTTTCGATTACATAC
AATTTGCACTATTTCCGGCAGCTAGTTGATACTATAACATCCTACATTTTTTACTTGTTTTA
CGTTCATTTTTTATTTGAAGTTTGTAACTTTATCAGAAAAGAAAACAAGAAGAGGAAAAAG
GAAAAGAGGGGTGAGGTAGTATCAATAAAAAAAGAGAGTAAACAAAACAATACAGAC
TCAATTGAAGCACTATAAGAATGGTAAAGATTGCGATAATTACTTACTCTACCTACGGGC
ACATAGACGTTTTAGCCCAAGCTGTTAAGAAAGGTGTGGAGGCAGCTGGTGGTAAAGCTG
ATATATACAGGGTCGAGGAACTTTACCTGATGAAGTCCTCACCAGATGAACGCTCCTC
AGAAACCTGAAGATATTCCTGTTGCCACTGAGAAAACGTTGCTCGAATATGACGCCTTTT
TGTTCCGGTGTTCCTCAACTAGGTTTGGTAATTTGCCGGCTCAATGGTCCGCCTTTTGGGATA
AAACCGGTGGATTATGGGCCAAGGGCTCTTTGAACGGCAAAGCTGCGGGGATATTCGTTA
GTACTTCCAGTTACGGAGGTGGTCAAGAAAGTACCGTTAAAGCCTGTTTGTCTTATTTAG
CTCATCACGGAATTATCTTTTTACCACTGGGTATAAGAATTCATTTGCTGAGTTAGCCA
GTATAGAAGAGGTACACGGTGGCTCTCCATGGGGTGCTGGTACCCTTGCAGGACCTGACG
GCTCAAGAACTGCGTCTCCACTTGAATTGAGAATTGCTGAAATTCAGGTAACATCTCT
ACGAAACCGCCAAAAAACTTTTCCCTGCAAAAGAAGCCAAGCCCTCCACTGAAAAGAAGA
CCACTACTTCTGATGCGGCTAAGAGACAACTAAACCTGCAGCAGCTACAACCTGCAGAAA
AGAAGGAGGACAAAGGATTATTATCTGCTGTACTGTCTATGTAA

YCR004C, 247 aa (SEQ ID NO 70)

MVKIAIITYSTYGHIDVLAQAVKKGVEAAGGKADIYRVEETLPDEVLTKMNAPOKPEDIP
VATEKTLLEYDAFLFGVPTRFGNLPQWSAFWDKTGGLWAKGSLNGKAAGIFVSTSSYGG
QESTVKACLSYLAHHGIIFLPLGYKNSFAELASIEEVHGGSPWGAGTLAGPDGSRTASP
LELRIAEIQKTFYETAKKLFPAKEAKPSTEKTTTSDAAKRQTKPAAATTAEEKKEDKGL
LSCCTVM

YCR013C, 1148bp, CDS: 501-1148 (SEQ ID NO 77)

TGAAAATGATGAAGGCACATTGTTAATTGAAGAAGAAGAAGAAGAAGAAAACAAAATTAA
AACCGATTGACCAATATATGTCTCTGAATGCCAAGGATGGAAATTATTGCAGAAGATTAG
ACTTTTTTTTGTGCAAGTGGGATGAGCTTGGAGCAGGAAGAATACACTATACTGGATCTA
AAGAGTACAATAGATGGATAAGAATATTGGCAGCGCAAAAAGGCTTCAAGCTTACACAAC
ACGGTTTATTTGCAATAATATCTTCTCGAAAGCTTTAACGAACGCAGAATTTTCGAGT
TATTAACTTAAATACGCTGAACCCGAACATAGAAATATCGAATGGGAAAAAAAACCTG
CATAAAGGCATTAAAGAGGAGCGAATTTTTTTTTTAATAAAAAATCTTAATAATCATTA

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AGATAAATAATAGTCTATATATACGTATATAAATAAAAAATATTCAAAAAATAAAATAAA
CTATTATTTTAGCGTAAAGGATGGGGAAAGAGAAAAGAAAAAATTGATCTATCGATTTC
AATTCAATTCAATTTATTTCTTTTCGGATAAGAAAGCAACACCTGGCAATTCCTTACCTT
CCAATAATTCCAAAGAAGCACCACCACCAGTAGAGACATGGGAGATCTTGTCAAGTACAC
CGTACTTCTTAGCGACAGTGGCAGTGTACCACCACCAATGATGACGGTGTACCAGCAG
CAGAGCTCTTGACAACCTTCGTCTAACAAAGCCTTAGTACCAGCAGCGAACTTTTCGAATT
CGAAAACACCTGGTGGACCGTTCAGACAATGGTCTTAGCCTTTGCAACAGTAGCAGCAA
ACAACCTTTCTAGATTCTGGACCATTGTCCAACCTTGCCAGCCAGCTGGAATACCTTCCT
TGTCAGTGACAGTCTTGGTGTGGCATCAGCAGAGAAAGCATCAGCAATGATGAAGTCGA
CTGGCAAGACGACTTCGACACCCTTGGCCTTGGCCTTTTCCATCAACTTTGGAACGATTT
CAGCACCAGCCTTGTGAAGATGGAGTCACCGATTTCAGTGTTCCTCAAACCTTCTTGA
AGGTGAAAGCCATACCACCACCAATGATGATAGAGTCGACCTTGTCCAACAAGTTGTCAA
TCAATTGA

YCR013C, 215 aa (SEQ ID NO 78)

MGKEKRKKLIYRFQFNSIYFFSDKKATPGNSLPSNNSKEAPPPVETWEILSVTPYFLATV
AVSPPPMMTVLPAEELLTSSNKALVPAANFSNSKTPGGPFQTMVLAFATVAANNFLDSG
PLSNPCQPAGIPSLSVTVLVLASAEKASAMMKSTGKTTSTPLALAFSINFGTISAPALSK
MESPISVFSKTFKVKAIPPPMIESTLSNKLIN

YDL059C, 1217 bp, CDS: 501-1217 (SEQ ID NO 83)

AAAGTATCAAGTTCGCTAAATTTACTTCGAAGACAGAAGCCAGTAAATTTTGTTCCTTC
ATGGAAATAGTTTCCAAAAGTTCTTAGTAATTACCATATGTTCTTGTATGTGGCGCTGC
GAAAGAAAGGTTAGCCGACCGGCATCACCATAATTGTATAATATAGCAATGAAGCAACT
TGTTGAAGTTTCTTTAAAGTACTATAGTATTGAATAATATCATGTTCACTTGATAAAAT
TGGGTATTTTATTGACCATTATATCGCGTTGGACACTAATGTCTTCAAGTTGGTGTAC
GTCACGTGCTTTTCAATGTACTGGGGCAAATTGATTAGAGGAAGCCACAGTTTGGCAAGG
GCAGATATGATAGGAAGCAGTAACGGCAAGGAAGGATAAGAACATCATTGAGGGAGTCTG
TGGCAGTTTAGCACATGCTTTGGACCATTAAAGGGTTACGTAGAGGAGAAGAGCATATTT
CAGGATAAACAGACAAAATAATGACGATACAAGCGAAGCCAGTTCGAGCATATCGTATG
ATTTCGACTACATACGGCACAGCACCGGGCTTGGATATAAAAGAGTTCCAAATCATCGAAG
ATTGGAATGGAAGACCTGCCAGCGCTTGGTTCGGTGCAGAGGATTGGGCTTCTACAGTCCA
AGATGGAAGGTACACGTACAATATTTACCACAATAATAAATATGGGAAGCACAACTTAT
CTAAGCTGATACCAGGGCATGCTCTCATTCACTTCGCTAATGAAACATTCCGGGTATGATG
GTTGGCGAATGGATGTTATAGATGTTGAGGCCCGGGAGTGCCAGCCCTTACCAGCAGTAA
ATAATGGAGAAAACACCAACACTAGTGAGGTCAAGTATACAGTTGTGGCAGAAGCCCAAG
TAAAGGTTACCTTAAAGGATGGCACCAACACACAGTGTGGTGGGCTAGGTAGAATTACTT
TGTCCTCGAGAGGTGAATGTTATAACAGGTGCAAAAAAGAGGCTGTAGGCGATGCGTTAA
AGAAGGCGTTATTGAGCTTTGAAAAATCATACTCGATTATGAGACTAAGATTACAAATA
ATTACTATGTCGATGGCTTGTATGGCTCAAAAAAATTAAAAATGAAGCTAACACCAATT
ACAACCTATTGTGTCAGCGACTAATAGCAAGCCGACTTTTATCAAATTGGAGGATGCTAAAG
GCACGCATATCAAATAA

YDL059C, 238 aa (SEQ ID NO 84)

MTIQAKPSSSISYDSTTYGTAPGLDIKEFQIIEDWNGRPASAWSVQRIGLLQSKIERYTY
NIYHNNKYGKHNLSKLIPGHALIQFANETFGYDGWRMDVIDVEARECQPFTAVNNGENTN
TSEVKYTVVAEAQVKVTLKDGNTQCGGLGRITLSSRGECYNRSKKEAVGDALKKALLSF
EKIILDYETKITNNYYVDGLYGSKKIKNEANTNYNLLSATNSKPTFIKLEDAKGTHIK

YDL147W, 1838 bp, CDS: 501-1838 (SEQ ID NO 87)

ACTCTTCTCTGATTTAGCAATGGCCTTTTTTTTTTCTTACGATCATACTCCTTCGCTT
GTCCTTTTGAATTCCTTTTATTCTTACTTTTGACGTTTGTGTGACCTGTGAGTCCACGGG
CCTTCAAGGCGGCCTTTAAATTCCTTAAGTTGTGAACCGCCATGATTTGATCTTCCCTT
TTATTTGCTTCTCAACTGTACTATTTACAGTAATAATTAGTGCAACCTTCAGATGCTTCT
CGCTAAATGCTCATCTCTAAATTATCATTATTATTCCTAATAAATCCTAAAATTTTTCAC
TCGTTCTGTACGGCTCATCGCCCAATATTACCGTCTTGTATGTGATCTTTTGTGACTTT

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TCGGTGGCAAAATGCAAAGGGGAATCCAAGGAAAAACCATAACAGGACACTACATCAGAG
ATAATCTTGAAATTAAGAGAGTAGAGGAATATACTGCTGGGCTCACTACCATTTTTGTTGC
TAGAGTAAACGTAGAGAAAGATGTCAGAGATGCACCAATTAAGGCTGACAAGGATTATA
GCCAAATTTTGAAGGAAGAGTTTCCTAAGATCGATTTCGCTCGCTCAAAATGATTGTAAC
CTGCTTTAGACCAACTGTTAGTGTGGAGAAAGAAAACCAGACAAGCTTCAGATCTGGCCT
CCTCGAAAGAGTTTGGCCAAGATTGTAGATCTGCTAGCATCAAGGAATAAGTGGGACG
ACCTAAATGAGCAATTGACTCTACTCTCAAAAAAGCATGGTCAGTTGAAATTGTCAATTC
AGTATATGATACAAAAGGTTATGGAATATTTGAAAAGCTCGAAATCTTTGGATTAAACA
CCAGAATTAGTGTCAATTGAACTATCAGGGTGGTTACAGAGAACAAAATATTTGTAGAAG
TGGAAAGAGCTAGGGTCACCAAAGATTTGGTGGAAATTAAGAAAGAAGAGGGTAAGATTG
ATGAAGCTGCAGACATCTTGTGTGAGTTACAGGTTGAGACCTATGGCTCCATGGAAATGT
CTGAGAAAATTCAGTTTATATTAGAGCAAATGGAATTGAGTATATTAAGGTTGATTATT
CCCAAGCCACGGTGTCTTCAAGAAAAATCTGAAAAAACTTTTAAAAATCCAAATACG
AGTCATTGAAGCTAGAAATATTATAATCTTCTGGTAAAAATTAGTTTGCACAAGAGAGAAT
ACCTAGAAGTTGCGCAGTATCTGCAAGAAATTTATCAAAACAGACGCCATTAAATCAGATG
AGGCTAAGTGGAAACCTGTTTATCGCACATTGTATATTTCTTAGTCCTTTACCTTACG
GCAATTTACAAAATGATTTAATTCACAAAATCCAGAATGATAACAACCTGAAAAAATTAG
AAAGCCAAGAATCTTTAGTAAAATTTGTTTACTACGAATGAGTTGATGAGATGGCCAATTG
TTCAAAAAACCTATGAGCCCGTCTTAAATGAGGATGATTTGGCATTGGTGGAGAAGCTA
ATAAGCATCACTGGGAAGATTTACAAAAAAGGGTCATCGAGCACAATTTAAGAGTCATTT
CCGAATACTATTCCAGAATTACTTTACTAAGATTGAATGAATTGCTGGACCTAACGGAGA
GCCAGACGGAACATACATCAGTGATTTGGTAAACCAGGGCATCATATACGCTAAAGTTA
ATCGCCCAGCCAAAATCGTGAAATTTGAAAAACCAAAAACTCAAGCCAATTATTGAACG
AATGGTCACATAATGTTGACGAATATTAGAACATATAGAAACAATAGGCCATTTAATTA
CAAAAGAGGAAATCATGCACGGTTTGCAGCTAAATGA

YDL147W, 445 aa (SEQ ID NO 88)

MSRDAPIKADKDYSQLKEEFPKIDSLAQNDCNSALDQLLVLEKKTRQASDLASSKEVLA
KIVDLLASRNKWDLLNEQLTLLSKKHGQLKLSIQYMIQKVMYELKSSKSLDLNTRISVIE
TIRVVTEENKIFVEVERARVTKDLVEIKKEEGKIDEAADILCELQVETYGSMEMSEKIQFI
LEQMELSILKGDYSQATVLSRKILKKTFFKNPKYESLKLEYNNLLVKISLHKREYLEVAQY
LQEIYQTDIAKSDEAKWKPVLSHIVYFLVLSPLYGNLQNDLIHKIQNDNMLKLESQESLV
KLFTTNELMRWPIVQKTYEPLNEDDLAFGGEANKHHWEDLQKRIVIEHNLRVISEYYSRI
TLRLNELLDLTESQTETYISDLVNQGIYAKVNRPAKIVNFEKPKNSSQLLNEWSHNVD
ELLEHIETIGHLITKEEIMHGLQAK

YDR253C, 1076 bp, CDS: 501-1076 (SEQ ID NO 113)

TTTCCCCGCTAAAATAACGCCAGATGCTTTCTATGCTTCTAATCTTTTACCATTTACCTT
TGTTTATTTCAATATAAACTTTAATTTACAGTCCCTATCTATTGCCCGACTGGACTAACA
TGCACGTGACATTTTGTGATGGTTTTTCGTCCCTTACTTAGTACGCTTAGTACGCCACAG
TTTATATTTTCTTGACAATAATAAGAACCTGATTGTGGGTTAGAACTTGCTATACTTTT
AGTTTAAAAATAAGCAGGAAATAATCTTGAGTTCTGTATCATTATTATAAAATAAACTATA
TTTGTCTCTTTGTCGCCCTCGGAACCTTCTCATTACATTGACGAGGTATATATAGATA
TAGTAGATATACATATCTATCCATGGTATATATGTATGCATCTGGATAATTGAATAGGGT
TTCATGTCAATATGCCAAGAATTTGTTAATAATATAGTGGAAAAAGTCAAGAGGTATTAT
AAATTTCAAAAAAGTACCAAATGGAGGATCAGGATGCTGCATTTATCAAACAGGCTACAG
AAGCAATAGTGGATGTATCATTAATAATATAGATAACATAGATCCTATAATAAAGAGTTAT
TAGAAAGGGTAAGGAATAGGCAAAACAGGTTACAAAATAAAAAACCAGCACTCATACCGG
CAGAAAATGGTGTGATATAAATAGTCAAGGCGGTAACATAAAAGGTTAAAAAGGAAAAACG
CATTACCAAAAACACCGAAGTCCAGCAAAAAGCAAAACCCCAAGATCGTAGAAAATAGTACTG
GTGAAAAAGATTTAAATGTGCGAAATGTTCTGTTGGAATTTTCAAGATCATCAGATTTGA
GAAGGCACGAAAAGACACACTTCGCCATATTGCCTAACATTTGTCCTCAATGTGGCAAAG
GTTTTGCAAGGAAAGATGCATTGAAAAGACATTATGATACACTGACATGTAGGAGAAAACA
GGACTAAATTACTAAGTGCAGGTGGTGGGGTATCAATGAATTACTGAAAAAGTCAAGC
AATCCAACATCGTTTCATCGTCAAGATAACAACCACAATGGTAGCAGTAATGGCTGA

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YDR253c, 191 aa (SEQ ID NO 114)

MEDQDAAFIKQATEAIVDVSLNIDNIDPIIKELLERVRNRQNRLQNKKPALIPAENGVDI
NSQGGNIKVKKENALPKPPKSSKSKPQDRRNSTGEKRFKCAKCSLEFSRSSDLRRHEKTH
FAILPNICPQCGKGFARKDALKRHYDTLTCRRNRKLLTAGGEGINELLKKVKQSNIVHR
QDNNHNGSSNG

YDR276C, 668 bp, CDS: 501-668 (SEQ ID NO 117)

ACCTTTAGTTCTTAGCATCACCAATCGCAGACATCCAACGTATCCGTGCGCGTAATCCTT
CTCTTGGTAGTTGAGCACAGCATACAGAAGAAGCCGCGCGCAAGCGGTAATGTCTTTCC
TCCGGCCTTCTAACCACCAAAACCGATCTCGGAACATGGGGGGGGGAAGGTCTCTGAAT
CGAAAAACCCGAGACAGCGAGAGGGATTTTGCAGAAAAATTACAAAGATCACTATTTACTG
CTCCCTCACCTCCGCGAGTCCCTTAATAGCGGAAGATGCAATGGGTGTGGGCTCTGGGTG
CCCTTTAACCACGCCCTCAAAGGGGGTCTTGGTTATTTGCGATGGGCGCCTCTATAAA
TACAAAAGAGGAAGTGAGTGTCTTTTGTCTTGGGAAGAGGGAAAGGAAAAAGAAAGAAAT
TTACTATCGGTTGTGTCTTTTCGCCAGTATAATACAATTGATTATACATTTTGAACATAA
CAGCACAGCACAAATACAACAATGGATTCTGCCAAGATCATTAACATTATATTTATCCCTTT
TCTTACCACCAGTCGCCGTCTTTCTAGCCCGTGGGTGGGGTACTGACTGTATAGTGGATA
TCATTTTGACCATTTTGGCTTGGTTCCCAGGTATGCTATATGCCTTGTACATTGTCTTAC
AAGATTAA

YDR276C, 55 aa (SEQ ID NO 118)

MDSAKIINIILSLFLPPVAVFLARGWGTDCIVDIILTLAWFPGMLYALYIVLQD

YDR377W, 806 bp, CDS: 501-806 (SEQ ID NO 127)

AATACAAGACTTGGTGGTCAGCGGAGCGCTATCCTTAGAGAATTCTATCGACCTCTCTAA
TATCAAGCACACCACATGGAAGGATTGGGAAAGAAATCAACAAGAGGAATTGCTTCGGGG
CAAAAAGGAACACAAAACCTCGGTCAAAGTTTCTTAACCTTTTGAAGAGTTGTGGAACGGTGT
AGAAGGCATATAAAATAGATCGTTAATATATTTCTAACATCTTCTTGTAAATGTAAATAT
TTTAAAGGGTTGATCTTATTACGGAGAGAACCAATCATATCGAAGGATTTCTCAATAGT
AAGTATCCCGCGCGTGGTCTCCTCGGGGAAATAGAACGAGAACTTCAAGTACTTGATAGCA
AGAAAAGTGAGTGCTTGGCTTCCCATTTTGTATTATAAAGAAAGGCATTATTTCTAGGGC
AAGAAAAGACATTGTTGAAATTGTTCCAGAAACTTTCAATTTAAAGTCTTTTCGTGAAAGGA
GTGGACGTCAAAAAGAAATAATGATTTTAAACGTGCAGTATCTACATTGATTCTCTCAA
AAGTTGTGTCTTCCAAGAATATAGGTTCCGGCACCAAATGCCAAGCGCATTTGCTAATGTTG
TTCACTTTTATAAGTCTTTGCCCTCAAGGACCAGCACCAGCCATCAAGGCTAACACTAGAT
TGGCCAGATACAAAGCCAAGTACTTTGATGGGGATAATGCTAGTGGTAAACCATTGTGGC
ATTTTGCTCTAGGTATAATTGCCCTTGGCTATTCCATGGAATATTATTTTCATTTGAGAC
ATCATAAAGGTGCGGAAGAGCATTGA

YDR377W, 101 aa (SEQ ID NO 128)

MIFKRAVSTLIPPKVVSSKNIGSAPNAKRIANVVHFYKSLPQGPAPAIKANTRLARYKAK
YFDGDNASGKPLWHFALGIIAFGYSMEYFHLRHHKGAEH

YEL039C, 842 bp, CDS: 501-842 (SEQ ID NO 141)

AGTAATTGTCTCCCATTTTGGTATACGAGCTAGCAGGACCTTTTGCCCAATGACCATT
CATATTCAATCCCACTCACCACCGTCATCGTTGGTATTATTATTATCATTCGCTTGAAGA
AAAAGAAACGAAAAAGAAATGGATCAGCAGCCGGGTATAGCGCCCTTATTGAATTAT
TTTCTTTCGTGCTTCTCTGAGAAGGGTCTGCGAGTCCCCGCGGAGGGGTCTTTTCCAC
CTTCTCAAAGCTAATAGCGATAATAGCGAGGGCATTATTCAAGTTCCAACACTATAAG
TGGCCGCAAGGGGCAAGACAAAGGCACACAACATATATATATATCGTGTGTGAAGCTC
GAGAAGATTAGATCAGAATAGTTCTCTTTTGTGAGGTTGAAACAAAATCAAAGACTTA
TACAAGAAGATCACATACAAGCATTTATTACATTACTTTAAGTAAACTTCAGTAAACTA
CATTACATCATAAACAAACATGGCTAAAGAAAGTACGGGATTCAAACCAGGCTCTGCAA
AAAAGGGTGCTACATTGTTTAAACGAGGTGTCAGCAGTGTACATAATAGAAGAGGGTG
GTCCTAACAAAGTTGGACCTAATTTACATGGTATTTTGGTAGACATTCAAGTCAGGTAA
AGGGTTATTCTTACACAGATGCAACATCAACAAGACGTCAAATGGGATGAGGATAGTA

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TGTCCGAGTACTTGACGAACCCAAAGAAATATATTCCTGGTACCAAGATGGCGTTTGGCCG
GGTTGAAGAAGGAAAAGGACAGAAACGATTTAATTACTTATATGACAAAGGCTGCCAAAT
AG

YEL039C, 113 aa (SEQ ID NO 142)

MAKESTGFKPGSAKKGATLFKTRCQQCHTIEEGGPNKVGPNLHGIFGRHSGQVKGYSYTD
ANINKNVKWEEDSMSEYLTNPKKYIPGTKMAFAGLKKKEDRNDLITYMTKAAK

YER112W, 1064 bp, CDS: 501-1064 (SEQ ID NO 147)

TACTGAAGTCCCTCTAAACCTACTGCCTTTTATTTTAGGCTCTAAAATAACCATGGACA
ACGTGAATTGGGTAGCATCTTTTTTTTAAATAGATAGTTTATTATGTATAACAATAATTTA
AAGATATTCATAGTGATAAGTAATTTTAAATGAGTTTAAAGTACTACTTTTCCTTTACCG
CCAGTTTCCGTACTATGAAAAAGGCAAATTCGCATTTGTAGCCGCCACACGCATTTTG
ATCATCAATTACGAAATTTGCCGCACACGTGTACGTGATAAGCACCTCTTACTATCATGT
TTTACGGAGTAGCAATGATGTTCAATTATTGCAGCTTTCTTTTCGTGAAATCGTAGTATCA
TAGACCTTCCCTAATGATGGAAGCGGTAAAGAAGGAAATCGTAAAAGTAAATTAACGAAGT
AGTATTAGTAAAACAGAGTTGAAAACTGATAAATCTTCAACTCGAACTGAAAAGAAACA
CAATAGAATATTTTCTCAATGCTACCTTTATATCTTTTAACAAATGCGAAGGGACAAC
AAATGCAAATAGAATTGAAAAACGGTGAAATTATACAAGGGATATTGACCAACGTAGATA
ACTGGATGAACCTTACTTTATCTAATGTAACCGAATATAGTGAAGAAAGCGCAATTAATT
CAGAAGACAATGCTGAGAGCAGTAAAGCCGTAAAATTGAACGAAATTTATATTAGAGGGA
CTTTTATCAAGTTTATCAAATTGCAAGATAATATAATTGACAAGGTCAAGCAGCAAATTA
ACTCCAACAATAACTCTAATAGTAACGGCCCTGGGCATAAAAGATAC'TACAACAATAGGG
ATTCAAACAACAATAGAGGTAAC'TACAACAGAAGAAATAATAAACGGCAACAGCAACC
GCCGTCCATAC'TCTCAAACCGTCAATACAACAACAGCAACAGCAGTAACATTAACAACA
GTATCAACAGTATCAATAGCAACAACCAAAATATGAACAATGGTTTAGGTGGGTCCGTCC
AACATCATTTTAAACAGCTCTTCTCCACAAAAGGTCGAATTTTAA

>YER112W, 187 aa (SEQ ID NO 148)

MLPLYLLTNAKGQQMQIELKNGEIIQGILTNVDNWMNLTLNVTSEYSEESAINSEDNAES
SKAVKLENIYIRGTFIKFIKLQDNIIDKVKKQINSNNNSNSNGPGHKRYNNRDSNNNRG
NYNRRNNNGNSNRRPYSQNRQYNNNSNNINNSINSINSNNQNMNNGLGGSVQHFNSS
SPQKVEF

>YFR010W, 2000 bp, CDS: 501-2000 (SEQ ID NO 153)

GAAAAATTTCAACGGTGGTGTCTTAATGGTTTCCCATGATATCTCTGTTATTGACTCTGT
TTGTAAAGAGATTGGGTTTTCAGAGCAAGGTACTGTCAAGAGGTTTCAAGGTACAATTTA
CGACTATAGAGATTACATCTTGCAGTCTGCTGATGCTGCAGGTGTGGTTAAAAAGCATTG
ATTATTTAGGAAGCACCTCAGAATATATTTTCCATAGAAGCCTAAATTAAGTATGCATTC
ATAGCCCCATGATAC'TTTTTTTTTTACTACTTGTATTGGAATCTAATTGACCTAACTGG
GCATTCTGGGTCATTGGTATATGTATCACTTTTACGTAAAAAAGTAGTGGCTAATATAA
AACATAAAATCTACAAGAAGGGTGAAGTGCTTTTTCGAATTTTGCCACTGCAAGTAATTGG
TGCAATTGAAATACGAGATTTCTGTTCTTAAGAGGATATAAAAAAAGGAAATTAGCCCT
ACCTATCCTTGTGTTAAATATGAGCGGAGAAACGTTTGAGTTCAATATTAGACATTTCTG
GTAAAGTTTACCCAATAACACTTTCCACTGATGCTACTTCAGCAGATTTGAAAAGCAAAG
CAGAGGAATTGACCCAAGTCCCAAGTGCCCGCCAAAAATACATGGTTAAAGGTGGCTTGT
CTGGCGAAGAGTCCATTAAAAATATATCCCTTAATCAAGCCAGGATCGACAGTAATGCTAT
TGGGGACTCCAGATGCTAACCTGATTTCTAAACCAGCCAAAAAGAATAATTTTATTGAAG
ACCTTGCGCCTGAGCAACAAGTCCAACAATTTGCTCAATTGCCTGTTGGTTTCAAGAATA
TGGGCAACACCTGTTATCTGAATGCTACCTTACAGGCTTTATACAGAGTGAACGATTTAA
GGGATATGATTCTTAATTATAACCTTCTCAAGGTGTGTCTAACAGTGGTGCACAAGATG
AAGAGATTCACAAACAAATCGTTATTGAAATGAAGCGTTGTTTGAATAATTACAGAATA
AAAGTTTCAAGAGTGTTTTGCCAATTGTGTTATTAAACACGCTAAGAAAGTGTATCCAC
AATTTGCTGAACGTGATTCACAAGGTGGGTTCTATAAACAGCAAGACGCTGAGGAGTTGT
TTACACAACATATCCATAGTATGAGTATTGTTTGGTGACAAATTTTCCGAAGATTTCA
GGATTCAATTTAAACTACCATCAAAGACACAGCTAATGATAACGATATTACTGTAAAG

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AAAATGAAAGCGATTCTAAATTACAATGTCATATTTCTGGTACTACAAATTTTCATGAGAA
ATGGGCTCCTGGAAGGTTTGAATGAGAAAATTGAAAAAGATCAGACTTGACTGGCGCCA
ATTCCATCTATAGCGTCGAAAAGAAAATATCAAGATTACCAAAGTTTTTAACTGTTCAAGT
ACGTTAGATTTTTCTGGAAGGTCACCAACAAAAATCTAAAATATTGCGTAAGGTCG
TTTTCCCATTTCAATTAGATGTTGTCAGACATGCTTACCCAGAAATACGCAGCAGAGAAGG
TAAAAGTTCGTGACGAAGTGAAGAAAGTTGAAAAGGAGAAAAATGAAAAGGAAAGAGAGA
TCAAAAGGCGTAAATTTGACCCATCATCCAGTGAAAATGTCATGACACCAAGAGAACAAT
ATGAGACACAAGTGGCTCTTAACGAAAGTGAAGAAAGATCAATGGCTCGAAGAGTATAAGA
AACATTTTCTCCAAACTTGGAAGGTTGAAAACCCATCTTGTGTTTATAACTTGATCG
GTGTCATTACACATCAAGGTGCAATTCTGAGTCTGGACACTATCAAGCTTTCATAAGGG
ACGAAGTGGACGAAAATAAATGGTACAAATTTAATGATGATAAAGTTAGCGTTGTTGAAA
AGGAAAAAATTGAATCTTTAGCCGGTGGGGGCGAAAGTGATAGTGCCTGATCTTAATGT
ATAAAGGATTTGGTCTGTAA

>YFR010W, 499 aa (SEQ ID NO 154)

MSGETFEFNIRHSGKVYPITLSTDATSADLKSAAELTQVPSARQKYMVKGGLSGEESIK
IYPLIKPGSTVMLLGPDPANLISKPAKKNFIEDLAPEQQVQQAQLPVGFKNMGNTCYL
NATLQALYRVNDRDMLNPNPSQGVNSGAQDEEIHQIVIEMKRCFENLQNKSFKSVL
PIVLLNLTLRKCYQFAERDSQGGFYKQDAEELFTQLFHSMSIVFGDKFSEDRIQFKTT
IKDTANDNDITVKENESDKLQCHISGTTNFMNRGLLEGLNEKIEKRSDLTGANSIYSVE
KKISRLPKFLTQYVVRFFWKRSTNNKSKILRKVVFFQLDVAADMLTPEYAAEKVKVRDEL
RKVEKEKNEKEREIKRRKFDPSSENVMTPREQYETQVALNESEKDQWLEEYKKHFPNL
EKGENPSCVYNLIGVITHQGANSESGHYQAFIRDELLENKWKFNDDKVSVEKEKIESL
AGGGESDSALILMYKGFGL

>YFR052W, 1325 bp, CDS: 501-1325 (SEQ ID NO 157)

CAGAGACATGTTTTAATTCAAGTGATGAGGCGAAACGTGCAAGATCCTAAATGAAGGAT
AAAAAGAGTTCTTAAAAAGGGAAGTAAGGAATAACAGAGTAGAAAAACCGAAAAGACAAC
TTAACAAATCGGCAACACTTTTATGGGGCCCCGCTCGCCTGTGTGCAAGTAGTATTCGAC
CTGGAACACGCAATTTACCACGAGAAGACAGCAATAGTCCGTACAACATTAATTAGTTTTCG
ACAATTGCTCGCCTTTATAAGCCATGCTAGTGCCCAATCAAACACTTTACTTGCCCTGAA
GTTCCTTTTTTTCGCTAGCCTGTAACCTAAATAAGCCATCTAACCTTTTTTTTTCTAAAAAT
TTTCTTTATTACCCTGTGCGCTTATTTTCTATTCTACACATTATTTGCCACCCATTGAAA
TTGTAGCTTGTATTAATAGGGAAAAGCCGGAAGTATAACCGGTGGAAGTACTATTGAAG
TGAGATAAGAAGCCATCGTAATGCCCTCGTTAGCCGAATTGACCAAGTCGTTAAGCATAG
CCTTTGAAAACGGCGATTATGCCGCGTGTGAGAAGCTCTTGCCCCCTATCAAGATCGAAC
TTATCAAGAATAACCTTTTAAATACCTGACTTATCCATTCAAATGACATCTATTTGAATG
ATTTGATGATTACTAAAAGGATCCTGGAAGTAGGTGCCCTTGCTAGCATCCAACTTTCA
ATTTTGACAGCTTCGAGAATTACTTCAACCAATTGAAGCCTTACTACTTTAGCAACAATC
ATAAATTATCTGAATCTGACAAGAAATCGAAGCTGATAAGTCTGTATTTGTTGAACTTAT
TGTCTCAGAATAACACAACCAAGTTTCACTCGGAATTGCAGTATCTAGATAAACATATCA
AGAACTTGAAGACGATTCACTTTTGTCTTACCCTATCAAACCTAGACAGATGGCTCATGG
AAGGGTCGTACCAGAAAGCATGGGATCTTCTGCAATCTGGGTCGCAGAAATATATCAGAA
TCGACTCTTTTACCGATATCCTAAAATCAGCTATAAGAGACGAAATTGCTAAAAATACCG
AGCTATCCTACGACTTTCTCCCTCTCTCCAACATAAAGGCTTTGCTCTTTTCAACAACG
AAAAAGAACTGAAAAATTTGCACTAGAGAGAACTGGCCTATTGTCAACTCGAAAGTTT
ACTTCAATAACCAATCAAAGGAGAAAGCTGATTACGAAGATGAAATGATGCATGAAGAAG
ACCAAAAGACAAACATTATCGAAAAAGCAATGGATTATGCCATAAGTATTGAAAATATTG
TGTA

>YFR052W, 274 aa (SEQ ID NO 158)

MPSLAELTKSLSIAFENGDYAAACEKLLPPIKIELIKNNLLIPDLSIQNDIYLNLDLMITKR
ILEVGALASIQTFFNDFSFNQYFNNHKLSESDKSKLISLYLLNLLSQNNNTT
KFHSELQYLDKHIKNLEDDSLSPYIKLDRWLMESYQKAWDLLQSGSQNISFDSFTDI
LKSIRDEIAKNTELSYDFLPLSNIKALLFFNNEKETEFALERNWPVNSKVYFNNQSK
EKADYEDEMMEEDQKTNIIKAMDYAI SIENIV

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>YGL072C, 860 bp, CDS: 501-860 (SEQ ID NO 159)

ACTCTTTTGTCTAGGGAGTTTCTGTCTGCTAAGAGGTTTGTCAATGACACCGAAAAGAGGAT
AATAGGTAATACTTTTTGTAACTGTAAAGAAATATTAAATCGTTTTTCACGGAATTGGCCTC
TTCCCTATATTCTATCCGAGGTTGTGTACTGTAGCGGTTTATACTTCAACCTGTGAAAGT
TATGTAATATGCGAATTCTGTTTCTGCTTGATAATCTGAAGAAATAGTCTCGAGCACGC
GATGGAGCAGAAAAGGGGAGAAATGAATACTGATGAGCTTAACGATGAGGAGGCCGTTTCC
GTTTCTCTTGATTACCCTTTTCATCCAACAGTCAATATAAGTACGCCAACTTGCGTTAAAA
CGGCCAATGTGACACCAGTTCACCTCGGCAAGCCCTTCTCAGGCTCTCACTAGCTCGAATA
ACGAGAACTCTTCACGACTCATCTACTTTGGCATTTTTCCGGGTGCAGTTCAACCTCACTCG
CGTGCGCGGCTGTGAGGTGCATGGGTGCCGTTATTTTTTTAGTTTCGCTCTGCGCCTTAC
GCGATCAGCTTCGAGAACATACTATATTAAATGATTATATACGCTATTTAATGACCTTGC
CCTGTGTACTATTCTTAGCTCGTTTGGGCAGGCGGTGATCGTTGTACTCTGTGCGGTTCC
TGTATTTGACTATAGCCGGTTCCGGTATTTCTCCACAAATCTTTCTTAGCGTTCTCG
GGCGCGGTGTCGGCTGGGTGGAATAACTGTGGTCATTAAAGCTTGGCAGGTTATCACTC
ACTTTAGTGTTTTTCAGTGGCGTGAACTTTATATCGGGGGACACCCTTGTAATTCCCTCA
CTAGTGTATTGTCTGTTTAG

>YGL072C, 119 aa (SEQ ID NO 160)

MGAGIFFSSLCALRDQLREHTILNDYIRYLMTLPCVLFLLSSFGQAVIVVLCRVLYFDYSR
FRYFLHKSFLSVLGRRVGLGGITVVIKAWQVITHFSVFSGAELYIGGHPCTSLTSVIVV

>YGL080W, 893 bp, CDS: 501-893 (SEQ ID NO 161)

GAAGAAAAAGAAGAGGGGATGATGAGGAAGGAGAAATAGAACTTGAAATTATTAGAGTA
AAAAGATAAAAGGCAGGACGAAGATAAAGAACGCTTACTTGCTTCTCGAAAAACAAG
AAAATTATTACCCCTCAGCACTCCAATAGTATGTGGTTACTACTAATAGTAATCTTGATT
TTTGACCGCCTACTATCGAATTAAATATAATTTTATAACCCAGTTCTATATTGCTGGGTG
GTATTATAGCTTCATGGCTAGTCAAATAAGTGGAGTTTTTGTCTCTGGACGTGGCCTGTA
AAGTTCTCTTTTGCAGCGGCCCCCGCTTTAACCGAGGCGAAATGACAAGTGCTTTCTGG
CAAAGAAGGAATAGCCACTACAACCTGCGGTCTCCACCTTTCTCCACCGATAATCTATTT
AAACACTCACTTGCCAATCAGCAAACGTCAATACATCTACATATATACGTATAGATTTTA
TTGCACTGTGATCAAAAAGAAATGTCTCAACCGGTTCAACGCGCTGCAGCACGCTCATTTCC
TTCAAAAATACATCAATAAAGAAACTTTGAAATATATTTTCAACAACACTTCTGGGGTC
CCGTATCAAAATTTGCGGTATCCCAATTGCTGCTATATATGATCTGAAAAAAGACCCCTACAC
TAATCTCTGCCCCAATGACTTTTGCTTTAGTTACCTATTCAGGTGTTTTTCATGAAGTATG
CTCTTTTCAGTATCACCCAAAACTACTTACTGTTTGGATGCCACCTTATTAATGAAACTG
CGCAATTAGCTCAAGGCTATAGGTTTCTCAAATACACGTATTTCAACAACAGATGAGGAGA
AGAAAGCTCTAGATAAGGAATGGAAAGAGAAAGAAAAAACTGGTAAACAGTAA

>YGL080W, 130 aa (SEQ ID NO 162)

MSQPVQRAAARSFLQKYINKETLKYIFTTHFWGPVSNFGIPIAAIYDLKKDPTLISGPMT
FALVTYSGVFMKYALSVSPKNYLLFGCHLINETAQLAQGYRFLKYTYFTTDEEKKALDKE
WKEKEKTGKQ

>YGR008C, 755 bp, CDS: 501-755 (SEQ ID NO 165)

CGCAATAGTTATGAACTTAACCGAGCTCAAATAATTTAAAGATAAAAAGATAAAAAGATAAA
AGATAAAAGACAAAAGAAAATTCATAGCCCATGTTGAAGTATCCCAGCGGGAAATGTTGC
TATCCAACAGAAAGTACCAAGCCAGTTTCAAAAAGGTACAGAAATTAAGTGATGCTATCCG
TCCCACAATAATTTTCTCCAGCGGAGGAAATATACGCGGAGGGGGGAGGAAAACCTCT
CAGTAAGCAATGAAGGGATAGATAAATGGGGCGCGCTGCCTAGCTTAGGCTAAGAACT
CCTTCGAAAAACAGGGGGCTGCGAGCGCAGAAGCGAACACTTGTCATTTGTATAAAAGGAC
TATTTATAAGTTTGTCTTTTGTCACTCTCTTGCCCTAATTACCCATACTATTGTAACAA
TTGTTGTGTAACTCAATTATACAAATAAACGAACAATCAACAGTAACAAACCGCTCAAG
TGTACAACCAATCAGAAAAAATGACGAGAACAAACAAGTGGACCGAACGTGAAGGAAAGG
CTGATCCAAAGTACTTTTCGCACACTGGTAACCTACGGTGAATCTCCAAATCACATCAAGA
AGCAAGGTTCCGGCAAGGTAATTGGGGTAAGCCAGGCGATGAGATTGATGACTTAATTG
ATAATGGTGAAATACCCCCAGTGTCAAGAAAGATAGAAGAGGCTCAAATTTGCAATCGC

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ATGAACAAAAGTTTGAAAACGTCCAAAAGGAATGA

>YGR008C, 84 aa (SEQ ID NO 166)

MTRTNKWTTEREGKADPKYFSHTGNYGESPNHIKKQGSKGKNWGKPGDEIDDLIDNGEIPP
VFKKDRRGSNLQSHQKFENVQKE

>YGR023W, 2156 bp, CDS: 501-2156 (SEQ ID NO 167)

TTAGATCATGGCTAGGGGGATCTGGAAGTACAATGATGTGCTCTCCCCCTCTCAAACACA
ACACCAGGATGAACTAAGGGCTCATCTCGAAAGTCGAAGGTGCCTCATTCAAGTTATTAG
TGGTGCCTGTTGTGTCTTCCATGAACAAGGAGCACTTAATTACTTGTGTGTCATGAGAT
ATCATTTTTTTTTTTCCCTCTTTCTTGGGGTCTTGACAGTCATCAAATCGAAGTTTTTAG
TTTTTCTTCTTCGGGAAGATCAATTTAGGTAGAAAAGTGTAGATGAAAACGAAGGATA
CTGCTATTTACTGTAAGTACTCTTCGGTCCATATTGGAAGACCAAGGCATAATAAGGATA
TATTCCGAGGAGATAAATTGGGATATAATCCTCCATTGCTTCCGAAATTTGTTTAAACACT
TCTAGTTCATTTTCGGGTGGTTCGATCTTTCGTTTCCACTTTTAACTTACTCCAGTTAGT
ATAATATAAGTAGTTAAGGTATGGCAAGCTGCAATCCGACCAGGAAGAAGAGCTCTGCTT
CAAGCCTATCTATGTGGAGAACGATTCTCATGGCGTTAACAACACTACCGCTAAGTGTTT
TTTCGCAGGAGTTGGTTCAGCTAATAGCACAAACATCGAGCACAGCTCCTTCCATCACTT
CGCTTTCCGCAGTTGAGTCATTTACGTCCAGTACCGATGCAACGAGCAGCGCAAGTTTAT
CAACGCCGAGTATAGCTTCAGTATCCTTTACTTCCCTCCACAAAGTTCTTCACTGCTTA
CTCTTTTCGTCAACATTATCCTCAGAACTTTCCTCTTCGTCCATGCAAGTTTCGTGCTCTT
CAACATCGTCGTCTTCTTCGGAGGTTACGTCATCATCGTCATCATCAATATCTCCTT
CCTCTTCATCATCAACAATAATATCATCGTCATCATCACTGCCGACATTCAGTGGGCAT
CAACATCTTCGACAGTTGCCTCCTCCACACTTTCCACTAGCTCATCGTTGGTTATCTCTA
CGTCTTCGTCAACGTTTACGTTTAGTTTCGGAAAGTTCAAGCTCTTTGATTTCTCTTCAA
TTTCAACATCCGTTTCGACTTCTTCAGTGACGTTCCCTCCTCTTCAACTTCATCTCCAC
CTTCGTCTCATCCGAATTGACATCATCCTCGTACTCATCATCCTCATCCTCATCCACCC
TCTTTTCTACTCCTCCTCATTTTCATCATCCTCATCCTCATCCTCATCATCCTCTT
CATCCTCATATCATCATCATCATCATCATATTTACCCTCTCCACATCTTCTCTT
CATCTATATACCTGTCCTTCGTATATCCTTCATTTTCATCTTTCATCTTCTCCTCAAACCTA
CCTCATCAATCACTTCTACATCCGCTCATCTTCTATTACTCCGCTTCCGAATATTCCA
ATTTGGCAAAAACCATAACTAGTATAATAGAAGGCCAGACCATCCTCTCTAACTACTATA
CCACAATAACGTATTCACCGACAGCATCCGCATCTTCAGGAAAAAATTCACATCACTCAG
GCTTATCAAAAAGAATCGTAATATTATCATCGGTTGTGTGGTTGGCATAGGTGCCCCC
TCATCCTAATTCTACTAATATTGATTTACATGTTTTGTGTTTCAGCCTAAAAAACGGATT
TCATTGACTCTGACGGTAAAATTGTACAGCTTATCGTAGTAACATTTTACCAAAATAT
GGTATTTCTTGCTGGGTAAAAAATTGGTGAAACAGAAAGATTACAGCTCAGATTCCCCCA
TCGGCAGCAATAATATTCAGAATTTTGGTGATATCGATCCAGAAGATATACTTAACAATG
ACAACCCCTACACCCCTAAACACACTAATGTTGAAGGCTACGACGACGACGACGACGACG
ACGCTAATGATGAAAACCTATCATCCAACCTCCATAACAGAGGCATAGATGATCAATACT
CACCTACTAAATCTGCATCATATTCAATGTGCAATAGTAATAGTCAAGATTACAACGACG
CAGATGAAGTAATGCACGATGAAAACATTCATCGTGTATTATGATGACAGCGAAGCTAGCA
TCGACGAGAACTATTACACGAAACCAACAACGGCTTAAATATCACGAACCTATTAA

>YGR023W, 551 aa (SEQ ID NO 168)

MASCNPTRKKSSASSLSMWRTILMALTTPLSVLSQELVPANSTTSSTAPSITSLSAVES
FTSSTDATSSASLSTPSIASVSFTSFPQSSSLTLSSLSSSSMQVSSSSSTSSSS
EVTSSSSSSSISPSSSSSTIISSSSSLPTFTVASTSSTVASSTLSTSSSLVISTSSSTFT
FSSESSSSLISSSISTSVSTSSVVPSSSTSSPPSSSELSSSYSSSSSSSTLFSYSS
FSSSSSSSSSSSSSSSSSSSSSSSYFTLSTSSSSSIYSSSYPSFSSSSSSNPTSSITST
SASSSITPASEYSNLAKTITSIIEGQTILSNYYTTITYSPTASASSGKNSHHGLSKKNR
NIIIGCVVGIGAPLILILLILIYMFVQPKKTDIDSDGKIVTAYRSNIFTKIWFLLGK
KIGETERFSSDSPIGSNNIQNFIDIDPEDILNNDNPYTPKHTNVEGYDDDDDDDANDENL
SSNFHNRGIDQYSPTKSASYSMSNSNSQDYNDADVMHDENIHRVYDDSEASIDENYYT
KPNNGLNITNY

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>YGR034W, 1244 bp, exon1: 501-525, intron1: 526-879, exon2:
880-1244 (SEQ ID NO 169)

TATAAAAAAAAAATTCCTGTAGACAATAAAAAAAGAAATGCCCCATTTTGTAACTTAGCGAAA
GATGCCCCAGTACATCCCTTTTACACCCGTGCATTAAAGGTGTTTGGGTTTAATAGGAGCT
TTATCATATCTCTTTGATTTTTTTTCTGCTGTCCTCGGCTTGAGGGACTCACAGAGATCT
GGAAATTTTCAGATTGTCAGTGCCTTAGGATGGGTTGTCTAGTAGACGGTGGCCGCCGTGGA
TGGGAAATCTCATACGTTTACACACATAGTGTGTTGGAAATTAATAGTAGCAATAGCTATC
TGGCTACTGTTTTAAAGTATTAGCCCGTTCTCAGTGCCTCTTTTTTAAGGAATAACAACG
GCAAGACCAAAGATATATCAAATATGGCTAAGCAATCTCTAGGTATGTTTGGAGGATACG
AATAACGATAGAAAACATGAGTGAATTTCCGTCCACGAAAAAATGTTAACATAAAATGCA
AGAGAACAATTAATCGAATAATGTTAAATTATTGTAAAAACAATGTGTATGATGAGGAGGA
ATTGACCTAAGCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGAAACAGCTTTTGCAT
ATTCAATCCAGGCATAGGGCGACTATTAGCACTCAACGATTTTAAAGCTTGTGTATTGCT
TGACATAAATTTCCGGCTTTAGAATCCAATATTGAAAAACGTGAGTACGCAGAGGAGATAG
AAGAAAAGTAGGAAGTTACCGTTTATATTGATTTGTGAAATGCATACTCCGTTGGATGTG
GGGCAACATAGATTTAAGTGTGGATGAAAATTATGTGCTCATTGTGAAAAAAAGTTTTG
CTTTTACTAACAAATTTTTTTTATTATTTGTTTTCAATAGACGTTTCCTCTGACAGAAGAA
AGGCCAGAAAGGCTTATTTCACTGCTCCATCCTCTGAACGTCGTGTTTTGTTATCTGCTC
CATTATCCAAGGAATTGAGAGCTCAATATGGTATCAAGGCTTTGCCAATCAGAAGAGACG
ATGAAGCTTTGGTTGTTTCGTGGTTCCAAGAAGGGTCAAGAAGGTAAGATTTCACTCTGTTT
ACAGATTGAAGTTTGCTGTTCAAGTTGACAAGGTCACCAAGGAAAAGGTCAACGGTGCTT
CCGTTCCAATTAACCTTGCACCCATCCAAGCTTGTTATCACTAAGTTACACTTGGACAAGG
ACAGAAAGGCTTTGATCCAAAGAAAGGTTGTTAAATTGGAATAA

>YGR034W, 129 aa (SEQ ID NO 170)

MLNYCKTMYVSSDRRKARKAYFTAPSSERRVLLSAPLSKELRAQYGIKALPIRRDDEVLV
VRGSKKGQEGKISSVYRLKFVQVDKVTKEKVN GASVPINLHPSKLVITKLHLDKDRKAL
IQRKGGKLE

>YGR069W, 836 bp, CDS: 501-836 (SEQ ID NO 171)

TTCGAATTATTTTTGTGAAAACAGGGCTCGAAAGTGATCTCTTGCTTAGAAATATTGCGT
TGCCGCTGGTGTCCATATCTTGGTTGCTTGTACTGCGACCGCTACTACTGTTATGTTGAT
TTTCCGCATTTTCCCCACCGACTAAAAACATCCCTTTTGAAGAAACCAATAAGTTGTCCC
AATAGCATTCGAAAATCTTACGCTTTTCCCTTAAGTACTTGCCAAACTACTGCTATTCT
TCTTATATCGGCCAACTTGCAAAACTCCAATTTGAATCTTCTACCAATCTCAGCGAAA
TTTTCTTCACTACGATCTCATTTTTCACTGAAATCACTAAGTTTCTGATAAAGGTATAG
ACGACAGTTCCAACGGTGACCCTTGGATCAAAATTATGTCCTTGACGGGGAGTTTATTC
TAATATCAAATAACTTATTCTCTCTCTTTCTCTGCTCTGAATGCCACCGCTGCTAG
ATAGCGAACTAAGTAAAAACATGGTCTTGCTTCACCCATATTCTCGCCGAGAGCTGTACAA
GATATTTTTTACTTTTGCCATCTTATACTCATCCTAATCATCTGTTTCATTTTCTTTCTA
TTTCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTCAGTTTTCGAAGAAACTGCCTTTTTTA
GAATTGTAAAAGACGAAGTGAAGTATTCAGGAGTATATTATTACATACATACAAAGCAAG
ACAAAGAAACATTTTAGATCTAACATTTTACTTCAATTGTTTTTGTATTCCCTTATAATA
AGAAAGACCTGCTGTTTAATGTGGGAGTAATCCGTCCCCCTACTCGATCTTCAATAA

>YGR069W, 111 aa (SEQ ID NO 172)

MVLLHPILAESCTRYFLLLPSTHPNHLFHFPSISFFFFFFFFFFFFSFRNCLFRIVKDEV
KYSGVVYIHTKQDKETFLDLTFYFNCFCIPYNKKDLLFNVGVI RPLLDLQ

>YGR070W, 3968 bp, CDS: 501-3968 (SEQ ID NO 173)

AAGAAACATTTTTTAGATCTAACATTTTACTTCAATTGTTTTGTATTCCCTTATAATAAGA
AAGACCTGCTGTTTAATGTGGGAGTAATCCGTCCCCTACTCGATCTTCAATAAATTGTCA
TCTTGATATCTAAAGGAGCGCTCCAGTACTCCAATTAAGCACCACCTAGTGCGTCTAGTGT
CGATTTTTTTTTTTCACGCATACGTTTGTATGTTTCTTAAATTTCCCATGATTTTTTGTGTC
CAATGTCATATCTACAACTCTATACGAAAGTAAACGCACTTCATCTTTTTTGGCCCTAAA
ACGGCAATATTTAGACATATCATAAGGGGCCCAAGGGAGAATCGTTAATTTTTAACTTTT

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CTTTGCTCTTGAATGAAAAAGTAAATAAAATAAACTAAATCAAAAAAAGAACGCCACGT
TTGAATTTTAAAGCAAAAATTTTGTGATTTAGTAATGATATAAAATAAAACCAAGTCGTT
GGTAAGAATTTGGTTAGGTATGAATAGTAATGAACGGATCTAAGAAATAAATATTTTT
ATGAGATATTCGGTAAGAAAAGAAAATCAGATACTTCAACCCCTACTCAGTTGTTCTCCG
GCTCCAAAGTTCAGACAAACATCAATGAAATTTCTATCACTAACGATGAGGATGAAGATA
GTACTGAAGATGAAAATAAGGCTTCATTGAAGGATTATACACTAGGGCACGACACCGGTG
CACGGTATAGGATAGCACCGGACTGTTCTTCCCACCAATTAAAGGCATCTCCTGTCTTAC
ATATTTCAACAAACCTTAATTCAAGTCCACAATCCTTCACAGGCGATCAGATTTACCTA
CTAATAAAAAAATTTCAATAAATGATTCGACCAGACAAGATAAAGGTAACAGTTGCACTA
CCACTTCATCACCTTCTCAAAAAAGATCGAATGTTTTGTCTCCTCACGTAAGAAAACATT
CATCTCCTTCACTATTATCATTTTCCAAAAACAGTGGCAGTCATATGGGGGATCCAAACC
AGCTATCTACGCCCTCAACTCCCAAAAGTGCAGGTACACGATGGAGTTACACAGTTTAT
TCAATGGAAAACATAGTTCTTCTAGCACCTCTTCTTTATTTGCATTAGAGTCACTGAAAA
CCCAAAATAGACGCTCATCAAACTCTTCCAATCATTTAGTCAATATCGACGCCATACTA
ATCAACACCAACGTCATCATTTCAAGGTCCAAATCAAGTCCCTGTCTCTCTGACGGAAATAT
CCATGATCAAAGGCACGCCTTTGGTTTTATCCTGCACTTTTATCACTAATAGCAATTAAAT
TCAAACAGACCATCAAATTGAGCACGCATAAAAAGATGGGGTTACTTTACAGAGATTCCT
TTACAGGAAAACAAGCAATTGATACTTTATGCTTGATCATAGGAAGCTTAGATCGTAATT
TGGGCATGTTGATCGGAAAATCGCTGGAAGCTCAAAAATGTTCCATGACGTACTTTATG
ACCATGGCGTAAGAGATTCTGTACTGGAGATTTACGAGTTATCTTCAGAATCAATTTTTTA
TGGCACATCAGTCGCAGAGTTCTACTTCAATTGCCAACACATTTTCTTCATCATCTTCTT
CAGTTAATTCGCTCCGTACTAAACTGAAATATATGGTGTTTTTGTCCCATTTGACACATT
GTTATTCCTCTACATGCTCTCTGGA AAAACTTTGCTACTCTATTTCTTGCCCCAATCGTT
TGCAACAACAGGCTAATTTACATTTAAAATTAGGTGGTGGTCTTAAGAGAAATATTTTCGT
TAGCACTCGATAAGGAGGATGATGAACGAATTTCTGACAAATTTCTGTACCAAAGAGCG
TATGGGAATCATTTATCCAAACAACAAATCAAAGGCAGGAGGCAATATATGAGTTGTTTA
CTACAGAAAAGAAGTTTGTA AAATCTTTGGAATCATCCGAGATACTTTTCATGAAGAAAT
TATTAGAAACGAATATTATTCATCTGATGTAAGGATAAATTTTGTAAGCACGTTTTCG
CACATATCAATGAAATATATTCTGTCAATAGAGAATTTTGAAGGCTTTAGCACAAAGGC
AATCATTAAGCCCAATTTGTCTGGAATTGCAGATATATTTTGCAGTATCTTCTCTTCT
TTGATCCTTTTTCTGTACATACATCAAGACCATACGCAAAAGTATCTAATTGAAACCC
AAAGATCAGTTAATCCCAATTTTGCTCGTTTTGACGATGAAGTGTCTAATTTCTTCCCTGA
GGCATGGGATCGATTATTCCTATCTCAGGGTGTTCAGACCTGGTAGATATTCACTGT
TGGTAAGAGAAATAATACACTTCTCGGACCCAGTAACAGACAAAGATGATCTACAAATGC
TAATGAAAGTCCAAGATCTTTTAAAGGATCTAATGAAAAGGATTGATAGAGCAAGCGGTG
CAGCACAAAGATCGTTATGACGTTAAAGTGTTAAAGCAGAAAATTTCTATTCAAAAATGAAT
ACGTTAATCTGGGTTTGAATAACGAAAAAAGGAAAATCAAGCATGAAGGTTTACTCTCAA
GGAAGGACGTGAACAAAACAGATGCGTCCTTTTCAGGAGACATTCAATTTTACCTACTCG
ACAAATATGCTATTATTCTTGAATCAAAAGCTGTAAACAAGTGGCACCAACACACTGTAT
TTCAGAGACCAATTCCTACTCCCTTTACTGTTTTATTTGTCCGGCTGAGGATATGCCACCCA
TAAAAAGATATGTGACAGAAAACCCAAATTGCTCAGCGGGTGTGCTCTTACCCCAATATC
AAACGAGCAATCCCAAGAATGCTATTGTATTTCGCTATTACGGTACGAAACAACAAATATC
AAGTTACTTTGTACGCGCCGACGCCGGCGGATTACAGACATTAATAGAAAAGGTGAAAC
AAGAGCAAAAAAGGCTCCTTGATGAACTAAACATATTACTTTTAAGCAAATGGTAGGTG
AATTCCTTCACTCATACATAAATACTAATCGCGTCAACGATGTCTAATCTGTCTATGCTG
GTAAAATTTTATTGGTTGCAACAAATATGGGACTCTTTGTTCTTAATTATGCTACATCGA
TCAATCAAAAACCAAGTGCACCTTCTGCACAAAATATCAATTTACAGATCTCTGTATTGG
AAGAATATAAAGTTATGATTTCTTAATTGACAAAAAAGTACGGCTGTCTCTTTAGACG
TAATCGACGATGCAGAAAATGCAGATTTTCTTTTCAGAAAAAATTTAAAGTGTTATTTA
AATATGTTGCAATGTTCAAAGACGGTTTCTGTAATGGTAAAAGAATCATTATGATTGCAC
ATCATTTTTTGCACGCCGCACAATTATTGATTGTTAATCCTTTGATATTTGATTTTAATA
GCGGTAATTTTTAAAAAAAACCTAAAGGCAGGCTTGGTAGATTTTAGCGTTGATTCTGAAC
CTCTGTCTTTTTCTTTTTTGGAGAATAAGATCTGCATTGGTTGTAAAAAAAATATCAAAA
TATTAACGTACCGGAAGTGTGTGATAAAAATGGATTTAAATGAGGGAGCTTTTAAATC
TACATGATAACAAAGTTTTAGCGAACATGTATAAAGAGACGTTCAAAGTAGTTTTCCATGT
TTCCGATAAAAAATTCAACTTTTGCATGTTTTCCAGAACTCTGCTTTTTTCTCAATAAGC

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AAGGGAAGAGGGAGGAGACAAAGGGATGTTTTTCATTGGGAGGGGGAACCAGAACAGTTCG
CGTGTTCCTACCCCTTATATTGTGGCAATTAATAGTAACCTTTATTGAAATTAGACATATAG
AAAATGGGAGAACTTGTCCGCTGTGTACTTGGAAACAAGATACGTATGTTAAATCATATG
CCAAGAAGATCTTATATTGTTATGAGGATCCTCAAGGATTTGAAATTATCGAACTGTTAA
ATTTTTGA

>YGR070W, 1155 aa (SEQ ID NO 174)

MNSNELDLRNKYFYEIFGKKRKSSTSTPTQLFSGSKVQTNINEISITNDEDEDSTEDENK
ASLKDYTLGHDTGARYRIAPDCSSHQKASPVHLHISTNLNSSPQSFTGDQISPTNKKISI
NDSTRQDKGNSTCTTSSPSQKRSNVLLPHVRKHSSPSSLFSKNSGSHMGDPNQLSTPPT
PKSAGHTMELHSSFNKGHSSSTSSSLFALESKTQNRSSNSSNHSSQYRRHTNQHQHH
SRSSSPVSLTEISMIKGTPLVYPALLSLIAIKFKQTIKLSHKKMGLLYRDSFTGKQAI
DTLCLIIIGSLDRNLGMLIGKSLEAQKLFHDVLYDHGVRDSVLEIYELSSSIFMAHQSQS
STSIANTFSSSSSVNSLRTKTEIYGVFVPLTHCYSSSTCSLEKLCYSISCPNRLQQQANL
HLKLGGLKRNISLALDKEDDERISWTNSVPKSVWESLSKQQIKRQEAIYELFTTEKKFV
KSLEIIRDTFMKKLEETNIIPSDVRINFVKHVFHINEIYSVNREFLKALAQRLSPIC
PGIADIFLQYLPFFDPFLSYIASRPYAKYLIETQRSVNPNFARFDDEVSNSSLRHGIDSF
LSQGVSRPGRYSLLVREIIHFSDPVTDKDDLQMLMKVQDLLKDLMKRIDRASGAAQDRYD
VKVLKQKILFKNEYVNLGLNNEKRKIKHEGLLSRKDVNKTDAFSGDIQFYLLDNMLLFL
KSKAVNKWHQHTVFQRPILPLLFICPAEDMPPIKRYVTENPNCAGVLLPQYQTSNPKN
AIVFAYYGTQYQVTLYAPQAGLQTLIEKVKQEQKRLDETKHITFKQMVGFHFSYI
NTNRVNDVLICHAGKILLVATNMGLFVLNYATSINQKPVHLLHKISISQISVLEEYKVM
LLIDKKLYGCPLDIVDAENADFLFRKNSKVLFKYVAMFKDGFNGKRIIMIAHHFLHAA
QLLIVNPLIFDFNSGNFKKLNKAGLVDFSVSEPLSFSFLENKICIGCKKNIKILNVPEV
CDKNGFKMRELLNLHDNKVLNMYKETFKVVSMPFIKNSTFACFPELCCFLNKQGKREET
KGCFWHEGEPEQFACSYPIVAINSNFIEIRHIENGELVRCVLGNKIRMLKSYAKKILYC
YEDPQGFEEIELLNF

>YGR132C, 1364 bp, CDS: 501-1364 (SEQ ID NO 177)

CATACATGTATCAGACGTATAGCTCCTACGATTCTCAAGAATCCAGAAAGTTTGCCATATT
ATGTATAAAGCGCATGATTATGTATATTTTATGTTGTCTCCAGTAAGTGGCAGCATAACC
CGCCAGTCTGCGCTGCATGCTGTGAAGCAGTAATATGCGATATATACCACATATATTCC
GCTTCCGTTTCAGGATTTTCGAAAAGAGAAACCTTCAGTGAAAGTACTATGACTACATAGTTGG
AGTCTTAGACCATTTGCAAATGAGTTATTTCAAGTATGAGAGATCAACACTGATGAGAAATAA
ACTCGTCTTCATGATGATACGGGTAACGCGAATGTATCGCATCAATAAAATTTTCAGGGAAA
GGGAGTTTGACGATCTCATGGATGCAACGGTTGAGGTATATAATATTAAGCAGAAAGAAG
AGGAAAAAAAATAAATCGGTAAACCAACCATCAACGGTACGAACTTACATTCAAAATCA
ATAATTTACTTTAGAAAAGAATGTCTAATTCGCCAAACTTATCGATGTCATACCAAGG
TGGCGTTGCCCATTTGGTATAATTGCTAGCGGGATTCAGTACTCCATGTATGATGTGAAGG
GTGGTTCTCGTGGTGTATTTTCGACAGAATCAATGGTGTAAGCAACAGGTTGTGGGTG
AAGGCACTCATTTCTTGGTGCTTGGCTACAGAAGGCGATCATATACGATGTGAGGACGA
AACCAAAAGACATTGCTACCAATACTGGTACGAAGGATTTGCAAATGGTGCTATTGACCT
TGAGAGTCTTACATAGACCAGAGGTCTTACAGCTACCCGCAATATACCAAAATTTGGGTC
TCGATTACGACGAAAGAGTGTTACCATCTATCGGCAATGAGGTTTTAAAGTCTATAGTAG
CTCAATTTGATGCTGCTGAGTTAATTACTCAGAGAGAAATTAATTTCTCAAAAAATCAGAA
AAGAGCTTTCTACGAGGGCCAACGAATTCGGTATTAAGTTGGAAGATGTCTCTATCACTC
ATATGACGTTTGGTCCCGAATTCACGAAAGCAGTTGAGCAGAAGCAGATTGCACAGCAAG
ATGCCGAAAAGGCCAAATTCCTTGTGAAAAGGCAGAGCAAGAGAGACAAGCTTCTGTTA
TCAGAGCTGAAGGTGAAGCAGAAAGTGCTGAATTCATTTCAAAGCCTTAGCTAAAGTTG
GTGATGGTCTGTTATTGATTAGAAGATTAGAAGCTTCTAAGGACATCGCTCAAACATTAG
CAAACCTCATCTAACGTTGTCTATTTACCAAGTCAACATTCTGGTGGTGGTAACAGCGAGT
CTTCGGGATCACCAAAATTCCTTGCTTTTGAACATTGGCCGTTAA

>YGR132C, 287 aa (SEQ ID NO 178)

MSNSAKLIDVITKVALPIGIIASGIQYSYMDVKGSRGVIFDRINGVKQQVVGEGTHFLV
PWLQKAIIDVVRTKPKSIATNTGTQDLQMVSLTLRVLHRPEVLQLPAIYQNLGLDYDERV

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LPSIGNEVLKSIVAQFDAAELITQREIISQKIRKELSTRANEFGIKLEDVSITHMTFGPE
FTKAVEQKQIAQQDAERAKFLVEKAEQERQASVIRAEGEAESAEFISKALAKVGDGLLLI
RRLEASKDIAQTLANSSNVVYLPSQHSGGGNSSESGSPNSLLLNIGR

>YGR135W, 1277 bp, CDS: 501-1277 (SEQ ID NO 179)

TTCTGAACTGAATCTGAAATTGTTAAACCTGTTTCCCTCAAAGCCTGCAAACAAAGACGA
TAGTTCCCCTATTAAACACGTTGCGTAGTTTTATCGCTGATTACTCCTTCGACACCCAGGT
GAACCCTCCAGGAAGAAGGGTGGTGTCTACGATGGTAAGATTTTGCCATTGCCCAAAGC
CGATAAGCCTATCCCACCTTCATGAATATATAACACTCGCAGAGCTCGATGTTGGAGACAG
TGAGTGAGCAGTGAATTGCTCATGTTTTCTCTGCATCCTCATTTAATGACAATTAGCCAT
GTAATAACATCTTGAGGCAGTTAAATATTCTGTTACCCTGCAGGTGGCAAAAAATTTATAG
ACAGACTGCTTTCTATAAAAAGTTTTCGATCAGTCTCTATTTTAATAATTGATTATTGGA
TATAGTTAGTAGTGTTAAACATGGGTTCCAGAAGATACGATTCCAGGACAACAATTTTCT
CCCCTGAGGGACGTCTATATCAGGTTGAATACGCGCTAGAATCCATTTACATGCAGGTA
CCGCAATTGGGATTATGGCATCTGATGGGATTGTTCTTGCAGCAGAACGCAAAGTCACAA
GTACTTTACTAGAACAAGACACCTCTACCGAAAACTTTATAAGTTAAACGATAAAATTG
CGGTTGCCGTTGCTGGACTGACTGCAGATGCAGAAATTTCTAATAAATACGGCTAGAATTC
ACGCTCAAAATTACCTTAAAACCTATAATGAAGATATACCAGTAGAAATTTTGGTGAGAA
GGCTAAGTGATATAAAACAAGGTTACACGCAACATGGTGGTTTAAGACCATTTGGTGTGT
CCTTTATCTACGCCGTTATGACGATAGATACGGTTACCAATTGTATACATCTAATCCAT
CGGGAACTATACAGGGTGAAGGCTATTAGTGTGGCGCTAACACATCAGCAGCACAAA
CCCTACTTCAAATGGACTACAAGGATGATATGAAAGTCGATGATGCCATTGAACTGGCTT
TAAAAACGTTATCCAAAACCTACCGACAGTAGCGCGCTGACTTATGACAGGTTGGAATTTG
CTACTATCAGAAAGGGTGCTAATGACGGAGAAGTGTATCAGAAGATTTTCAAGCCTCAAG
AGATAAAGGATATATTGGTAAAGACTGGTATTACCAAGAAGGATGAAGACGAAGAAGCTG
ATGAAGATATGAAATAA

>YGR135W, 258 aa (SEQ ID NO 180)

MGSRRYDSRTTIFSPGRLYQVEYALESIHAGTAIGIMASDGIVLAAERKVTSTLLEQD
TSTEKLYKLNDKIAVAVAGLTADAELINTARIHAQNYLKTYNEDIPEILVRRLSDIKQ
GYTQHGGRLRPFVGSFIYAGYDDRYGYQLYTSNPSGNYTGWKAI SVGANTSAAQTLQMDY
KDDMKVDDAIELALKTLSKTTDSSALTYDRLEFATIRKGANDGEVYQKIFKPQEIKDILV
KTGITKKDEDEEDEDMDK

>YGR155W, 2024 bp, CDS: 501-2024 (SEQ ID NO 181)

GTGTTCTCATCCGACCCTCTGATTCATTTGGTGGCCATTACATTTTCCCTCAATGACACA
TTCCCCTATTTTCATAACTGATTAATAATGGTAATGGCACGTGATAGTAGTGGCTCACAAAA
CAAAATTTTCTTCTCAGCGCTGACAAAGCTTCATTTGCATTCTAACCTTATCACAACAA
CTTCAACTTCACCCAAGTAAGGATAATCAGCTCTGTCTGCTGACTGATAAATGCTATATCCG
GCATATGCAGTCCACACGGCATTACCGTTTCACTAATTTATTGCCATCTTCTCCACAGT
TTTGCACCGAAAGGAAAAAAGAAACCAACACCGAAAAATTTTTTCTCTAAAGGTTAAA
GTAAACGCAAGGCACCTTACCAGGCTTGTATATATAAATGTCGTGATGCTTCTATGCCAA
AGTAAAAGGCAACACTTGAAGATTTGCTTGTAGGCCACTTGCTCAAAGGACATCTAGATA
AATACGACGTAAGAATAAAAATGACTAAATCTGAGCAGCAAGCCGATTCAAGACATAACG
TTATCGACTTAGTTGGTAACACCCCATTTGATCGCACTGAAAAAATTGCCTAAGGCTTTGG
GTATCAAACCACAAATTTATGCTAAGCTGGAACATATAAATCCAGGTGGTTCCATCAAAG
ACAGAATTGCCAAGTCTATGGTGGAAGAAGCTGAAGCTTCCGGTAGAATTCATCTCTCCA
GATCTACTCTGATCGAACCTACTTCTGGTAACACCGGTATCGGTCTAGCTTTAATCGGCG
CCATCAAAGGTTACAGAACTATCATCACCTTGCCGAAAAAATGTCTAACGAGAAAGTTT
CTGTCCTAAAGGCTCTGGGTGCTGAAATCATCAGAACTCCAAGCTGCTGCTGCCTGGGATT
CTCCAGAATCACATATTGGTGTGCTAAGAAGTTGGAAAAAGAGATTCTGGTGCTGTTA
TACTTGACCAATATAACAATATGATGAACCCAGAAGCTCATTACTTTGGTACTGGTCGCG
AAATCCAAAGACAGCTAGAAGACTTGAATTTATTTGATAATCTACGCGCTGTTGTTGCTG
GTGCTGGTACTGGTGGGACTATTAGCGGTATTTCCAAGTACTTGAAAGAACAGAATGATA
AGATCCAAATCGTTGGTGCTGACCCATTGCGTTCAATTTTAGCCCAACCTGAAAACCTTGA

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ATAAGACTGATATCACTGACTACAAAGTTGAGGGTATTGGTTATGATTTTGTTCCTCAGG
TTTTGGACAGAAAATTAATTGATGTTTGGTATAAGACAGACGACAAGCCTTCTTTCAAAT
ACGCCAGACAATTGATTTCTAACGAAGGTGTCTTGGTGGGTGGTTCTTCCGGTTCTGCCT
TCACTGCGGTTGTGAAATACTGTGAAGACCACCCTGAACCTGACTGAAGATGATGTCATTG
TTGCCATATTTCCAGATTCCATCAGGTTCGTACCTAACCAAATTCGTTCGATGACGAATGGT
TGAAAAAGAACAATTTGTGGGATGATGACGTGTTGGCCCGTTTGTACTCTTCAAAGCTGG
AGGCTTCGACGACAAAATACGCTGATGTGTTTGGTAACGCTACTGTAAAGGATCTTCACT
TGAAACCGGTTGTTTCCGTTAAGGAAACCGCTAAGGTCCTGATGTTATCAAGATATTAA
AAGACAATGGCTTTGACCAATTGCCTGTGTTGACTGAAGACGGCAAGTTGTCTGGTTTAG
TTACTCTCTCTGAGCTTCTAAGAAAATCAATCAATAATTCAAACAACGACAACACTA
TAAAGGGTAAATACTTGGACTTCAAGAAATTAACAATTTCAATGATGTTTCTCTTACA
ACGAAAATAAATCCGGTAAGAAGAAGTTTATTAATTCGATGAAAACCTCAAAGCTATCTG
ACTTGAATCGTTTCTTTGAAAAAACTCATCTGCCGTTATCACTGATGGCTTGAAACCAA
TCCATATCGTTACTAAGATGGATTTACTGAGCTACTTAGCATAA

>YGR155W, 507 aa (SEQ ID NO 182)

MTKSEQQADSRHNVIDLVGNTPLIALKKLPKALGIKPQIYAKLELYNPGGSIKDRIAKSM
VEEAEASGRIHPSRSTLIEPTSGNTGIGLALIGAIGYRTIITLPEKMSNEKVSVLKALG
AEIIRPTAAAWDSPESHIGVAKKLEKEIPGAVILDQYNNMMNPEAHYFGTGREIQRQLE
DLNLFNLRVAVAGAGTGGTISGISKYLKEQNDKIQIVGADPFGSILAQPENLNKTDITD
YKVEGIGYDFVPQVLDRLIDVWYKTDDKPSFKYARQLISNEGLVGGSSGSAFTAVVKY
CEDHPELTEDDVIVAI FPD SIRS YLT K FVD DEWL K KNNL W DDD V LAR F DSS KLEASTTKY
ADVFGNATVKDLHLKPVSVKETAKVTDVIKILKDN GFDQLPVLTEDGKLSGLVTLSELL
RKLSINNSNNDNTIKGKYLDFKKLNNFNNDVSSYENKSGKKKFIKFDENSKLSDLNRFFE
KNSSAVITDGLKPIHIVTKMDLLSYLA

>YHR095W, 935 bp, CDS: 501-935 (SEQ ID NO 207)

GACACCTTTTCCGGTGTGTTGGAGGGGCAACGGCGGGTGCCTTGACTTTCACTTAAGTT
GTCGTGAAAACCTTCATTTTACCTTCGGAGTATTCATGGCCTTTGAACGACCAGATTTC
CAATTCATATGAGTTGGATGAATTGGATTTCTGAGGAGATATTAGATCGGGAGTTGAATT
CATGATTTTACGTATATCAACTAGTTGACGATTATGATATCTTTATAGATTTTAAAGTGG
GGAAAGAACATGAGACCCAGATGGAATTGATTATGGGGACATTGTTGCCTTTATATATA
ATTTCAATATACTAATTCAAATGATTA AAAACGTGAGGGGGACACGCAACTTCGGGTGTT
AAGAAATATTTTGCTACATTAGATAATGGTGGAGTTTCCTGGCTTGTCGGATAAAAGCCA
TCAAATGTCGCAGCAGCTCATGTTTACGTTTGCTGTCTTCTGCCCACGTCATATGAGTGG
TATTCCTCTATCAGCACTTGATGAATATTCTTTTCTCATATATCTGAAAGACAAAAGAT
CGGCACGGCAATGCCCTGCAGCATTCTTCTTAGTTTTTCCGAATTTCCATTACGTATTG
GATCTTGTGCGCATATTTGTCACTCCTTCACGGAAAAAAGAGCACTGGGTCACTT
CGGAAAAACCTTTGACTCAATGCAACAGTGTCAATCCTTTGCGCTGTCTCTTTGAAGA
AAAATCAGGAGTGCAAGATATCGATTAATTCCTTGGAAGTTATGATGGTTAGTCTTAGTT
TAACCTCTTTGAAGAAGGGTTTTTTTCAAGTTGGTCAACACTCTTTAGAGGTAAAAA
AAAAAAGAGAAATCTTTCATGTAATTTACCATGATTCTACGTTTTTGCAAG
CAAAATGAAGATAATCCGAGCGCATGCGAAGTAG

>YHR095W, 144 aa (SEQ ID NO 208)

MNILFLIYLDKRSARQCPAFLPSFSEFPLRIGSCAHICQSFTEKKKEHWVTSEKLLTQ
CNSVILCAVSLKKNQECKISINSLEVMMVSLSLTLLKKGFFSWSTLFRGKKKKKKKKR
ILHVIYHDSTFLQAKMKIIRAHAK

>YHR138C, 845 bp, CDS: 501-845 (SEQ ID NO 209)

CTACGAAAATAAGCAAAAAATAAATAAAAAACAAAAACAAAAACAAAAACAAAAAC
AAAAACAAAAACAAAAACACATATTGTTATGATGACTGGACGAAAGAAAGATCGTCGTTA
CTTTCCTAATTGTTTGTCTTCAGTACAGTTATTATCAGTGTCTCTTTCTTTTTTATTGT
ACTATGTGATGTTACTGATACATCACGCGCTTCCTTTATGTTTTCTTTTTTTATGTTTCGT
TACAGGATTTATAGTTTTTACAGTATATTGACTTCAATAATTTCTAATATTCAAGTTCCTA
TTAAATTTGATTATTCCGATTAGATCGGTGCGCGCTACCAAAAGAGGCGAAGAAAAGAG

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GAAAACGCAAGTGGATAAAGGGGTGGGGGGCAAAGTATTTAAGAAAAAGCGATGCGATG
GAGAGAACAAATGGATAAGTTGCGTTTCCTCGTTATATTACAACATTTAAATCTATTGTG
TAACAGACTATAGCATATATATGAAGGCCAGTTACTTAGTTTTGATTTTCATTAGCATAT
TCTCCATGGCACAGGCATCTTCCTTATCATCATACATCGTAACTTTCCCCAAGACGGATA
ATATGGCTACGGACCAGAATAGCATTATTGAAGATGTCAAAAAATATGTGGTGGACATAG
GGGGTAAAATAACACACGAATATAGCTTGATAAAGGGCTTTACAGTGGACTTACCTGATA
GCGACCAAATTTTGGACGGTCTGAAAGAACGTTTGAGCTATATTGAAAGCGAGTACGGTG
CTAAATGCAATTTGGAAAAGGATTCAGAAGTTCATGCTCTAAACCGTGACCATTTAGTTG
CTTAG

>YHR138C, 114 aa (SEQ ID NO 210)

MKASYLVLFISIFSMAQASSLSSYIVTFPKTDNMATDQNSIIEDVKKYVVDIGGKI THE
YSLIKGFTVDLPDSDQILDGLKERLSYIESEYGAKCNLEKDSEVHALNRDHLVA

>YHR179W, 1703 bp, CDS: 501-1703 (SEQ ID NO 215)

ATATCTTACGTAATGAACTTCCGTAATGAACTTCCGTAATTCAGATCTCTTAGCATCTC
TTGTTCAATCTTCAGACTCTACTAAGTGTCTTACCAACCATTGGATGCTCATTAACAAT
GAATGAATATATTGCACGGAACGGAAGCGGCATGCTTTTTCCGTCTCGTGTGCTTAGTAA
AGCAAAACGGAGTAGAATCGGTAAGAACTTCCTTTTGGGTGGAAAAATCATTGCCATTG
TTTGGACACCTTTCTTTTTCCGTATTGTTGAGCACC CGCTTCTTTTTGGGTACTTGAT
GAGGTAGCAGATTCCGTGAACGTGCTTTCTCTCGAGGTAACTGCCTTGTTCCTCCGGT
GACTTTCATAAAATATAAAAGGAAAAGCATATCTCTAGTTTCGAGTTTTTCTTCATACATT
TATTTCCTTATGTTAAACGGTCCAGATATAGAATAAATCATCATATTAAGCTAAATATAG
ACGATAATATAGTATCGATAATGCCATTTGTTAAGGACTTTAAGCCACAAGCTTTGGGTG
ACACCAACTTATTCAAACCAATCAAAATTGGTAACAATGAACTTCTACACCGTGCTGTCA
TTCCCTCCATTGACTAGAAATGAGAGCCCAACATCCAGGTAATATTCCAAACAGAGACTGGG
CCGTTGAATACTACGCTCAACGTGCTCAAAGACCAGGAACCTTGATTATCACTGAAGGTA
CCTTTCCCTCTCCACAATCTGGGGGTACGACAATGCTCCAGGTATCTGGTCCGAAGAAC
AAATTAAGAATGGACCAAGATTTTCAAGGCTATTCATGAGAATAAATCGTTCCGATGGG
TCCAATTATGGGTTCTAGGTTGGGCTGCTTTCCAGACACCCTTGCTAGGGATGGTTTGC
GTTACGACTCCGCTTCTGACAACGTGTATATGAATGCAGAACAAGAAGAAAAGGCTAAGA
AGGCTAACAACCCACAACACAGTATAACAAGGATGAAATTAAGCAATACGTCAAAGAAT
ACGTCCAAGCTGCCAAAACTCCATTGCTGCTGGTGCCGATGGTGTGAAATCCACAGCG
CTAACGGTTACTTGTGTAACCACTTCTTGGACCCACACTCCAATAACAGAACCGATGAGT
ATGGTGGATCCATCGAAAACAGAGCCCGTTTCACCTTGGAAAGTGGTTGATGCAGTTGTG
ATGCTATTGGCCCTGAAAAGTCGGTTTGAGATTGTCTCCATATGGTGTCTTCAACAGTA
TGTCTGGTGGTGTGTAACCCGTTATTGTTGCTCAATATGCTTATGCTTAGGTGAAC TAG
AAAGAAGAGCTAAAGCTGGCAAGCGTTTGGCTTTCGTCCATCTAGTTGAACCTCGTGTCA
CCAACCCATTTTTAACTGAAGGTGAAGGTGAATACAATGGAGGTAGCAACAAATTTGCTT
ATTCTATCTGGAAGGGCCCAATTATTAGAGCTGGTAACCTTGTCTGTCACCCAGAAGTTG
TCAGAGAAGAGGTGAAGGATCCTAGAACATTGATCGGTTACGGTAGATTTTTTATCTCTA
ATCCAGATTTGGTTGATCGTTTGGAAAAGGGTTACCATTAAACAAATATGACAGAGACA
CTTCTACAAAATGTCAGCTGAGGGATACATTGACTACCCTACGTACGAAGAAGCTCTAA
AACTCGGTTGGGACAAAAATTAA

>YHR179W, 400 aa (SEQ ID NO 216)

MPFVKDFKPQALGDTNLFKPIKIGNNELHRAVIPPLTRMRAQHPGNI PNRDWA VEYYAQ
RAQRPGTLIIITEGTFPSPQSGGYDNAPGIWSEEQIKEWTKIFKAIHENKSF AWWQLWVLG
WAAFPD TLRDGLRYDSASDNVYMNAEQEEKAKKANNPQHSITKDEIKQYVKEYVQA AKN
SIAAGADGVEIHSANGYLLNQFLDPHSNNR TDEYGGSIENRARFTLEVVD AVVDAIGPEK
VGLRLSPYGVFNSMSGGAETGIVAQYAYVLGELERRAKAGKRLAFVHLVEPRVTNPFLTE
GEGEYNGGSNKFAYSIIWKGP IIRAGNFALHPEVVREEVKDPRTLIGYGRFFISNPDLVDR
LEKGLPLNKYDRDTFYKMSAEGYIDYPTYEEALKLGWDKN

>YIL074C, 1910 bp, CDS: 501-1910 (SEQ ID NO 219)

TGGGAGTCTTTAGCAAGTTCCGGCAAATATCGATATCAATAGTATTGCTAAATAAACCTTT

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TTTATTCCATTTACTGTCGTTTATACTGGCTGACCCTTAATTCCTTAGCAATCTTTGCCT
GCACCCGTACCAGGAAGCGTGATAGAATCGGTAGCTACAAAATTTTAGCATAGTTAATA
AGTGCTATTGTTTTTTCATAATGTCACGTGCACTATCAATAATATTACACTCTTGTCTTG
CCAAATATACACAAAATGCCACATTTTTTTCTTTACACCGAAGAATTTGGCCGTCAGCCG
GACAGCGCTCAGATTAATTGTGGGCTAGATTCTTCACGCTGGAACGAGTCACCGTTATG
AAAACTAATGGAATCTCCAGGTTTAATACATAAGAAGGTTACGAGCTACTACATTAAAA
AATACTTTGTCTGTTTTAGCTGTAGATTATTGTAACATTAAAAAGTAACAAACACTGATT
TCGGGTATTTCTCCCTAACATGTCTTATTACGCTGCCGATAATTTACAAGATTCAATCC
AACGTGCCATGAACTTTCTGGCTCTCTGGTGCAGTCTCAACCTCACCAACTCAGTCAT
TTATGAACACACTACCTCGTCGTGTAAGCATTACAAAGCAACCAAGGCTTTAAACCTT
TTTCTACTGGTGACATGAATATTCTACTGTTGGAAAATGTCAATGCAACTGCAATCAAAA
TCTTCAAGGATCAGGGTTACCAAGTAGAGTTCCACAAGTCTTCTCTACCTGAGGATGAAT
TGATTGAAAAAATCAAAGACGTACACGCTATCGGTATAAGATCCAAAAC TAGATTGACTG
AAAAATACATACAGCATGCCAGGAATCTAGTTTGTATTGGTTGTTTTTGCATAGGTACCA
ATCAAGTAGACCTAAAATATGCCGCTAGTAAAGGTATTGCTGTTTTTCAATTGCCCATTCCT
CCAATTCAAGATCCGTAGCAGAATTGGTAATTGGTGAGATCATTAGTTTAGCAAGACAAT
TAGGTGATAGATCCATTGAAC TGCATACAGGTACATGGAATAAAGTCGCTGCTAGGTGTT
GGGAAGTAAGAGGAAAACTCTCGGTATTATTGGGTATGGTCACATTGGTTTCGAATTAT
CAGTTCTTGCAGAAGCTATGGGCCTGCATGTGCTATACTATGATATCGTGACAATTATGG
CCTTAGGTACTGCCAGACAAGTTTCTACATTAGATGAATTGTTGAATAAATCTGATTTTG
TAACACTACATGTACCAGCTACTCCAGAACTGAAAAAATGTTATCTGCTCCACAATTCG
CTGCTATGAAGGACGGGGCTTATGTTATTAAATGCCCTCAAGAGGTACTGTCTGGACATTC
CATCTCTGATCCAAGCCGTCAAGGCCAACAAAATTGCAGGTGCTGCTTTAGATGTTTATC
CACATGAACCAGCTAAGAACGGTGAAGGTTCAATTTAACGATGAACTTAACAGCTGGACTT
CTGAGTTGGTTTTCAATTACCAATATAATCCTGACACCACATATTGGTGGCTCTACAGAAG
AAGCTCAAAGTTCAATCGGTATTGAGGTGGCTACTGCATTGTCCAAATACATCAATGAAG
GTAACCTCTGTCGGTTCTGTGAAC TTCCAGAAAGTCAGTTTGAAGTCTTTGGACTACGATC
AAGAGAACACAGTACGTGTCTTGTATATTATCGTAACGTTCTGGTGTTTTGAAGACCG
TTAATGATATCTTATCCGATCATAATATCGAGAAACAGTTTTCTGATTCTCACGGCGAGA
TCGCTTATCTAATGGCAGACATCTCTTCTGTTAATCAAAGTGAAATCAAGGATATATATG
AAAAGTTGAACCAAACCTTCTGCCAAAGTTTCCATCAGGTTATTATACTAA

>YIL074C, 469 aa (SEQ ID NO 220)

MSYSAADNLQDSFQRAMNFSGSPGAVSTSPTQSFMTLPRRVSITKQPKALKPFSTGDMN
ILLLENVNATAIKIFKDQGYQVEFHKSSLPEDELIEKIKDVHAIGIRSKTRLTEKILQHA
RNLVCIGFCIGTNQVDLKYAASKGIAVFNSPFSNSRSVAELVIGEIISLARQLGDRSIE
LHTGTWNKVAARCEVRGKTLGIIGYGHIGSQLSVLAEAMGLHVLVYDIVTIMALGTARQ
VSTLDELNLKSDFTLHVPATPETEKMLSAPQFAAMKD GAYVINASRGTVVDIPSLIQAV
KANKIAGAALDVYPHEPAKNGEGSFNDELNSWTSELVSLPNIILTPHIGGSTEEAQS SIG
IEVATALSKYINEGNSVGSVNFPEVSLKSLDYDQENTVRVLYIHRNVPGLKTVNDILSD
HNIEKQFSDSHGEIAYLMADISSVNQSEIKDIYEKLNQTSKVSIRLLY

>YIR037W, 992 bp, CDS: 501-992 (SEQ ID NO 221)

GTTTTCCATGCTTTTGCCGATTTCCTCCACCAACGCTTCCATTCGAGACCTGTCCGTGA
TGTCGAGGACACGATAGACAAATTTGTCTGCACCGTATTCTCTTTGCAAAGACTGCAGAC
CAGCTTCCGTTCTTGTCTACGCCGTAGACGATGCATTCATCGTCTCTTTCGATAACAGTTT
TCACCAATTGACAGGCAATCCCACGGGAGGCACCTGTAATCAAATAACCTTGCCCATAT
CCCTTCTTTTGACAGATTATAAGTTGTTTCTCTTGTGCTGTTTCGCGACAGCCCTTATTTC
CTGTATTCTTCTTCTTTTCTGCATTATCGTTTTTAGCCACTTTACGAAAAAGGTCAAA
AAGTGAAAAAAGAGGGAAAAAACCATGAGGAACAGTATGCTCCCTTAATATCGGAAAAG
CAATAGTAATAAAAAACAGCATCAGAGCTTTCACGTCTCTCTCTTCCAAGCTGTCATCTC
GTAAAGTATTCAAGTTTATCATGTGAGAATTCTATAAGCTAGCACCTGTTGACAAGAAAG
GCCAACCATTCCCTTCGACCAATTAAAGGGAAAAGTGGTGCTTATCGTTAATGTTGCCT
CCAAATGTGGATTCACTCCTCAATACAAAGAACTAGAGGCCTTGACAAACGTTATAAGG
ACGAAGGATTTACCATCATCGGGTTCCCATGCAACCAGTTTGGCCACCAAGAACCTGGCT
CTGATGAAGAAATTGCCAGTTCTGCCAACTGAACTATGGCGTGACTTTCCCATATTATGA

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AAAAAATTGACGTTAATGGTGGCAATGAGGACCCTGTTTACAAGTTTTTGAAGAGCCAAA
AATCCGGTATGTTGGGCTTGAGAGGTATCAAATGGAATTTTGAAAAATTCTTAGTCGATA
AAAAGGGTAAAGTGACGAAAGATACTCTTCACTAACCAACCTTCTTCGTTGTCCGAAA
CCATCGAAGAACTTTTGAAAGAGGTGGAATAG

>YIR037W, 163 aa (SEQ ID NO 222)

MSEFYKLAPVDKKGQFPFQDLKGKVVLIWVASKCGFTPQYKELEALYKRYKDEGFTII
GFPCNQFGHQEPGSDEEIAQFCQLNYGVTFPIMKKIDVNGGNEPVPYKFLKSQKSGMLGL
RGIKWNFEKFLVDKKGKVYERYSSLTKPSSSLSETIEELLKEVE

>YJL161W, 1043 bp, CDS: 501-1043 (SEQ ID NO 229)

TCATAAGTCTGGCGCGTATTCCTTGCAATTTTCATATCTTCCCATATGAATACCTG
TATAGTCGGTATCACCAAGTGTAACCTGTTCTTTACAATGAGAACATCTAGAGTCTTTCTG
ATATGCGTAACCTCTGCCTCATTAATTTAAAAATTTCTTCATAGTAAATAGCTTATTTGC
TTGGAGCAGATGATCGACATGTATTTTAGGAACATAAACTGCCTAAATATAATAGATCA
GCCTAAAAATAAGAATGCCAATCAACAAAGTTGTATTTTCTATCTTCCGATATTCGCAGT
CCACCATTTCAGACCTCTGGTGAGATAGTTTGCTGCTTTTGCTCCCTTCCAAAGTGCTGA
TAAAAACCTCCGTGATTTTTTGAATACTCCCCTGAATGTCTATTTTAAAGTATATTATAAA
ATTAGTTTAAAGTTGGTGCGGATAACGAAAACCTTGATGCAAGGTAAATAAATCAAGTATAT
CATAGAGTTCTTTTCATTCATATGCTATACACAAGGTTGTTACGTCACAACCTACAATTCA
CCAAGTTTTCAGGCACATCGCCCAATCTTGGCTCAAAACCTTTATTTTTCGAAGGGTAATT
TGTAAGTACTAGTCTTTTAGTGACACACTGTATGGGACAGGTCTGGCATGCCTATATCTAG
AATCAAAATAGCTTGAATAAGTCCAAAGAGCAAGAAGATCCCCATGCCATCGCAGAAGACG
ACATTTGTAAATATAGTCCATGACGCTCCCAATAGAATATTCAAGCCAGCACTTGATACCT
ATCAAGAGAAAAGAGCTTGACTTACAAAAGAGTGACCTCCATAAAAGTACTTCATTCTTTGA
CGTACAGTGATGTCTCTCAATTTTCGATTGTTTGGGGGTTTCTCATTCAACTTTTCGAGCC
TAATAGGCAATTCACCTTAGGCAAAAAATCCATTCTTTATAAGGGAAGTGTCGTTAGTG
TTTTAGGGTTCCACCGTTGATTTATATGGCACTTAACTTAGGATGAAACAGCTGGAAA
AAGCTGGAGTGCGCTTTGAGTAA

>YJL161W, 180 aa (SEQ ID NO 230)

MLYTRLLRHNSQFTKFSQTSPLNGSKPLFSKGNLYTSLLVTTLYGTGLACLYLESNSLNK
SKEQEDPHAIAEDDIVNIVHDAPNRIFKPALDITYQEKELDLQKSDLHKVLHSLTYSVDVSQ
FSIVWGFLLIQLSSLIGNSTLGGKSILYKGSVSVLGFPLIYMALKLRMKQLEKAGVRFE

>YJR096W, 1349 bp, CDS: 501-1349 (SEQ ID NO 233)

GTATATTCAAGAAGATGACACACCAAGCCAAAGCCATTAAAGTAGATGATGAACAATG
GGACTACAAAATGAAATAAAGAAAAATAGAAATAGGCTAGAAGATCAATTATTAATCGC
CCTATTTCTTCTTATTACCTACACAAAATAAAGCAGCAACATAAGAAACAAAAACAAAT
GAAAAACAAACCAATAAATCTATGTAAGCATACTCATTTCAATTTGATATTCAATTACTTG
ACTTTTTTTGTCCTTATTTGAGGCTCCATAAGCGCGCCATTTTTCCCTACTCCCTTTTTTC
GTAAATAGTAATAATGTGCTGAAAAGAACATGAAGTAGTTATCATACATATTTCCGTCGT
GTCGATATGAGGGGAGGTGTCTCTTTCTTTTCATCCCTTGTGCGCAACCTCCAATATATAAG
AGCATAAGCAACTGATCTTACTTTAGTAATTAACCTTAGCATACCTAGCCCGAAGGAAGAA
AAAAAATTCACCTCAACAACATGGTTCCCTAAGTTTACAAACTTTCAAACGGCTTCAAAA
TCCCAAGCATTGCTTTGGGAACCTACGATATTCCAAGATCGCAAACAGCCGAAATTTGTGT
ATGAAGGTGTCAAGTGCGGCTACCGTCATTTGATACTGCTGTCTTTATGGTAAATGAGA
AGGAAGTTGGCGGATGGTATCATTAAATGGTTGAACGAAGATCCAGGGAACCATAAACGTG
AGGAAATCTTCTACACTACTAAATTATGGAATTCGCAAAACGGATATAAAAGAGCTAAAG
CTGCCATTTCGGCAATGTTTGAATGAAGTCTCGGGCTTGCAATACATCGATCTTCTTTTGA
TTCATTTCGCCACTGGAAGGTTCTAAATTAAGGTTGGAAAATTTGGCGCGCCATGCAAGAAG
CGGTTGATGAAGGATTGGTTAAGTCTATAGGGTTTCCAACATATGGGAAAAAGCACATTG
ATGAACCTTTGAACTGGCCAGAACTGAAGCACAAGCCAGTGGTCAACCAAAATCGAGATAT
CACCTTGGAATTATGAGACAAGAATTAGCAGATTACTGTAAATCTAAAGGTCTCGTCGTCG
AAGCCTTTGCCCCATTGTGTCACGGCTACAAAATGACTAATCCAGATTTATTTAAAGTTT
GCAAAAGAGGTGGACCGTAATCCAGGTCAAGTTTGTATTCGTTGGTCTTTACAACACGGTT

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ATTTACCACTACCGAAGACTAAACTGTGAAGAGGTTAGAAGGTAACCTTGCAGCCTACA
ACTTTGAACTGTCAGACGAACAGATGAAATTTCTTGATCATCCTGATGCTTATGAGCCTA
CCGATTGGGAATGCACAGACGCGCCATAA

>YJR096W, 282 aa (SEQ ID NO 234)

MVPKFYKLSNGFKIPSIALGTYDIPRSQTAEIVYEGVKCGYRHFDTAVLYGNEKEVGDGI
IKWLNEDEPNHKKREEIFYTTKLWNSQNGYKRAAAIRQCLNEVSGLQYIDLLLIHSPLEG
SKLRLETWRAMQEAVDEGLVKSIGVSNYKKGHIDELLNWPELKHKPVVNQIEISPWIMRQ
ELADYCKSKGLVVEAFAPLCHGYKMTNPDLLKVCKEVDNRNPGQVLIRWSLQHGYPPLPKT
KTVKRLEGNLAAYNFELSDEQMKFLDHPDAYEPTDWECTDAP

>YKL065C, 1121 bp, CDS: 501-1121 (SEQ ID NO 241)

CTGGGCTAGGTTTCACATATCAAAAAGAAGTTATGGCTTATGTGCTCTTTCTAAGTTTGA
CTTTTATGCCAAAAATTTCTCCGTAGATCGCCGCCCGTTGAAGCAGCAGAATATTTTAAGT
GCGCCATAAAAACCTAGATAGAAAAGAAGGGAGAGAACAATAAACGCAGAACACCCTACT
TTTAAGGCGTACGCAAACTGTTGGGCTTATCTATATTGTACTATCTACCTACTTGCAACG
TCTTTTACCTCCTCGATACGTACTGCTTATGCCCTGAACAATTTACATGTAACCCGCGAGC
TGCATGCTATATCACAGGATACGTTAACATAAAGGGGGCGCTACTAAACCCCTCTGGCGCA
GTGCAAAAATAGAAATATATGCCAAGTGGGACCTTGTATAGTTTCTGGTTTAAAGCTATT
CGTTCATTGCAACGCTCCTTTCTGCTATCCTTTTCGCAAAGTGGCAAGTACTGAAAACCGA
GAAGAATAAATAATATTGCGATGAGTTTATACCTTTACGACATTATTTTTATTGCTCACTG
TTGAGGTGGTAATGCTCTTCATCTTCGTTTTGCTTTTGCCATTCCGGATCCGTAGGGGTA
TTTTTAGCACCTATAACCAATTGACAGCGAAGCAGCAAATAAAAACTATAATCTTTATAA
CGGGTTGTCTTGTGGCCTGTTGTTTTATTGATTCATGGAAAAGGTCCAAATTCGTGTTT
CATTATACCACAACGACAACAGTGGCTCAATCGGGTCATCTGCTGTAACCTCCAATACAGG
CACTAGCATCAAGAGCGTACAATCAAAGAAATATGTATATTTCCGGGTTTCATATTGTACT
TTTCTATCTGTATCCCAACTGTCATGTCTATTGTCAAGAGACTGGTGAAATACCAAGGCT
TAATCAACGAACAAGAAAAGCAAAAATTGAACAAACCTTCCTCAAACAGCAAGAAAGACT
CAAATGAAGCTGATTCCACCAAACCTCAAGAGGAACTAAGGAAAAGCAAATTTCTCTGG
AGGGCCTACAAAAGCAAGTCAAAAACCTGGAGAAATATTTTGATGAGAAGAATCAACCTG
GAAATGTAGCAGCTGCTGAAGCTTCCAAGAAAGGAAACTAA

>YKL065C, 206 aa (SEQ ID NO 242)

MSLYFTTLFLLLTVEVVMLFIFVLPLPFRIRRGIFSTYNQLTAKQQIKTIIFITGCLVGL
LFIDSWKRSQIRVSLYHNDNSGSIGSSAVTPIQALASRAYNQRMNMYISGFILYFSICIPT
VMSIVKRLVKYQGLINEQEKQKLNKPSSNSKKDSNEADSTKLQEELRKKQISLEGLQKQV
KNLEKYFDEKNQPGNVAAAEASKGN

>YKL196C, 1103 bp, CDS: 501-1103 (SEQ ID NO 253)

AAAGAGGCTTCCTATTAGGAGCAATAAAATATAAAGCACCAGCCATAGAAAGAATCCCCA
TTATAAAGCCCGCTGTTTTTTCTCTGATTGGAGTTCTTACCGAACTGAGGGGAGGACGCCA
TGAGACGCTCTGTTTGGTGTCTGGCATAACCCCTTGCCACTTGAATTGACGGCCTGTTTC
TGCACGCATTCCTGACGACTAAGTTGCGAAGCATTTTACTGATAATATACACTCTTTGGA
TCGAGCCTACTTCCAGTTGGTAATTGGTGTTCACAAATTTACGATTATATGTTTTTAAA
CCAAAATTCGGCTCCTTTTCCCTTTTTTCTTATTGGGTGGCGTGCCGTACAGAACGATT
GGCTTGGTGTGAAATCAAGAGCAAGCACAATAGATATCAACATGAACAATATACAAAAGT
CTCTGGCACAGTTTGACTGCGTTAGACCAGGCTAGGGCATTCTGAAGCTTTACGTATCA
CTAGAGAAGTTATTTTGGCAATGAGAATCTACTACATCGGTGTATTTTCGCTCTGGGAGGAG
AAAAGGCTCTAGAGTTGAGTGAAGTTAAAGACTTGTCACAATTTGGTTTCTTTGAAAGGT
CTAGTGTGGCCAGTTTATGACTTTTTTTGCTGAAACGGTCGCTTCTAGAACTGGTGCAG
GACAAAGACAAAGTATAGAAGAAGGCAACTATATTGGCCACGTTTATGCCAGGAGTGAGG
GCATATGTGGTGTTTTGATCACCGACAAAGAATATCCTGTCAGACCAGCATACACACTAT
TAAACAAAATATTGGATGAATATTTAGTCGCACATCCTAAGGAAGAGTGGGCAGATGTGA
CTGAGACCAATGATGCATTGAAAATGAAGCAACTGGACACTTACATTAGCAAATATCAAG
ATCCTTCACAGGCTGACGCTATCATGAAAGTTCAACAAGAAGTGGATGAGACGAAAATCG
TTTTGCACAAAACGATTGAGAATGTTTTACAAAGAGGTGAAAAGTTGGATAATTTGGTGG

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ACAAATCGGAGTCATTAACGGCAAGTTCCAAAATGTTTTATAAGCAAGCTAAAAAATCCA
ATTTCGTGTTGCATCATCATGTAG

>YKL196C, 200 aa (SEQ ID NO 254)

MRIYYIGVFRSGGEKALELSEVKDLSQFGFFERSSVGQFMTFFAETVASRTGAGQRQSIE
EGNYIGHVYARSEGICGLITDKEYPVRPAYTLLNKILDEYLVHPKEEWADVTTETNDAL
KMKQLDITYISKYQDPSQADAIMKVQQELDETKIVLHKTIENVLQRGEKLDNLVDKSESLT
ASSKMFYKQAKKSNSCCIIM

>YKR076W, 1613 bp, CDS: 501-1613 (SEQ ID NO 259)

TAAATAGTTGAGGCTTTTCTGCATTCTGTCAAGAAGGGTATGTGTATGAACATGCAAAT
GACACTGHTAAAATGATTCAATACCCCTGATTATGGAGTGATTTTCTTTCTTTTCTTTT
ACATTTAGTTTTCATTATTATGCAAATTAGAGGGTATACAGTTGAGATTTTAACACTTTTGA
ATTAAAAAGTGTACAGAGGAAACCGACGCAAAAGGCTTGGTGACGCAAACTTTTCCATC
TTTATTTTACCCTCTTCAGACGGTCCTAAGACCCTTTTGAACGTATCAATATAGTTTATCA
TCTGTTCTCTGTTGTTCTCCGTTACTAAGATATTAGTCAGCTCTTGAAATTTACACCCCC
TATTTATTTGTCTTAGCGTCCAACCCCTCTCAACCCCTTTTCCATTTCTTGTATAAAGGTA
GTAAATTAGGTAACGCTGCTCTTACCATCACTACAGTGCTTACGAGAATTTACCCAAACC
CTGCGCAAGATAAATAAGAAATGTCGAAACAGTGGGCGAGTGGTACAAACGGAGCTTTCA
AAAGACAGGTTTCGTCCTTCAGAGAAACAATCTCTAAGCAACACCCAATTTATAAGCCAG
CAAAGGGAAGATATTGGTTGTATGTTTCACTTGTCATGCCCATGGGCCCATAGAACACTAA
TTACGAGGGCTTTGAAGGGATTAACCTCTGTTATAGGATGTAGCGTAGTCCATTGGCACC
TTGACGAGAAAGGATGGAGATTTTTGGACATGGAAAAGCAATTGGAGGACAGTGAAGATT
TTTTGGAACATTGGGCACGATGTTGCAGGTGGTATTAGAAGTGTAAAGAGGATTCCAGCA
AGAGCTTCGCCGAGATCAAGAATGACAGTCAAAGATTTCATGGTTGATGCTACCAATGAGC
CTCACATATGGATACAAGAGAATCAGTGACTTATATTACAAGAGCGATCCTCAATACTCGG
CAAGGTTTACCGTCCCAGTCCCTGTGGGACTTAGAAACCCAAACAATTGTTAACAACGAAA
GTAGCGAAATTTATAAGGATTTTGAACCTCTAGTCCGTTTCGATGAATTTGTTCGACGACGATC
ACAAGAAAACGGACCTTGTTCCTGCTCAGTTGAAAACACAGATCGATGACTTCAATTCCTT
GGGTTTACGACATCAACAATGGTGTATACAAGACCGGATTCGCAGAGAAAGCAGAAG
TTTACGAAAGTGAAGTCAACAACGTATTTGAACATTTGGACAAAGTGGAGAAAAATCTTGA
GTGACAAATATTCCAAATTGAAGGCCAAATACGGTGAAGAAGATAGACAAAAAATCTTGG
GTGAGTTCTTCACTGTGGGTGATCAATTAACAGAAGCTGACATTAGATTGTATACTACCG
TCATAAGATTCGATCCTGTGTACGTCCAACATTTCAAATGCAATTTTACCTCTATTAGAG
CCGGATATCCATTTATTCATTTGTGGGTAAGAAATTTTACTGGAATTATGATGCCCTTCA
GGTACACAACAGATTTTGACCATATCAAGTTACACTACACGCGTTCCACACAAGGATCA
ACCCCTTGGAATTACGCCCCCTGGGACCCAAGCCAGATATTCGTCCTTTATAA

>YKR076W, 370 aa (SEQ ID NO 260)

MSKQWASGTNGAFKRQVSSFRETISKQHPYKPAKGRYWLIVSLACPWAHRTLITRALKG
LTSVIGCSVVHHLDEKGRFLDMEKQLEDSEDFLEHWHDVAGGIRTAKEDSSKSFAEIK
NDSQRFMVDATNEPHYGYKRISDLYYKSDPQYSARFTVPVLWDLETQTIWNNESEIIRI
LNSSAFDEFVDDHKKTDLVPALKTQIDDFNSWVYDSINNGVYKTGFAEKAEEVYESEVN
NVFEHLDKVEKILSDKYSKLKAKYGEEDRQKILGEFFTVGDQLTEADIRLYTTVIRFDPV
YVQHFKCNFTSIRAGYPFIHLWVRNLYWNYDAFRYTTDFDHIKLHYTRSHTRINPLGITP
LGPKPDIRPL

>YKR092C, 1721 bp, CDS: 501-1721 (SEQ ID NO 261)

TCAAGGATACCTGGTTGATTCTACGTCGTCCTTCACTTTGGTTAATTCACCTTTGCC
TTCACCTTGTTGGTGTGCGGGTGTGTCAGTCATTAATGTTCTTTATCGCGAGAGGGGGTCT
ACATAATCTTGTTTTTTTCACTCCAATAAGGCAGTTATAGTGAATTTGTTTTATTACAGAA
GGTGTACCTTTCGTTTCGAGTTATTTTACTCTTGTGTTTGTAGTTTGTACATCTCTTTATGT
CTGGATCAAAACGATAATTGCAAGCTTATTGCAATTTAGTTCTCTTACCCATTTCTTTAC
AACGGGCCGAGAAAAAGTGGAGTTGGTCCGAGGAAGCTTTGAACGGGAAGAGGAAAAAAC
CTTCCCATCGCTCGAGCATACAATTTTTTTTTTTTCAATGCAGGCTGAAAAAAAATTT
CACTTGATGATTGAACTCATCGCACTTTTATACAAAGCAAGAAAGAAACCCAAGTCGCAG

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AGGGGTGGGATGCGCGAAATTCATGCCTACAGTAGAAAGCGGTTGTTGCACAAATGATT
AAATCTTTATCTCCAACCTACAATACTATCGCGATAGATGCATAATATGTGCAGCTTCTA
AACAGCACGGAGTGATGATAAATACGCATATATGTATATATATATGTATGTGCATATGCA
CGTCCTTTTAAAACTCAAAATACAACATTCTTAGTAAATCCTTTTGTGACACACGTCGG
AACAACCTCAGGACGGAGTTAATGGATATGCTTCATAATAAATGTAGTGATGCTATCAAAA
GCACCTCCAATAGCAATTTGAGTAATGAGGTAGACAAACAAAAATTGCAATACGATGACC
TCGGGAACACCGGATTTTCTGAACATTTGAGATGGAATCTCAAGATAATAATGATAGCA
TAGAGGATTTCTTGTCTCTTAATATAAAATTTAACCCAGGAGGTTGAGTTGAGAACCAAA
GACAATATGAGCACACGAAAAAGACAAAGAAGCATAACCCATTCTATGTACCGTCAGAGG
TAGTGCGAGAGATGGTCAAGAAACACGCATTGAATGGCAGAATATAG

>YLR053C, 108 aa (SEQ ID NO 272)

MDMLHNKCSDAIKSTSNSNLSNEVDKQKLQYDDLGNLTFSELFEMESQDNNDSDIEDFLFF
NINLNTQEVFENQRQYEHTKKTKKHNPFPVSEVREMVKKHALNGRI

>YLR390W, 839 bp, CDS: 501-839 (SEQ ID NO 291)

GTGAAATTGAGACTGATAGGTGAGAGGTGAACCAATTGAGTGAGGAGTGGTTTAGTTACA
AATGCAGAAGAAGAAGCTAAAAGAGATACGCCCATACAGAGCAATATCAAAATGAGCAAG
AATGAGGTCTTCCGAATGGTTGGTTCTGACTTACTATTTGATTTCACTTTCTCTGATTCA
TTCAGGAAGAAAAGGGCGAAGTCCTCGAAATGAAAATTTCAACATCATTAACAGACCGGC
GCGCGCCTTTACAATTTAGTATGTACGCCACCAATAAAAGCTGCTTAAACAATAAGCTAG
AAAGCCCAAAGGGTGTTAAATAGTACAGCGAACCCCTCAGCAACGGTACATCAACAACCC
CTTGAAAAGAATAGAGACAATACAGCTACAGTCATCCCCCTTCTCTTGTATTTTTGGCCAC
AATTGATTGTATTACATCATATTTTGCTGTGCGCTTCTTCTATCTTTTCCGCATAAACT
AGGGGAAACGCGATGAAGAAATGGATTGGCTGAAAAATACAACAATTGTAGTGTTATTCA
GTCATTTCAACTGACAAAAGTAACAAACACAAGAAACGTCAAGTCCAGTGCAATATGCGAA
AGAACACTTTAGATATGGTCACTATAGGTATCGCATGCCTTGTGGGAGTCTACACGGGCA
CGAGATTTTTCGAGCCCATTTGTTATCGATAGATTGCGTAAGGATGGAAGCTTGGAACGG
ACATTTCCCATCCCAAGTAACGACGAGGACGGAAATCTGTTAAAGGTCACGCCGTCTTTAT
CATCCACACCAGCTGCACCACCTACACCACCTACACCTCCTACTCCACCACAACAGTAA

>YLR390W, 112 aa (SEQ ID NO 292)

MDWLKNTTIVVLFSSHSTDKSNKHKRQVQCNMKNTLDMVTIGIACLVGVYTGTRFFEPI
VIDRLRKDGNLRTDIPPEYDEDEGNLLKVTPSLSSTPAAPPTPPTPPTPPQQ

>YMR251W, 1601 bp, CDS: 501-1601 (SEQ ID NO 315)

ACTCCAGAGCGCAAGAGTTCGTTTCATCTACGAAATGTTGCTGGCATTGGCATCTCCACAA
GATGACATCCCAACGCCGGATGAAATCGAAAAGAAAAATAAGCTAAAGGAAACAACAACG
AGAAACTATAGAGGAACATGTTGAGTTGAAAAGGTTCATCCAATATACCGCCCCCTATATG
TATGTACCTTTACCTTTTATTTAAGTACTAGTGCTGTTTAGTTAGGTTATGTGAAGGCAC
GGGTTTTGTCTTTTTTTTTTTTTTTTTTTTACTATTACTTTCTTTTTTCAAGCTTTTAAGCG
CCGAAATGATATTTAAGGGAAGATGACTAAAGGGACAGCGACGAGGATTACAGCCTGGACA
GTGATAGAAAAGTTATGCGGGAATACGTATATATAGTTGTATAAATTGTGGTTATAGAAC
ATCGCAGCGCCTTTAAATATATTGTCTTTTTATTTCAATCTTATTCCATCTCTCTCTTGCA
ACCACGGCAAAGCTGGAGCTATGTCTGAAAAATCAGCTAGCAATAACAAAGCTGAATTC
AAAGGCAGTCATCGCCATTACAGAGAAATCATCTCTGCGGATCACCCAATTTATAAACCTG
CTAAGGGAAGGTACTGGCTGTATGTGGCGCTACCATGCCCATGGGCACAAAGAACCTTGA
TCACCAGGGCCCTGAAAGGGCTAGCGCCTATAATCGGGTGCAGTGATAGCGCATTGGCACC
TGGATGACAAAGGCTGGCGATTCTTTGAAGAAGGAGATGGGAAAACCAATGAAAGGCACT
GGTTTGACATTGCAGGCGGAATTAGCTCAGTAAATTTAAATACCAGTACTCCTGTGGCTA
ACATACCCAATAACGCGCATCGGTTGTTGGTGCACGGAACAGATGAACCGCATTACGGGT
ACAAGAGACTAAGCGACTTCTATTTCAAAACAAGCCAGACTATAAGGGAAGATTACCGG
TACCTGTTCTTTGGGACTTGGAACATGCACTATAGTAAACAATGAAAGCAGTGATATCA
TCGGAATTATGAATTCGCTGCGTTTGATGAGTTTGTGCGGCGAAGAATACCGTCAAGTCC
GTCTGGTACCTCGGTCTCTAGAGGCACAGATTACAGAGTTCAACTCTTGGGTGTACGATA
AAATCAACAACGGTGTATACAAGGCCGGTTTTGTCAGAATGTGCAGAGGTATACGAGAGGG

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AGGTAACAAGCCTTTTTCAATATCTTGACAAATTGGAAAATCTTCTGGACAAGAAGTACA
CAGATTTGGAGGCGGAGTATGGTAAGAACAACAAGGACAAGATACTAGATCGCTACTTTG
CCATCGGAGACACTCTGACCGAGGCGGACGTGAGACTCTACCCAACGATAGTAAGGTTCCG
ACGTGGTATACCATCAACACTTCAAATGCAATCTGGCCACCATCAGAGATGATTATTCCC
GTATACACACGTGGCTCAAGAATATATACTGGCGCCACGAAGCCTTCCAGCGCACAAACGG
ACTTTACCCACATAAACTCGGATATACTCGCTCGCAGCCACGGGTCAACCCGATTGGGA
TCACCCCACTGGGGCCCAAGCCTGATATCCGACCTCCATGA

>YMR251W, 366 aa (SEQ ID NO 316)

MSEKSASMNKAIEFKRQSSPFREIISADHPIYKPAKGRYWLIVLPCPWAQRTLITRALKG
LAPIIGCSVAHWLDDKGWRFLLEEGDGKTNERHWFDIAGGISSVNLNTSTPVANIPNNAH
RLLVDGTDEPHYGYKRLSDFYFKTKPDYKGRFTVPVLWDLETCTIVMNESSDIIGIMNSA
AFDEFVGEERYQVRLVPRSLEAQITEFNSWVYDKINNGVYKAGFAECAEVYEREVTSLFQ
YLDKLENLLDKKYTDLEAEYGNKNDKILDRYFAIGDTLTEADVRLYPTIVRFDVVYHQH
FKCNLATIRDDYSRIHTWLKNIYWRHEAFQRTTDFTHIKLGYTRSQPRVNPIGITPLGPK
PDIRPP

>YMR273C, 3248 bp, CDS: 501-3248 (SEQ ID NO 321)

AAATTGGTCTCAATCTGGAATAAGTGCTACTTCGCACTGCTGGTCCTTGGATTAATATCC
CTGAAGGATACCTTACAACTCTGGTAGGAACTCCTGGTTATAGAATAACCTTTAGCCT
TTTTTACGTACTTGTATACCGTTTAAAATTTCTATGTACTATAACCTTTTTTCACTACT
ATTATGGAATTTCTATCGAGCGACCGGGCTTTTGTACGGAAGAGTGAAAAAATCGAGTTT
TGGTGTTTTGGTGAAAGAATTTGGAGGACTATAAAGTACCTATACTTTGTATTACGGACT
CAATAACAAGTCGTTCGTGTCAGTGGTATTGAAGTTGTCAGATCTAAGAGTAGAGAGAAG
GTGGCATCTAATAGGTTTCGACGTTTTTCTTTTTTTAAGGTTTTTATTTGGTCTCCTAGA
ATTTAAGGTCTTAGTTAGTTTGGTTTTGTTTTGTGGGTTACATATTTTCAATTCAAAGGA
GAATTTAGCTGTCTTTTATAATGTCCAATAGAGATAACGAGAGCATGCTGCGTACTACAT
CAAGCGATAAGGCGATCGCTAGTCAAAGGGATAAACCGGAAGTCTGAAGTTTTGATTGCTG
CACAGTCCCTTGACAATGAAATCCGCAGCGTAAAAAACCTAAAAAGATTGTCGATTGGGT
CAATGGATTTACTTATTGATCCAGAATTAGATATAAAATTCGGTGGGGAATCTAGTGGGA
GACGATCATGGTCTGGCACGACATCCAGTTCTGCGTCAATGCCAAGTGACACAACACCCG
TTAATAACACACGATATAGCGATCCAACTCCGCTAGAGAACTTGCATGGGAGGGTTAACT
CAGGGATAGAATCCTCCAATAAGACTAAACAAGGTAAGTACTTAGGTATAAAAAAAGGTG
TTCACTCTCCATCCAGGAAATTAATGCTAACGTATTAAAGAAAACTTATTATGGGTTT
CCGCCAATCAACACCCCTAACGTTAAGCCTGATAATTTCTTAGAGCTTGTACAAGATACTT
TACAAAATATACAACCTAAGCGACAATGGTGAAGATAATGATGGGAATAGCAATGAAAATA
ACGATATTGAGGATAATGGGGAGGATAAAGAATCACAATCATATGAAAATAAGGAGAACA
ACACTATCAACTTGAACAGGGGGCTGTCAAGGCATGGAAACGCGTCACTAATACGAAGGC
CTTCAACATTGCGGAGGTATATACAGAGTTTGATGATAACGAAGATGACGATAATAAGG
GAGACAGTGCCTCTGAAACAGTAAATAAAGTCAAGAAAGAACTCTCCAAAATAAAAGAGA
GACCAGTGTCGTTAAGAGATATAACTGAAGAACTGACAAAGATCTCAAATAGTGCAGGAC
TAACCGACAATGATGCCATTACATTAGCCAGAACTCTTAGTATGGCTGGTTCATATTAG
ATAAAAAAGATCAACCACAACCGGAAGGGCATTTATGATGAAGGAGATATTGGT'TTTTCAA
CTTCACAAGCGAATACTTTGGATGATGGTGAATTTGCCCTCCAATATGCCCATCAATAATA
CCATGACATGGCCTGAACGATCGTCACTGAGAAGGAGTAGATTCAACACTTATCGAATCA
GGTCACAAGAGCAAGAAAAAGTAGAACAAAGTGTGGATGAAATGAAAAACGACGACG
AAGAAGCTCTAAAAATTGACCAAGAAATACAATAAAGGTCGAAATAGATCCGCACAAATCCC
CTTTTAGACAGCAAGATGAGGATTTCTGAGAATATGAGTTTCGCCCTGGGTCAA'TTGGTGATT
TTCAAGACATTTTATAATCATTTACAGACAGTCTAGTGGCGAGTGGGAACAAGAAATGGGAA
TAGAGAAAGAAGCCGAAGAGGTACCCGTCAAGGTTGCAATGACACAGTAGAACAAGACT
TAGAGTTAAGAGAGGGAACAACAGACATGGTAAAGCCAAGCGCAACGGATGACAACAAG
AAACGAAGCGACATCGTCGAAGAAACGGATGGACATGGTTGAACAATAAATGAGCAGAG
AAGACGATAACGAAGAAAACCAAGGGGACGATGAAAATGAAGAAAACGTGGATTACAAA
GAATGGAGCTCGACAATTCCAAAAAACATTATATTTCTCTATTTAATGGCGGTGAGAAGA
CGGAGGTGTCAAATAAAGAAGAAATGAACAATTCAAGTACTTCCACCGCCACATCACAGA
CAAGACAGAAAATCGAGAAAAC'TTTTGCGAACCTATTCAGAAGAAAGCCACACCACAAGC

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ATGATGCATCATCATCACCTCGTCGTCACCATCATCGTCACCATCAATACCAAATAACG
ATGCCGTGCACGTTTCGCGTGAGGAAAAGCAAAAAGCTTGGTAACAAAAGTGGAAGGGAGC
CGGTTGAACCCATTGTGTTGCGCAATCGCCCTCGTCCCTACCGTCACCATCACAGCCGTC
ATGGTTCCCAAAAAATAAGCGTAAAAACCTTAAAGATTCTCAGCCGCAGCAGCAGATAC
CATTACAACCACAATTGGAAGGCGCAATAGAGATAGAAAAGAAAGAGGAAAAGCGATTCCG
AGAGCTTGGCCCAACTACAGCCGGCCGTTAGTGTAAGTAGTACCAAAAGTAACCTCTAGAG
ACAGAGAAGAAGAGGAGGCAAGAAAAAGAACAGAAGAGGAGCAATACGACAGAAATTT
CCAACCAACAACACTCCAAACACGTCCAAAAGGAGAATACCGATGAGCAAAAAGCTCAAC
TACAAGCTCCAGCTCAAGAACAAGTCCAAACTTCAGTCCAGTTCAAGCTTCAGCCCCAG
TCCAAAATTTCAGCCCCAGTCCAAACTTCAGCCCCAGTTGAAGCTTCAGCTCAAATCAGG
CTCCAGCGGCACCAACCATTTGAAACATACCTCCATATTGCCCCCAAGAAAGCTTACATTTG
CAGAGTCAAAAAACCTGACAAACCAAACTCCCGGTTCAATTACAGACAGTGCCTTTG
GGTTCCCACTGCCTTTGCTGACAGTGTCTACGGTTATCATGTTCGACCACCGTCTACCAA
TTAACGTCGAAAGGGCCATATACCGGCTGAGTCACCTGAAATTGAGCAATTGGAAGAGGG
GACTGCGCGAGCAGGTATTACTAAGTAACCTTCATGTATGCTTATCTGAACTTGGTTAATC
ACACTCTGTACATGGAGCAGGTAGCCACGACAAAGAACAACAACAACAACAACAACA
AACCTGA

>YMR273C, 915 aa (SEQ ID NO 322)

MSNRDNESMLRTTSSDKAIASQRDKRKSEVLIAAQSLDNEIRSVKNLKRLSIGSMDLLID
PELDIKFGGESSGRRWSGTTSSSASMPSDTTTVNNTRYSDPTPLENLHGRGNSGIESSEN
KTKQGNYLGIKKGVHSPSRKLNANVLKKNLLWVPANQHPNVKPDNFLELVQDTLQNIQLS
DNGEDNDGNSNENNDIEDNGEDKESQSYENKENNTINLNRGLSRHGNASLIRRPSTLRRS
YTEFDDNEDDDNKGDSASETVNKVEERISKIKERPVSRLDITEELTKISNSAGLTDNDAI
TLARTLSMAGSYSDKKDQPPQEGHYDEGDIGFSTSQANTLDDGEFASNMPINNTMTWPER
SSLRRSRFNTYRIRSQEQEKEVEQSVDEMKNDDERLKLTKNTIKVEIDPHKSPFRQODE
DSENMSSPGSIGDFQDIYNHYRQSSGEWEQEMGIEKEAEVVKVRNDTVEQDLELREGT
TDMVKPSATDDNKETKRHRRRNGWTWLNKMSREDDNEENQDDENEENVDSQRMELDNS
KKHYISLFGGEKTEVSNKEEMNNSSTSTATSQTRQKIEKTFANLFRKPHHKHDASSP
SSSPSSSPSIPNNDVHVVRVRSKKLGNKSGREPVEPIVLRNRPVRPHRHHHSRHGSQKIS
VKTLKDSQPQQQIPLQPQLEGAIEIEKKEESDSESLPQLQPAVSVSSTKSNRDRREEEEA
KKKNKKRSNTTEISNQQHSKHVQKENTDEQKAQLQAPAEQVQTSVPVQASAPVQNSAPV
QTSAPVEASAQTQAPAAPLKHTSILPPRKLTFADVKKPKPNSPVQFTDSAFGFPLPLL
TVSTVIMFDHRLPINVERAIYRLSHLKLNSKRGLREQVLLSNFMYAYLNLVNHTLYMEQ
VAHDKEQQQQQQQP

>YNL112W, 3143 bp, exon1: 501-1773, intron1: 1774-2775, exon2: 2776-3143 (SEQ ID NO 327)

CTTGATGGATTTATGTGACGTTGTAGAATCTAAGTTTACTGAAAAATCAAGAGCATGTA
GATGTTACGGATCGACTCAAAGACCCTCTGTCACTCTGAAATTTCTAATAATTATGCACA
CCACGCTAGTATAGATACAGCTTGATTTGTGTATCCCGTTTATAGTCGTGCTATTTAAAA
TCTATGTATAATATAACCAGATAAAAAATACACCTTCGTACAAGGTGCTAATAATGTTGAG
AATTCGAAATTCCTTTTTTAAAGGCGTATTCGTATTGAATGATTGAAAAATTTATTTCTT
TTTTTATTTCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTACGCCGATGCTCATCGAGAAAAT
TTTCTCTTCAGTTTATTTGTCTTATAAAAAGACTGTCCTACGCTCAAATAACTTATACTT
TTCTGTATCTCATTCAAATTATTTTCTTGTCACCAACCTGTAACAGAATTAAGCACTATT
AAGGCAAATTTAGAGCAAATATGACTTACGGTGGTAGAGATCAGCAATATAACAAGACTA
ACTACAAGTCTAGAGGTGGCGACTTCCGCGGTGGAAGAACTCTGATAGAACTCTTACA
ATGACAGACCACAAGGCGGTAACCTACCGTGGTGGTTTCGGTGGTCGTTCCAATTACAACC
AACCCAGGAATTGATCAAACCAAACCTGGGATGAAGAATTACCCAAATTGCCAACTTTTCG
AAAAGAATTTCTATGTTGAACACGAAAGTGTTCGCGACAGATCGGACAGTGAGATTGCTC
AGTTCAGAAAGGAAAATGAAATGACTATTTCCGGACACGATATTCAAAGCCAATCACCA
CTTTCGATGAAGCTGGTTTCCAGACTACGTTTGAATGAAGTGAAGGCTGAAGGATTTG
ACAAACCAACTGGCATTCAATGTCAGGGTTGGCCAATGGCTTTATCTGGTAGGGACATGG
TTGGTATTGCTGCCACTGGTTCCGGTAAGACTTTGTCTTATTGTTTACCAGGTATTGTTT
ATATCAACGCTCAACCATTATTGGCTCCAGGCGATGGACCAATTGTTTTGGTTTTGGCTC

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AGTGAGTAACTTTTGGAGTAATACGAAGTAACCAAAGAGGTCAAAACGGAACATATATACC
CCAAAATAAGCATCATTCAAATGGTCTGAATTAAGTAAAGACGATGTCGTTCAAT
TAGACGAACCACAATTTTCCAGAAATCAGGCCATCGTGGAAGAAAAGGCCTCTGCAACAA
ACAACGACGTTGTCGATGATGAAGATGACTCTGATAGTGATTTTGAAGATGAATTTGATG
AAAATGAAACATTGTTGGACAGAATCGTTGCTTTAAAAGACATTGTCCCCCAGGTAAGA
GACAAACAATTTCTAATTTTTTTGGTTTTACTAGCTCTTTTGTGAGAAATGCTTTCACAA
AATCCGGAACCTTGCTTGGACTTTGACCACCCTGCTTTGTTACTCGGTGTGCCACTAT
CCTTATCTATACTTGCCGAACAACAGCTAATCGAAATGGAAAAGACATTTGATTTACAAA
GTGATGCTAATAACATATTGGCCCAAGGTGAAAAGATGCTGCAGCAACAGCCAATTAA

>YNL131W, 152 aa (SEQ ID NO 330)

MVELTEIKDDVVQLDEPQFSRNQAIVEEKASATNNDVVDDEDDSDSDFEDEFDENETLLD
RIVALKDIVPPGKRQTISNFFGFTSSFVRNAFTKSGNLAWTLTTTALLLGVP LSLSLAE
QQLIEMEKTFDLQSDANNILAQGEKDAAATAN

>YNL143C, 893 bp, CDS: 501-893 (SEQ ID NO 333)

GAAAATACACACGGCGGAAGCCATCATCGAGGCCCAAAGCAAGGATAAAGCATGCTTTTT
CCTGGATAAACCAGAATATAATAAACCAGATACCTGGGACCATAATCCACACACCTGCTGA
AGCCACACCGATCCATCCCATGTTGGCCAAGTCAAATTGTGTATTCAAATCTGTTGTCAA
CGAGTTACCACCCGTTCCCTTCGCCTGTAGGCGTACCTGTAAAATTGTAAGACATTGTTGA
TATTGTATTGTAATATATTAAGTATGATATATTACAAAATAAACTTCTTTCAAAGCTCT
GTGCAGACTTATTATTTAAGAAGGATATTTAATTTGAAAGGACGTGAAAGCACGAATGAT
TACTACCCACTGATGTTTGGTTAGCACATGTGTAACACTGCTTATATATGGTGCAGAAA
AGTGGCTCGGAATGAACACCTCTTGTACTGAATACTTCATTGATAAGGCACAGGGCTTTC
ACGCCGCTTAGTATTTCGTCGATGCGTGAGCAATTGAAGCTTTTACGAGGGAAATAGTCG
ATTTTACATTTCTTATCTTATCTGGCTTTGACTATTACCAGACACTCTTGATAAGCAGTA
ACAGCAGTAAGAAGAGACCGAAGGATTCTTCTTTGTTATCGGAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAGATGTCTTATCTTATCTTCTTATCTTAAAGACCTACCATTGTTC
CTTTTCTATTTTGGCAGCCCGGTTATTCGAAAGGGGAAAAAAAAACCAAGACAGCATTCCT
TGTTTATTATGACTATTACAAAGCCAGGAATGATTTTCGATGGCCGACATGAATTACGTCG
TTTCCAAGAACAGAAGCTTAAACCGTCCTGCTGAGCGGGGCGGTAATCGGTGA

>YNL143C, 130 aa (SEQ ID NO 334)

MREQLKLFRTREIVDFTLILSGFDYYQTLISSNSSKKRPKDSLLSEKKKKKKKKKDV
LSYLSYKDLFPVPFLFWQPGYSQREKNPRQHS LFIMTITKPGMISMADMNYVVSKNRSL
NRPAERGGNR

>YNL179C, 938 bp, CDS: 501-938 (SEQ ID NO 335)

ACAGCGGTTAATTTCAAATACCCTAATCGGAGGTCTTATCTTATTTTTCAAGGGCAAGGC
TCTCCACATCGGTAAGTGATGACCAGATAATGGAAAGTAGCAGAATTTTATTTATGTGCC
ATACAAGCCCGGAGAAACAGAGTAGCTAAAAAATTAAGGTGTGCAAAAGTGGTTTTGTTT
CCCGACGCCCGGGCCTTTCTCTCCCCTGAATCTTTTCGTTCCGGCCCCCTCTCTCAATA
CCAGATCTGCATCTATACTAAAGCTGCAGTGAGAGTAAACCGGAAAATTATCCTGCGTGT
TTGCTTCGGTCTTAGCTTTTACTTGGGTATGCGAGAACCTCTAAGAGCTTAGACCGGTCT
TCCTCCCTAAAAAAGAAATTATAAAAAGGTTATTATCTGGACTAAAGCAAAAAAAAAACAA
CGTTTCGGCGTCCGCTCAAATTTTATTACGCTTCTTGGTCAAATCAGTTACGTAACGG
GTTATGACGAATACGATGAGATGAGTAATTGCAGAAGGCTCCTATGCAGACAGCTAAGCA
GTGCTTACTTGAATTACCTTCCCTTTTATTTCTTGATATATCGTCCTTTTTCTCTCTATC
TTAGTTCTTGCGAGTACTGGCAATCATGTTTCTCCTTTTTTTTTCTTTTTTTTTTATTTT
TTTTTTTTTTTTTTTACTTTTTCAGTTTCTCGTAGCTTTTCTTATTTTGCTATTTAAAGTAA
GTTTAAATAGTACCCTCACTAAACACGTACGGCCGATCCACCAACGAACAAAAGCACGAT
CCTTGACCCATCATTGTATTCCAAAGCGTTGGAACATTCACTTTTTTTTTTCCGGTCTAT
TGCACAAGACAATATCCAGAATATTCAGTTGGATAGGAAATACAAGACAGGTGGCACCCA
CAAAGCACACGCCGAAATATTTATTAAATACAATATAG

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>YNL179C, 145 aa (SEQ ID NO 336)

MSNCRRLLCRQLSSAYLNYLPFYFLIYRPFSLYLSSCEYWQSCFSFFFLFFLFFFFFTF
QFLVAFPIILFKVSLNSTLTKHVRPIHQRTKARSLTHHCIPKRWNHFFFSGLLHKTISR
IFSWIGNTRQVAPTKHTPKYLLNTI

>YOL150C, 812 bp, CDS: 501-812 (SEQ ID NO 349)

TTCCCATTTTCCACTGCTATTCCTGTTGCTATTGTCAGAACCATTGTTTACTTGAATGTTA
TTACTACCATTMTTGTGAATCAAAAATATCTACTTCTTGTGGGGAGACGGGTAGAAGATTT
GTATTTTGGGAGACGTCCTCTCAAATATATGGCCAAAACACCTTGATATTCTAGTTTATTC
CATTCGTCCTTCTTGAAGTCCCATTATACAGTGACGCATGTGGTGTGTGAAAAAGTAGT
TGCTTTATTTTGGATCGTATCTCCCAATAACGTTGAAATTCAAAGCTTTTCTATAGAAT
TCTAACGTGTGTGGCAGAGTTTCTGCTGCAGTTGCTGCTCCGGTCATTGTGCACAGCTTT
TCTTGTGATGTGTGCAAAGATAAATGCTTATCTGAACGTTTCTCTATTGTTTTTTCGTC
AATTTTCTTTTCTTTCTTGCCTTCGCGTTTTCGACATATTAAGCTGTATATAGAAGAGAAA
AATGCGCAGAGATGTACTAGATGATAAAAAATAATGTAATAACGTTAATATATAGATAAAT
ATTATCTATTTTCATTTTAAAGTTTATATTCTGCCCTCAAATTTTAAATTTGGGAGGCAG
TGTCGTCAATGGTCTCTTTCAAGTTCTTGAACCTTGAACCTAACAAATTTCTTACTCTTTT
TATTATCAAGAGTAGCACCAGGGGTGTTATGGGTAGCACCAGAACCTGGTTTCCCCACTG
GAATATTCGCTTTTAGAACAGGGAAGTCTTCGTTAAGGATATCGAGAACATCCTGCATAG
TAAATCTGGCCTCCGATACGATTAGTCTTTGA

>YOL150C, 103 aa (SEQ ID NO 350)

MIKNNCNNVNIYKYLFSEFKVYILPSNFKIWEAVSSMVSFKFLNLKPNNFLLFLLSRVAP
RVLWVAPEPGFPTGILPFRTGKSSLRISRTSCIVNLASDTISL

>YOL151W, 1529 bp, CDS: 501-1529 (SEQ ID NO 351)

GCGTGAACATATGTCATATTTGCGATTTTAGGTACAATAAATATTATCATTATTATATTAT
GTTTGCATGTAGGTTCTACAAATACATTGTTGTACGCTATAGTTTCCTTTCAAACCTAGA
AAGAATTCGTAACAAAATAATCTCCAATATTTTATAGCACCTTATTAATATCAATGCTGC
AATACCTTCTCATTTCAACAATTTGGCCCTCACCTCTTTTGTACAAAAACGTCGCCATTG
ATAAAATAAGTAAGAAGCATATAAATTGGAATGTCCATTACGTAAAAGAAAAAAATCATG
TGTACATATTACGTAATAGAATACGGAATTTTCTCGCGGAAGTAGATCTTCCGTGGAAAA
AAAGGAAAAAGTCCGATCAATATTGAAAAAGGGATCCTTAGTTTCCCAACTATATAAGGA
GGAAAAGTCTATCTCTGTAGCGTTGATATAACGTGTACGATTTTCAAACAAACAGATAGC
AGTATCACACGCCCGTAAATATGTCAGTTTTCGTTTTCAGGTGCTAACGGGTTCATTGCC
AACACATTGTCGATCTCCTGTTGAAGGAAGACTATAAGGTCATCGGTTCGCCAGAAGTC
AAGAAAAGGCCGAGAATTTAACGGAGGCCCTTTGGTAACAACCCAAAATTTCTCCATGGAAG
TTGTCCCAGACATATCTAAGCTGGACGCATTTGACCATGTTTCCAAAAGCACGGCAAGG
ATATCAAGATAGTTCTACATACGGCTCTCCATTCTGCTTTGATATCACTGACAGTGAAC
GCGATTTATTAATTCCTGCTGTGAACGGTGTAAAGGGAATTCCTCACTCAATTAATAAAT
ACGCCGCTGATTCTGTAGAACGTGTAGTTCTCACCTCTTCTTATGCAGCTGTGTTTCGATA
TGGCAAAAGAAAACGATAAGTCTTTAACATTTAACGAAGAATCCTGGAACCCAGCTACCT
GGGAGAGTTGCCAAAGTGACCCAGTTAACGCCCTACTGTGGTTCTAAGAAGTTTGTGAAA
AAGCAGCTTGGGAATTTCTAGAGGAGAATAGAGACTCTGTAAAATTCGAATTAAC TGCCG
TTAACCCAGTTTACGTTTTTGGTCCGCAAATGTTTGACAAAGATGTGAAAAAACAATTGA
ACACATCTTGCGAACTCGTCAACAGCTTGATGCATTTATCACCAGAGGACAAGATACCGG
AACTATTTGGTGGATACATTGATGTTTCGTGATGTTGCAAAGGCTCATTTAGTTGCCCTTCC
AAAAGAGGGAACAATTGGTCAAAGACTAATCGTATCGGAGGCCAGATTTACTATGCAGG
ATGTTCTCGAATATCCTTAACGAAGACTTCCCTGTTCTAAAAGGCAATATTCAGTGGGGA
AACCAGGTTCTGGTGTACCCATAACACCCCTTGGTGTACTCTTGATAATAAAAAGAGTA
AGAAATTGTTAGGTTTCAAGTTTCAGGAACCTGAAAGAGACCATTGACGACACTGCCTCCC
AAATTTTAAAATTTGAGGGCAGAATATAA

>YOL151W, 342 aa (SEQ ID NO 352)

MSV FVSGANGFIAQHIVDLLLKEDYKVIGSARSQEKAE NLTEAFGNNPKFSMEVVPDISK
LDAFDHVFQKHGKDIKIVLHTASPFCDITDSERDLLIPAVNGVKGILHSIKKYAADSVE

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RVVLTSSSYAAVFDMAKENDKSLTFNEESWNPATWESCQSDPVNAYCGSKKFAEKAWEFL
EENRDSVKFELTAVNPVYVFGPQMFDKDVKKHLNTSCELVNSLMHLSPEDKIPELFGGYI
DVRDVAKAHLVAFQKRETIGQRLIVSEARFTMQDVLIDLNEFPVLKGNIPVGKPGSGAT
HNTLGATLDNKKSKLLGFKFRNLKETIDDTASQILKFEGRI

>YOR131C, 1157 bp, CDS: 501-1157 (SEQ ID NO 359)

TCCTGAACGGAAGCTGCAGTTTGCCTCAGTACCTACACGCTCCTCTGACATAGAAGATGAT
CCATCTGTGGTTGTTGCAGCAGGTTTCAAGATCTTCTCTGGGGCTCAGCAAATGGATTG
TTATCCAGATCATCATATGGATCATAAGGTACAGCCGAAGTCATTGTTTCAAGAGGATAGAT
GGATTGACTAAGGGTACAGTACGGCAAAAAAATTAGATCAGCTTTTCAAACAAACTA
TTTTGGCGTTTACCAAACCAAACAGTATATTCAACTAGTTCAATCACTCTTGAAAACG
TCCCCTTTCTACAAAATTAGGCTTTGAACCGGTGCTATGGAAAAAGTGTAAGAAAACG
AAAAAACAGAAAAGTCATATATATCTTATAACGAAATATCAGGGTGTTCGACTCAATCG
CCAGGTGCCGTAAACACAATCATTAGGATAGTCGGGCAATATATACGGTTCAATAGTCAC
TGAAAGTGTTATCACAGAATAATGACAAAGCTACAAGGACTACAGGGATTAAAACACATCA
AAGCGGTTGTATTTGATATGGATGGCACATTATGCCTACCCAGCCTTGGATGTTTCCAG
CAATGAGAAACGCCATAGGATTGGAGGACAAATCGATTGATATCCTTCATTTTCAATTGATA
CATTTGCCACAGAAAAAGAAAAAAGAAGCGCATGATAGAATAGAATTAGTTGAGGCAA
AAGCCATGAAGGAGATGCAACCGCAGCCTGGTCTGGTTGACATAATGAGGTATTTGACGA
AAAATGGTATTAGCAAGACATATGTACTAGAAATGTCGGAGCCCCGGTAGAGACTTTTG
TTAAAAGATTTATTCATCCGAGCTTTTCGAGGTTTGACTATATTGTGACAAGGGAGTTTA
GGCCTACAAAACCGCAACCAGACCCATTATTACACATCGCCTCGAAGCTAAATATAAGGC
CCTTGGAATGATCATGGTAGGAGATTCAATTGACGACATGAAATCCGGTAGATCTGCTG
GATGTTTACGGTATTACTCAAGAATCATGTGAATGGACATTTACTGCTCGAACATAAAG
AACTAGTAGACGTTTCACTAGAGGATCTTTCCGAAATAATTGAATTGATTCAAATATGA
ATAAAGAAAGTTTCTAA

>YOR131C, 218 aa (SEQ ID NO 360)

MTKLQGLQGLKHIKAVVFDMDGTLCLPQPMFPAMRNAIGLEDKSIDILHFDITLPTEKE
KKEAHDRIELVEAKAMKEMQPQPLVDIMRYLTKNIGSKNICTRNVGAPVETFVKRFIPS
ELSRFDYIVTREFRPTKPQPDLLHIA SKLNIRPLEMIMVGDSFDDMKSGRSAGCFTVLL
KNHVNGHLLLEHKELVDVSVEDLSEIIELIQNMNKESF

>YOR286W, 950 bp, CDS: 501-950 (SEQ ID NO 367)

CATCTGAGTACTCGATTGTTTCATATTCCTGCTTCCATCAATGTGCCATATAGATCGCACC
CTGACGCATTTGCCTTAGATCCTTTAGAAATTTGAGAAACAGATTGGCATCCCAAACCTG
ACAGTGCCAAGGAGCTAATATTTTATTGTGCTTCTGGCAAACGCGGGGAGAAGCTCAA
AAGTCGCCTCCTCATGGATATTCAAACACCTCACTATATCCTGGCTCTATGAATGATT
GGGTTTCTCATGGGGGTGATAAACTTGACTTATAGCCTTGTATACTCTAGGTATGTACCC
TGTGTATTTTCGTAAGCTAGTAACGTATTATGCCATTTATGTCACACCGTTTCATAATATT
TGCCTATTGCATTGGCTGTGATAGCGCGCGCAAAGAAATTAGGAAGTATAAAAAA
AATACAAAACCTTAATCTGAATGGAATAAGATAGCGATAACTCTCAACAAATGGAAGCGAG
ACAGAAGAAAAAGACCAACGATGTTCAAGCATAGTACAGGTATTCTCTCGAGGACAGTTT
CTGCAAGATCGCCTACATTGGTCTTGAGAACATTTACAACGAAGGCTCCAAAGATCTATA
CTTTTGACCAGGTCAGGAACCTAGTCGAACACCCCAATGATAAAAACTATTGGTAGATG
TAAGGGAACCCAAGGAAGTAAAGGATTACAAGATGCCAACTACAATAAATATTCCGGTGA
ATAGTGGCCCTGGCGCTCTTGGATTGCCGAAAAGGAGTTTCAAAAAGTTTTCAAATTTG
CTAAACCACCTCACGATAAAGAATTGATTTTCTTTGTGCGAAAGGAGTAAGAGCCAAAA
CTGCCGAAGAGTTGGCTCGATCTTATGGGTACGAAAACACTGGTATCTATCCTGGTTCTA
TTACTGAGTGGTTAGCTAAAGGTGGTGTGACGTTAAGCCCAAAAAATAA

>YOR286W, 149 aa (SEQ ID NO 368)

MFKHSTGILSRTVSARSPTLVLRFTTTKAPKIYTFDQVRNLVEHPNDKLLVDVREPKEV
KDYKMPPTTINIPVNSAPGALGLPEKEFHKVQFAKPPHDKELIFLCAKGVRAKTAEELAR
SYGYENTGIYPGSITEWLAKGGADV KPKK

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>YOR382W, 962 bp, CDS: 501-962 (SEQ ID NO 375)

AGTAAGCTCCTACAGTGAAATATCTGGGTGCTACTGACGCCAAGCCCTACAGCGATCGGA
ATGCGGGAACGGAAGTTAACGGGGCTTCCAGAACGGCGGAAGCGAATTGAACGAGGACGG
CAAACAAAAACACCCAAAATTTCTATTACTTAGAATGACCCTCAAGAGCAGGGTGCAATTT
ATCAAGCGATCATTGAACTAACTAAGTTCATATCCTGTATAGGATTTAAAACAATGCACC
CTAAGTTCAAATGCACCCCCCTCGCCCCGAGCGGACCCTTGAACAGAGAAC TGTTTCG
AGGTTACCCCAATTGGATCACTTGTATAATTTGTAATCGAGTTCCGATAAGATGTATACG
AATCTAACTGGGTGCAGTATAATTAGCATTTTATATTACCTAGCAATATATGTATAAAAC
AGGAATGTGTGCGTGCTTCAGGCAGAATTTACGGTCCTTGTAAGAAAGTCTATCATAAA
GCCATCACAAAACAATAATAATGAAATTTCTCAACTATTTTCGGAGCTACTACAGTTATGA
CTGCCGTCTCGGCAGCAGCTGTGTGAGTGTAATGACCACTAAGACTATTACTGCTACTA
ACGGTAATAAGTTTACACTAAGTTCGTTACCGACACCGCTGACCCTATCATTTGTACA
GTACCCTAGAACTGTCTGTTGTGAGTAATAGTGATGCTACTTACACAAAGGTTGTCCCG
AAGGACCAGATACCACCTCTGAAAAGAGTACAACAAAGACACTTACTTTGACAAACGGTT
CAGGTTTCATCAACCAACCTTTACACCAAGACCGTCACTCAAGCCGTGCAATCATCTACAT
CCTCCTCATCCTCCTCATCCTCCTCCTCCTCCTCCTGCTCCTCCTCCTGCTGCTCCTG
CTGCATTCCAAGGAGCAAGTGTGCGGTGCATTGGCCCTTGGTTTGATTTCTTACCTATTAT
AA

>YOR382W, 153 aa (SEQ ID NO 376)

MKFSTIFGATTVM TAVSAAVSSVMTTKTITATNGNNVYTKVVTD TADPIISYSTTRTVV
VSNSDATYTKVVTGPD TTTSEKSTTKTLTLTNGSGSSTNLYTKVTQAVESSTSSSSSSS
SSSSSSSSGAAPAFQGASV GALALGLISYLL

>YPL078C, 1235 bp, CDS: 501-1235 (SEQ ID NO 379)

TAAACTGTGTTGTGACGCAACTGCAACTCCCAGATGAAATACGGTCCGGTAAAGATAGGA
ATATTCTACTCTACAAGCATGAATATTTTAAACGCGGCGCAGTACTATACAGCATAACA
GGTCTTCCACGCATGAGAACTGTCCATGGCTAAATTAGTTCCTCACACAGAATTAGAAA
TGTGCTGTGACAAATGGCACATACGTAGATAAAAGATAAATATAATTGAGAATGGCTGTGG
CGACACTATTATCATAGAGGTGTCCCATCGAGCGAGCCTCATTGGCCGGGTAATCGACA
TCAATATTGAACCAATCACGACGCTTTTTCTCTTCACCGCTCATTCCGACCTTCACCACA
GGTTTGGGTAATTAAAATAGCAAGGGATTATAATTGCAGTTAGCAGTTTATGTTGACAAG
TTTATACTGTGCTAGGAAGGGTTATATTTTATTAAAAGACTGACGAGAATTCAGTACCTC
CTAAGTGCGCAAGAGATAAAATGAGCATGAGTATGGGTGTCCGTGGCCTAGCGTTAAGGT
CCGTTTCTAAAACATTATTTAGCCAAGGTGTTTCGTTGTCTTCGATGGTGATTGGAGCCC
GTTATATGTCTTCCACTCCAGAAAAACAGACAGATCCAAAAGCAAAGGCTAACTCTATCA
TCAATGCCATTCCAGGTAATAATATTTTGACAAAGACGGGGGTTTTGGGGACTTCTGCTG
CCGCTGTCAATTTATGCCATTTCCAATGAATTGTACGTTATCAACGATGAAAGTATTTTAT
TGCTGACTTTTTTGGGTTTCACTGGTTTAGTGGCAAAGTATTTGGCGCCAGCATATAAAG
ATTTTGGCGATGCAAGAATGAAGAAAGTCTCCGACGTTTTAAATGCCTCGAGAAACAAGC
ATGTCGAAGCTGTTAAAGATAGAATCGACTCTGTCTCTCAACTACAAAATGTTTGCTGAAA
CTACAAAGGTTTTGTTTGATGTTTCCAAGGAACTGTTGAACTTGAAAGCGAAGCCTTTG
AATTGAAACAAAAGGTAGAATTAGCTCACGAAGCAAAGGCAGTCTTAGATTTCGTGGGTTA
GATATGAAGCTTCCTTGCGTCAATTGGAACAAAGGCAACTAGCAAAATCTGTCTATCTCA
GAGTTCACTCAGAAATTGGGTAATCCAAAATTCGAAGAGAAAGTTTTGCAACAGTCTATAT
CTGAAATTGAACAATTGCTTTCTAAATTGAAGTAA

>YPL078C, 244 aa (SEQ ID NO 380)

MSMSGVRGLALRSVSKTLFSQGVRCPSMVIGARYMSSTPEKQTD PKAKANSIINAIPGN
NILTKTGLVLTSAAAVIYAI SNELYVINDESILLTFLGFTGLVAKYLAPAYKDFADARM
KKVSDVLNASRNKHVEAVKDRIDSVSQ LQNV AETTKVLF DVSKETVELESEAFELKQKVE
LAHEAKAVLDSWVRYEASLRQLERQLAKSVISRVS ELGNPKFQEKVLQQSISEIEQLL
SKLK

>YPL085W, 7088 bp, CDS: 501-7088 (SEQ ID NO 383)

TTTTTCATGAGGAAGAGCCAGTGACAGTAAATAATAAAAGGTGAAATGATTAAACAATGA

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AAGCGGCAGAAAAATAAAATCAAACAGTGGCAGTATTGACTTTTGAAAAATCAGAAGTTCA
TCCTAAGTTAAGACTTTCTTCTTTTAAGTGCTTTCTCCTTCTCTCACTGTCTTATCGCTG
TATATCTCATTGTTGAATAATATAACACAACGTTATAAGTGATCATCACTTTCTGATCCA
TAATTTCAAACCTCAAGCGACCGTACATGTGGCATTTCCTACTATAAACTTACGAGCAAG
AGAAAGATATACGGAAAAGGTTAATTGGCAGGTTACACAAGATTTTGGTCATTGAATATT
TGCAGCCCTCCTGCTTGAGAACTGGACAACAACCTGTTATCAATATTCCCTTTTCAAAT
AGTGGTATTTAACTGGCCATAACCAAGGAAAACCGTTGTACCTATTATTTTGTATAGTCTT
CATTTAATAACGTGTTAAGAATGACACCTGAAGCCAAGAAAAGGAAAAACCAAAAAGAAG
AGTTGAAGCAAAAAGCAAAAAAAGCTGCTGAGAAAGCTGCTAGCCACAGTGAAGAACCAC
TTGAATTACCAGAAAGTACGATTAACAGCAGCTTCAACGACGACTCGGTGAACCGTACAG
AATCTGACATAGCTTCAAATCTGATGTTCTCCGGTCTCATCATCTACCAATATCTCTC
CGGCTAATGAAACACAACCTAGAAATACCTGATACTCAAGAATTGCATCATAAACTGCTCA
ACGACTCTGATCAACATGATATTACCGCGGACTCAAATGATTGCGCAGACAACCTCAATCG
TTGAACATGACTCTGTTATTACCCAAACAAAACCAAGCCATGCTCTCAAGAATACGAAGAT
CTGCCGCTCACTTATCTTCGAGAAATCCATCGCTCGATGTAGTCGCGGAGAACTTCACA
ATAATAATGAACATACCCAGAAAATTGCCGTATCCGCTGTGGAAGAGGATTCTTTCAATG
AAGAAGAGGGGTGAAAATCACGACAGCATAATAATTTTCATCATTAACGATGCTACCCCTT
CTCAATATAATCATTTTCTCCCATCCGATGGCAATCTTCTTTCTCCAGAATTATCTTCTG
GTGATACGCCAACTCACAATGTTCTCTAGGCACAAAAGACAATGAAATAAATGACGATG
AGTATTGTAATGATAAGGAAATTAGTTTGAACGCAATAATGTGCTTCTGTATGAACCTT
CAAAGGAAGAAGATGAAAGATTAAACTAGAAACGCATGTATCAACCGAAGAAAAGAAAC
AGGATATCGCTGATCAGGAACTGCAGAAAACCTTATTTACGTCTAGTACAGAACCATCTG
AGAATAAAATAAGAAATTCTGGTGATGATACCTCCATGTTGTTTCAAGATGACGAAAGTG
ATCAGAAGGTTCCATGGGAGGAAGATGTGAAGAAAAGATTTTCATAATGAGAACACAAATA
ATACTCAAGAATCGGCACCGAACACAGATGATCGTGATAAGGGTTATGAAGGAAACGAAG
CTTTGAAAAAGTCCGAAAAGTTGTACAGCCGCGGACGAGAGGTCGTACTCTGAAGAAAACCT
CAGAAGATATCTTTCACGGACACGACAAAACAGGTAGTTGAAGGCCAAAATGATTTCACTG
GGAAAAATATTGAGAATGAAAGCCAGAAATTAATGGGGGAAGGGAATCATAAGTTACCGT
TGTCTGCCGAAGCTGACATTATAGAACCTGGTAAGGATATTCAAGATCAAGCCGAGGATT
TGTTTTACGACAGACGCGGAGACTTGGGAGAAGTTTGGCATGGGAATCTACTGATAAAA
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CACGACAGGAAAATAATCCAATTAAAATAGACAACGAGGCTTTATTACGCCGTCAATTTTC
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AAAGTTCCGGCACCACCCTCTCCAATCGTGAACGTAAGATGGCGGCCCAAGACAA

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AGCCACGTTTCAGGCCCATCAATAATTCCTACCTCCAGTACATGCCACATCAGTTATTC
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CCAATCCAAACAATTCTCCATCACCATCCTCTCCCATATCAAGGATTTCTGGCGTAAACT
TGACTAGCAAAAAGGCAAACGGTTTGGATGATTTATTGAGTTTGGCAGGAGGACCCAAAC
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TACAATAA

>YPL085W, 2195 aa (SEQ ID NO 384)

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EVS DGEVSSGKTENSMQTSTEKIAEQKFSFLENDDDLLDDDDSLASSEEDTVPNTDNT
TNLT SKPVEEKASRYKPIIEEEAGMRQEQVHFTNTTGIVTPQQPHGLTKTGLGTPNQV
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SASIQPHANIQPPTGILPLAPLRPLDPLQAATNLQPRASNITAANSLPLANLPLAENILP
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PPP KIGVPTKANSSQGS LMYSPSVEALPIDPVVPQVHETGYNDFGNKHSQKSMPEDESHT
SHDN SNADQNTL KDSADVTDETM DIEGPGFNDVKNLLPMEPNHQPTSTVNPIQTI SDDIQ
PILQTNVEVRGTDASKMENS LPSIENERSSEEQENISKSASSAYLPSTGGLSLENRPLT
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>YPL190C, 2909 bp, CDS: 501-2909 (SEQ ID NO 387)

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ATAATAACCATCTGCAAGCCATGTCAGATGAAAACCATAACAGTGATGTTCAAGATATTC

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CTTCACCTGAACTATCCGTCGATAGTAACCTCTAACGAGAATGAATTGATGAATAACTCAA
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>YPL190C, 802 aa (SEQ ID NO 388)

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DDAVAIFNNIKNNRNSRPTDYRAMSHQQNIYGAPPLPVPNGPAVGPPPQTNYQQYQYSMP
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>YPL201C, 1886 bp, CDS: 501-1886 (SEQ ID NO 389)

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>YPL201C, 461 aa (SEQ ID NO 390)

MGIPMQIYQDGKGVQFYHTRYQNVFDERASKYGNVTVNNDYPQLPDTIKEHIDQLTFSNV
GEDGGDVGNYSSEDDDGDEEKELEDVFRSNRGLFVRINNYFTTHDLQSFKSRNFNSKY
WIFYSNQAEDKKLLLYDFNGQHLIFIKQQFYGQLNLLLSDAIICMDCNFGYNSNTIQILV
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ITSLDHQQSNGSFQSFHTNIDLPLVLRITTNVKSVLNFPQFTLYKGNMDMIFHCKNLLGSD
ASTLNKEINFMLKIDEDVQKIDYLLKTNHILLETNMRYLSIPTDPIENSNSPPVSDSE
VYPIFYKTQELHVHASGTGRQIANNGKYIFITEQHLYGTALSVYKYSISFKRWLFVGYSD
IRAKYGIRSVKDLFVGNCPVSNPVLTLTDDNNIQTILLK

>YPR028W, 1176 bp, exon1: 501-551, intron1: 552-684, exon2:
685-1176 (SEQ ID NO 393)

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GACATAACCGCACTCCAATCATGTCCGAATATGCATCTAGTATTCACTCTCAAATGAAAC
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CAATGACCCGACACACGTAACCGAAGCAGTTATACTAACAAGAAAGCTAATTTTCACCC
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>YPR028W, 180 aa (SEQ ID NO 394)

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YDR145W, 2120 bp, CDS: 501-2120 (SEQ ID NO 99)

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CAAATGAATATCACGATTTTGGCTGTATTACCCGGGCAGTATACGCGGCG
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GCATATATAGCGCATAGGTTGCTAGTGTAAAGACAGGAGACTGTCCAATA
GCATTGCAATCATAACCGAATCTTTGCCAGTGTGTGTATAAAATACGACA
ATGTCTTCCAATCCAGAAAATCTGGTGTAAATGCGAATAATAATACGGG
CACTGGTAACGCTGATGCGATCACAGGAGCTCAGCAAATATGGTACTGC
AACCAGAGACAGTTGCAAGAAATGGCCGCTAAGTTTCAAGACATTACTGACT
GAAGCAAGAAATGTAGGTGAAACTACTCCTAGGGGCAAGGAATTGATGTT
CCAAGCCGCAAGATCAAACAGGTATATGATGCCCTTACACTGAATAGGA
GAAGACAACAGGCTGCGCAAGCCTACAATAATACTTCAAATTCAAATTCA
AGCAATCCAGCTTCTATTCTACTGAAAATGTCCCTAATTCATCACAGCA
ACAACAACAACAACAACAACAGACAAGAAACAACAGTAACAAATTTAGCA
ATATGATAAAACAGGTTCTCACCCCGGAAGAGAACCAAGAATATGAAAAG
CTATGGCAGAATTTCCAAGTCCGTATACGAGTATAAAGGAGAAAGAGAC
CTACTTGAAACAAAATATTGATAGGTTAGAACAAGAAATAAATAAACAGA
CGGACGAAGGGCCCAAGCAGCAGCTACAAGAAAAGAAAATTGAACTGCTT
AACGATTGGAAGGTGCTAAAAATTGAGTATACCAAGCTGTTCAATAATTA
TCAAAACAGTAAAAAACATTCTATGTAGAGTGTGCAAGACACAATCCGG
CTTTACATAAATTTTGAAGAAAGCACTCAACAGCAACGAGTGCAGCAA
CAAAGGGTACAACAACAACAACAACAACAGCAGCAGCAGCAACAGCA
GCAACAGCAACAGCAACAGCAACAGCAACGCCAGGGTCAAACCAAAGAA
AGATTTCTAGTTCTAATTCTACTGAAATACCCTCTGTAACCGGCCCTGAT
GCACTGAAATCGCAGCAGCAGCAGCAATAACAATAACTGCCACCAATAA
TCCCAGGGGCAATGTTAACTTCACTTACAGACTGAACAATCGAAAGCTAAGG
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AAATCGGCAATATTCAAACAACAGAGCCTGCCATACCCATATCGGAAAA
TATATCTACCAAAACACCAGCACCGGTAGCTTATAGATCCAACAGACCTA
CAATAACTGGAGGTTCTGCTATGAATGCCAGTGCTTTGAATACACCAGCA
ACAATAAATTACCACCCTATGAAATGGATACTCAGAGAGTTATGTCAA
GCGTAAATTAAGAGAGTTAGTGAAGACTGTCGGAATTGATGAGGGTGACG
GTGAAACTGTCATTGACGGTGATGTTGAGGAATTACTATTGGATCTTGCC
GACGATTTTGTTACTAATGTTACAGCTTTTTCTTGATAGATTGGCAAAACA
CAGAAAATCGGACAATTTGGAGGCAAGAGACATTCAATTACATTTGGAGA

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GAAATTGGAATATTAGGATTCTCTGGTTATTCCGCAGACGAAATAAGAAGT
ACAAGAAAATGGAATCCCTCTCAAAATTATAACCAGAAATTGCAGAGTAT
CACATCAGATAAGGTAGCAGCTGCAAAAAACAATGGAAACAATGTTGCAA
GCTTGAATACAAAAAATAA

YDR145W, 539 aa (SEQ ID NO 100)

MSSNPENSGVNNANNNTGTGNADAITGAQONMVLQPRQLQEMAAKFRTLTLT
EARNVGETTPRGKELMFQAAIKQVYDALTLNRRRQQAQAYNNTSNSNS
SNPASIPTENVPNSSQQQQQQQQQTRNNSNKFNNMIKQVLTPEENQEYK
LWQNFQVRHTSIKEKETYLKQONIDRLEQEINKQTDEGPKQQLQEKKIELL
NDWKVLKIEYTKLFNNYQNSKKTFFVECARHNPALHKFLQESTQQQRVQQ
QRVQQ
ALKSQQQQQNTITATNNPRGNVNTSQTEQSKAKVTNVNATASMLNNISS
KSAIFKQTEPAIPISENISTKTPAPVAYRSNRPTITGGSAMNASALNTPA
TTKLPPYEMDTQVRMSKRKLRELVKTVGIDEGDGETVIDGDVEELLLDLA
DDFVTNVTAFCRLAKHRKSDNLEARDIQLHLERNWNIRIPGYSADERS
TRKWNPSQNYNQKLQSITSDKVAAAKNNGNNVASLNTKK

YDR216W, 4472bp, CDS: 501-4472 (SEQ ID NO 109)

CAAAGAACAACGCCTTAAAAATAGGAAAACGTTTTTCGCTACAGGTGTTGT
TATTATTGTTGTTGTGCTGTTGTTTATTGTGCTATACTTGTGGTATTTAT
TCTGGACTTCCGATCGGAAATTTTCTTCCCTTGAAGACCTTTTGAAGACA
ACAGTTATATATCATTTGATCTGAATTTCTCAGGCTATTTTCAAATTTCCA
TACCTCCTTATTCCAACATTTGCTCGACTACTATAGAAAAGCCTTATTCT
TTTATCTTTGAAAGAAAGAAAAGGTGTCATAGCAAAGTTTATTTGTACT
CTGTTTTGATATACTCCCTCTTATTCTGTTGGAAGTATAAGATTGATTTGC
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ACACTTCAGAAAAATATTCTGCTACTATTCTTACTTTACTATAAGAATT
TTGTTTTTCCAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATA
ATGGCTAACGTAGAAAAACCAAACGATTGTTTCAAGGCTTTCCCGTTGTTGA
CTTGAATTCGTGCTTTTCTAACGGCTTCAATAATGAGAAACAAGAAATAG
AAATGGAAACGGATGATTCACCGATTTTATTAATGTCATCATCAGCTTCC
AGAGAAAACCTCAAACACTTTCTCTGTGATACAGAGGACGCCAGATGGAAA
GATCATTACCACAAATAATAATGAAGTCCAAGATTAACAAGCAACTGG
ACAAGTTGCCCGAAAATTTAAGGCTTAATGGTAGAACCCCAAGTGGGAAA
CTAAGGTCAATTTGTTTGCAGAGTTTGTACGAGAGCGTTTCGCAAGACAAGA
GCACTTGAAAAGACATTACAGATCGCATACAAATGAAAACCTTATCCCT
GTGGCCTCTGCAACAGATGCTTTACTAGGAGGGACTTACTGATCAGGCAT
GCTCAAAAAATCCATAGTGGTAATTTAGGGGAAACGATTTCCCATACCAA
GAAAGTGTGCGAAGTATAACTAAAGCTCGGAAAAATTTCTGCATCCTCAG
TCAAGTTTCAAACCTCAACCTATGGTACTCCAGATAATGGTAATTTTGTG
AATCGCACTACTGCCAATACAAGAAGAAAAGCAAGCCCTGAAGCTAATGT
TAAACGTAAGTACTTGAAAAAAGTACGCGCAGGGCTTCATTTAGCGCAC
AATCAGCATCCAGCTATGCTTTGCCCGACCAATCTTCGCTAGAACAACAT
CCAAAGGATCGTGTTAAATTTTCTACGCCTGAATTAGTTCCACTTGACTT
GAAGAATCCTGAACCTTGACTCTTCGTTTGACCTGAATATGAATCTAGATT
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TCTTCTGGATCAACAATGAATTTGGATTATAAATTGCCCGAATCAGCAAA
TAACTACACATATTCTTCCGGCTCACCAACCCGCGCATATGTGCGCGCTA
ACACGAATTCTAAGAACGCTTCATTTAATGACGCAGACTTATTGTGCTCG
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TGATGAAACTTCTCCAATGAAGTCTGAATTAAACGACACTAAATTAATCG
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TCTTGGACTGTTGCTATAGATAATAATAGCAATAACAATAAGGTATCAGA
CAACCAACCTGATTTGCTCGATTTTCAAGAAGTCTGGATAATGATACTT
TAGGTAATGATTTGTTAGAGACCACTGCCGTTTTTAAAGAATTTGAAGT

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TTACATGATGATAGCGTAAGTGCTACCGCCACGTCAAATGAGATTGACCT
TTCCCATTTGAACCTATCAAACCTCTCCAATTTCTCCTCATAAGTTAATTT
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GATCATCCTTCCAATCGCGAAGATGATCTGGATAAGCTATGTAATATGAC
CAGAGATGTTCAAGCCATATTCAGTCAATATTTGAAAGGAGAAGAGTCTA
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GATAGCGGCAACTATACTTTTTATGGGTTAGATTGTTTAACGTTATCGAA
AATATCAAGAGCTCTGCCGGCCTCCACTGTGAACAACAATCAGCCATCGC
ATTCCATAGAATCAAAGCTATTTAATGAACCAATGAGAAATATGTGCATT
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CATGGACTCTAATCCAAACTTGCTGTCCAAAGAATTGTTAATGCCAGCTG
TGAGTGAATTGAACGAATATTTAGATCTTTTCAAGAATAATTTCCCTCCC
CATTTCCCTATTATTCACCCAAGCTTGCTTGATTGGATTGGATAGCTT
GCAACGATATACTAATGAGGATGGGTATGATGACGCTGAAAACGCGCAGT
TGTTTGATCGATTAAAGTCAAGGGACAGATAAAGAATATGATTACGAGCAC
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TGTATGAGATGAGTAGAAGAATTCTACATTCTTTTTTGGAGACTAAAAGA
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AGAAAATTGACTCCTCTTTGATGAAAAGGCAATTGTCCGCATTATGTTCA
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CAGTTCTTGAAATGTTTCTTCCATATTAAATTCGATTTGTCTATAAAGGA
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GTGAATCGATAATATGTAATGGGCATGTTGTGCAAAAGCAAAATTTTTAT
GATTTTAGAACTTTTATTACAGTTTCACGTATGGACACTTACACTCAAT
ACCAGAATTTTAGGGTCATCTATGATTTATTATGAATACGATTTAAGAA
AAGGAACCAAATCACATGTGTTTTTGGATCGAATCGATACGAAAAGGCTA
GAGAGGATCTTGACACTTCTTCCATGGCAATGATAATATGGCAGCAAC
CAATAAAAAATTGCGATCTTAATTGATGACACCATAATTTTGAAAAATA
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TTTTAGTAGCGTTGAACTTTTCAATCCGTAATATTTGCTCTTTATACGTA
GAAGAAGAAAGTGATTGCTCCCAAAGAATGAATCTCCAGAGCTGCCAAG
GATCCACCTGAATAATCAAGCGCTTCTGTCTTCAATTTACAAGGCTATT
ACTATTGCTTCATCCTAATTATCAAATTTTTATTGGATTTTGAAGCAACT
CCAAATTTTAAGTTACTGAGAATTTTTATTGAGTTGAGAAGCCTTGCGAA
TTCTATTTTACTTCCCACACTTTCAAGATTGTATCCGCAAGAGTTTTCTG
GATTTCCCTGATGTTGTATTTACGCAACAATTTATAAATAAAGATAATGGT
ATGCTTGTCCTGGTTTATCCGCAAATGAACACCATAATGGTGCAAGTGC
AGCTGTTAAGACTAAGTTAGCCAAAAGATCAATGTTGAAGGGCTTGCAA
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AATATGGAGGATCCTATTCGAAATGAATTTTCTTTGATAATGGGGACAG
GGCAGTGACAGACTTGCCCTCGTTTCAGCACATTTCTATCGGATACCGGCC
TAGAAGGATTTAACTTCAGCGGCTTAAATGATTTCGCATCAAACGTGTTCT
ACTTTGAATCTTTTACGTTACGGGGAAAATCATTCATCAAACATAAAAA
TGGTGGAAGGGGCAAGGATTTGCCGAAAAGTACCAATTATCTCTGAAAT
ATGTTACTATTGCCAAGTTATTTTTTACCAATGTTAAAGAAAACATATT
CATTGTACATGTTAGATAAGATGGCAAGTGATTTCACACTTTGGAAAA
TCATCTAAAGGGAAACAGTTGA

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YDR216W, 1323 aa (SEQ ID NO 110)
MANVEKPNDCSGFPVVDLNSCFNNGFNNEKQEIEMETDDSPILLMSSSAS
RENSNTFSVIQRTPDGKIITNNNMNSKINKQLDKLPENLRNLNGRTPSGK
LRSFVCEVCTRAFARQEHKLRHYRSHNTNEKPYPCGLCNRCFTRRDLLIRH
AQKIHSNGLGETISHTKKVSRITITKARKNSASSVKFQTPTYGTPDNGNFL
NRTTANTRRKASPEANVKRKYLLKLTRRASFSAQSASSYALPDQSSLEQH
PKDRVKFSTPELVPLDLKNPELDSSFDLNMNLDLNLNLDNLFNIALNRS
SSGSTMNLDYKLPESANNYTYSSGSPTRAYVGANTNSKNASFNADLLSS
SYWIKAYNDHLFSVSEDETSPMNSELNDTKLIVPDFKSTIHHLKDSRSS
SWTVAIDNNSNNKVSNDQPDFVDFQELLDNDTLGNDLLETTAVLKEFEL
LHDDSVSATATSNEIDLSHLNLNSPISPHKLIYKNKEGTNDMDLISFGL
DHPSNREDDLDKLCNMTRDVQAFISQYLKGEESKRSLEDFLSTSNRKEKP
DSGNYTFYGLDCLTLKISRALPASTVNNNQPSHSIESKLFNEPMRNMCI
KVLRYYEKFSHDSSSEVMDSNPNLLSKELMPAVSELNEYLDLDFKNFLP
HFPIIHPSLLDLDSLQRYTNEDGYDDAENAQLFDRLSQGTDKKEYDYEH
YQILSISKIVCLPLFMATFGSLHKFGYKSQTIELYEMSRRLHSFLETKR
RCRSTTVNDSYQNIWLMQSLILSFMFALVADYLEKIDSSLMKRQLSALCS
TIRSNCLPTISANSEKSINNNEPLTFGSPLQYIIFESKIRCTLMAYDFC
QFLKCFHFIKFDLSIKEKDVETIYIPDNESKWASESIICNGHVQKQNFY
DFRNFFYYSFTYGHLSIPEFLGSSMIYYEYDLRKGTKSHVFLDRIDTKRL
ERSLDTSSYGNDNMAATNKNIAILIDDTIILKNNLMSMRFIKQIDRSFTE
KVRKGQIAKIYDSFLNSVRLNFLKNYSVEVLCEFLVALNFSIRNISSLYV
EEESDCSQRMNSPELPRHLNNQALSVEFLQGYCYCFILIIKFLLDFEAT
PNFKLLRIFIELRSLANSILLPTLSRLYPQEFSGFPDVVFTQQFINKDNG
MLVPGLSANEHNGASAAVKTAKKINVEGLAMFINEILVNSFNDSFSL
NMEDPIRNEFSFDNGDRAVTDLPRSAHFLSDTGLEINFSGLNDSHQTVS
TLNLLRYGENHSSKHKNGGKGQFAEKYQLSLKYVTIAKLFFTNVKENYI
HCHMLDKMASDFHTLENHLKGNS

YBR112C, 3401 bp, CDS: 501-3401 (SEQ ID NO 51)
GGGTGCCGTATCGGCTCTAATTATTTTATCTCTCTATTTTCTTTCTTTTC
TCTGCGCTACTCCTTTCTCGATCGTTGCTACTCCCGTCGCTAGCCACTGG
TCTCCCGCGTACTGTACTCCATCTTTTTTTGGCGTTTTTCCCCTATCCAA
CTCGAACAAGGTTTGTAAATTTATTTTATTTTCTTTCTTCGGTCGG
TCGTTCTTTTCCCTTCCGATTATCAAAGCAAAGCGCATTTTTTCTTTG
TCTTTTTGTGTTTTGTTTCTGTTCTCTGTTTTTTTACAAACCACGTCAG
GAGTTCAATTGAGAGAACTAGAATCAACAAAGCCAAATACGACAACGTCA
CTAGTCTTTGAACCAGAGGCGTATTCCCGTTACCTCTTTTCCCATATTTT
TGTTTTTCTTTTTCACTGCTATAAGCCTTTAGACTAGTACTACAACCTACA
ACAGCAACAACAACAACAAAACACGACTGGAAAAAAAAAATTAGGAAAA
ATGAATCCGGGCGGTGAACAAACAATAATGGAACAACCCGCTCAACAGCA
ACAACAACAGCAACAACAACAGCAGCAACAGCAACAGCAGGCAGCAGTTC
CTCAGCAGCCACTCGACCCATTAAACAAATCAACTGCGGAAACTTGGCTC
TCCATTGCTTCTTTGGCAGAAACCCTTGGTGATGGCGACAGGGCCGCAAT
GGCATATGACGCCACTTTACAGTTCAATCCCTCATCTGCAAAGGCTTTAA
CATCTTTGGCTCACTTGTACCGTTCCAGAGACATGTTCCAAAGAGCTGCA
GAATTATATGAAAGAGCACTTTTGGTAAATCCCGAATATCAGATGTGTG
GGCTACTTTAGGTCAATTGTTATCTGATGCTGGATGATCTGCAAAGAGCTT
ACAATGCCCTATCAACAGGCTCTCTACCACCTCAGTAATCCCAACGTACCG
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CTATGCCGAAGAAGCTTTTGCCAAAGTTTGGAAATGGACCCTCATTTTG
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GGTAAATGGTCTCAAGCTTTGGAATGCTTCAGATACATTCTCCCTCAACC
TCCTGCTCCCTTGCAGGAGTGGGACATATGGTTTCAGTTGGGTAGTGTTC
TGGAGAGTATGGGAGAGTGGCAAGGTGCGAAGGAAGCCTACGAGCATGTC
TTGGCTCAAAATCAACATCATGCCAAAGTATTACAACAATTAGGTTGTCT

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TTACGGTATGAGTAAACGCTACAATTTTATGACCCCTCAAAGGCCATTGGGATT
ATCTTCTTAAAGTCGTTAGAAGCAGATCCCTCCGATGCCACTACATGGTAC
CATCTCGGTAGAGTGCATATGATTAGAACAGATTATACTGCCGCATATGA
TGCTTTTCCAACAAGCTGTTAATAGAGATTCAAGAAACCCTATCTTTTGGT
GCTCAATCGGTGTTTTATATTACCAAATTTCTCAATACAGAGACGCCTTA
GACGCGTACACAAGAGCCATAAGATTAAATCCTTATATTAGTGAAGTTTG
GTACGATCTAGGTACTCTTTACGAAACTTGTAACAACCAATTATCTGACG
CCCTTGATGCGTATAAGCAAGCTGCAAGACTGGACGTAAATAATGTTTCA
ATAAGAGAAAAGATTAGAAGCTTTAAACAAAGCAGTTAGAAAACCCAGGCAA
TATAAACAAATCGAACGGTGCGCCAACGAATGCCTCTCCTGCCCCACCTC
CTGTGATTTTACAACCTACCTTACAACCTAATGATCAAGGAAATCCTTTG
AACACTAGAATTTTACGCCAATCTGCCAATGCTACTGCTTCAATGGTACA
ACAACAGCATCCTGCTCAACAAACGCCTATTAACCTCTTCTGCAACAATGT
ACAGTAATGGAGCTTCCCTCAATTACAAGCTCAAGCTCAAGCTCAAGCT
CAAGCACAAGCTCAAGCACAAGCACAAGCTCAAGCACAAGCACAAGCACA
AGCGCAAGCACAAGCACAAGCACAAGCGCGCAAGCACAAGCACAAGCACA
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CAAGCACAAGCGCGCAGGCACAACAACAACAACAACAACAACAACAACA
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AGCAGCAGCAATTACAGCCCCCTACCAAGACAACAGCTGCAGCAAAAGGGA
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TGGAACATCCGCAAAGCTCTCAACTGCCACCTCAACAGCAACAACCTACAA
TCTGTTC AACATCCACAACAACTTCAAGGCCAGCCTCAAGCCCAAGCTCC
CAAACCTTTAATCCAGCATAACGTGGAACAGAACGTTTTTACCTCAAAGA
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AGCACCCACACAGAGAATAACACAAAGTCTCCTCGTCAACCAACCCATGC
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CCACAGGAAGCTAGTCCTGCTGAAGAAGCTACCAAGCAGCTTCTGTTTC
TCCTTCTACAAAACCGCTTAATACGGAACCAGAGTCATCTAGTGTCCAAC
CAACTGTATCATCAGAAAGTTCAACAACAAAAGCAAATGACCAAAGCACT
GCTGAGACCATAGAACTTTCTACTGCTACTGTTTCTGAGAAAGCAAGCCC
TGTAGAAGACGAAGTAAGACAGCATTTCTAAAGAGGAAAACGGCACAACCTG
AAGCATCTGCACCTTCTACTGAAGAGGCGGAGCCAGCAGCTTCCAGAGAT
GCTGAAAAACAACAAGATGAAACCGCTGCTACAACGATAACTGTAATCAA
ACCTACTTTGGAAACAATGGAAACAGTGAAAGAGGAGGCCAAAATGCGTG
AGGAAGAGCAAACATCTCAAGAAAAATCCCCACAGGAGAACACACTTCCA
AGAGAAAATGTAGTAAGGCAAGTGGAAGAAGATGAAAACCTACGACGACTA

YBR112C, 966 aa (SEQ ID NO 52)

[illegible]

YMR043W, 1361 bp, CDS: 501-1361 (SEQ ID NO 305)
AAGCTGTGCCAAACAAGGTCATCTCCAAATACTTACCAAAAAGCTAGGGC
GTACTGTACTGGAATCTCTGCTTTTTTCTTTACCTTACTTCAATTTGCCCT
TGCTGCTTTTTTACGTGTGTTTTGGCGTTTCTGCTTTTCTTTTTTATTA
CTCGTTGTTGTAAATCATTTTCTAAGTATTATACATACTATATCATCGCA
TACCCAATCGGTTTCTTATTCTCACCACCTTTTTTCTGGAAAAATACATAG
CCTAACAAGCAATTTTATTTTACGTTTGTTAATTCAATTACTGATAATA
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CTGTTTTTTTTTCGATTTCAGTTATAGGGAAAAAACGGGAAAGGAAAGAGAA
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ATGTCAGACATCGAAGAAGGTACGCCCTACTAATAATGGGCAACAGAAGGA
GAGAAGAAAGATAGAAATTAAAGTTTCATCGAGATAAAAACAAGGCCCATG
TGACATTTTCCAAAAGGAAGCAGCGTATCATGAAAAAGGCGTTTGAGCTT
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AGCAACAAGTATTGAATGCACACGCAAATAGCTTAGGCCATCTAAATCAA
GATCAGGTACCGGCAGGCGCGCTGAAACAAGAGGTGAAGTCACAATTGCT
AGGCGGTGCCAATCCTAATCAAAACTCAATGATTCAACAGCAGCAACATC
ACACGCAGAATTCACAACCACAACAGCAACAGCAACAACAACCACAGCAG
CAAATGTACAGCAACAAATGTTCACAGCATCCTCGACCACAGCAAGGAAT
ACCACATCCGCAACAATCGCAGCCACAGCAACAGCAACAACAACAAC
AACTGCAACAGCAGCAACAGCAGCAACAACAACAACCCCTCACCGGCATT
CATCAGCCTCACCAACAGGCTTTTGCCAACGCTGCCTCCCCCTATCTGAA
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GCCAATACTAA

YMR043W, 286 aa (SEQ ID NO 306)
MSDIEEGTPTNNGQKERRKIEIKFIENKTRRHVTFSKRKHGIMKKAFEL
SVLTGTQVLLLVVSETGLVYTFSTPKFEPIVTQQEGRNLIQACLNAPDDE
EEDEEEDGDDDDDDDDDDGNDMQRQPPQQQQPQQQQQVLNAHANSLGHLNQ
DQVPAGALKQEVKSQLLGGANPNQNSMIQQQQHHTQNSQPQQQQQQQPQQ
QMSQQQMSQHPRPQQGIPHQQSQPQQQQQQQQQLQQQQQQQQQQPLTGI
HOPHOQAFANAASPYLNAEONAAAYOQYFOEPOGOY

YPL089C, 2531 bp, CDS: 501-2531 (SEQ ID NO 385)
TTCCACGTTTCGCAAAAAATACTTCCACGGTGACGAAGTCTGTCTCAGTCG
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TACTTCAGATTTCTGATAAAAAATAAACGGAAGAGATGAAAGCTAATAAT
AGAAACAGCTCGATCTTCCTCTGAACAATAATAATTAAAGGACAGACAAA
AAGAAACGTAAGAAAGAAGCGAGCCTGTTCTAAAGTGTTCAACGACTGAT
TCAATTAGAAGTGCCTACTCCTGATAGCCAACTCAACTTTTGACTCGTTA

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AAGTAATTGAAAGCTGGCAAGCAGAATTATTCCTTTTTTTTTTTCAAGGTT
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GGCTGTCACGTTTATAAAACGTAAAGCTGGCCTTTTTAAGAAGGCCCATG
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AATAACACGTTCTATGAGTTTTCTCTGTGGATACGAATGATTTAATCTA
TCACTACCAAATGACAAAACCTTGCTTCACGAAGTGAAAGATCCTTCCG
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GAACCAGTCAGAAAATGATGATGATGAGAACAATGATGAGGACGACGATG
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GCCATTTACAAATGCATCCTCAAGGACCCCTAAACAGGAGCACAAAATTA
ACAATAGTGGCAGCAATAATAATGACAACAGCAACTACACTCAGTCACCA
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ATTGTCCGCCAGACCGGTACTTCGTGTGAGAATCCGAACAACAATTTCA
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TTCCAACAAAATACATCTTTTTTTAGCTCAAAGACAAACCCAGCAATACCA
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CCTCCAATGGTTCACTGCCATCGAAGTTCGTACATGATTTGATGAGTAA
TTCTCCAAATGTTTCTTCTATATCGATGTTTCCAGACTGGTCAATGGGAC
CCAACAGTGCCAAGCCGGGAAACACAAACAATCCTGGTACTTTCCCTCCC
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CAACACTAACAACAACAACAATAACAACAACAACAGCAGCAACAACA
ACAGCAACAACGGCAACGACAATAACAGTAACAATAGCAATAACAGTTAC
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TACTACCGATGGTGACTCGAACAATCAGTCCAACCTCAAGTACATATGATG
CTGCTGCCACCGCATATAATGGAAATACCGGGCTGACTCCATACATAAAT
ACTGCTCAAACACCACTAGGCACATAAATCTTTAATTTTTTCGACTGATAT
TTCAGGAGAAAAAATTCAAGCAAAATATAA

YPL089C, 676 aa (SEQ ID NO 386)

MGRRKIEIQIRISDDNRNAVTFIKRKAGLFKKAHEL SVLCQVDIAVII LGS
NNTFYEFSSVDNDLIYHYQNDKNLLHEVKDP SDYGDFHKSASVNINQDL
LRSSMSNPKPSKNVKGMNQSENDDDENDEDDDDHGNFERN SNMHSNKKK
SDKNIPSAHMKLLSPTALISKMDGSEQNKRHPENALPPLQHLKRLKPDPL
QISRTPOQQQQQNI SRPYHSSMYNLNQPSSSSSSPSTMDFPKLPSFQNSS
FNGRPPPI SISPNKFSKPFTNASSRTPKQEHKINNSGNNNDNSNYTQSP
SNSLED SIQQT VKARRKLSARPVLRVRI PNNNFSSNSAIPSEPSSASSTS
ANGNSMGSSQIMKENKTSRSSKISPLSASASGPLTLQKGNNGRMVIKLPN
ANAPNGSNNNGSNNNHFPYFGSGSSPLFSATQPYIATPLQPSNIPGGP
FQQNTSFLAQRQTQQYQQMSFKQSQT VPLTTTLTGRPPSTFSGPETSNG

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PPTGSLPSKFVHDLMSNPVSSI SMFPDWSMGPN SAKPGNTNNPGTFPP
VQTAVNNGNSSNISSTNNTNNNNNNNNNNSSNNNSNNGNDNNSNNSNNSY
YSNNEDAPVNGAAI SEHTTDGDSNNQSNSSSTYDAAATAYNGNTGLTPYIN
TAQTPLGTFKFFNFSTDISGEKNSSKI

YOR372C, 2165 bp, CDS: 501-2165 (SEQ ID NO 371)

AAAATCGTGGTTACTTTTCATATTCCTTAAACACTTTACCACTGTTACTGT
GCGCGTTTCGAGCGTAGCTTTTCGTGGTGAATTTATTGTAAGATTCTCCAGC
TGGCTCGATAGTTCTGCCTCCTGCGTATCCATATCCATTTTCGGTATGCTT
TTACTATTCAACCTAGTCGGCAATTTTTTCACCTGAATATTGTTGAACAC
TTCTGGCATCCTAGATACTCATCTGTATTTATTTCATTATCTGTTGTGCAT
CGTTAATAGCATTCCAGTAAACAAGTTTAGGTCACCTACCCGCATAAGCCT
TTTGGCGTTTGGCGTAACCTCCTCGCGAAAAGAAACGGGACGCAAAAAA
AAAAACAACAAAACAAGAACAACAAAACAACAAATAGGACAGAGCCTTAA
GGAGCTGCAAGGATCTTCTGAATATTTGGCATCGGCATTGTGGGTGGAAA
AAGTGTCCAAATTGGAATAAATTGGTCAGAATAGAGCATTGATTCCAAC
ATGGACAGAGATATAAGCTACCAGCAAAATTATACCTCAACTGGGGCAAC
TGCAACTTCTCAAGACAGCCCTCTACGGACAATAATGCAGATACAAATT
TTTTGAAGGTAATGTCAGAATTCAAATATAATTTTAACAGTCCGTTACCT
ACAACGACTCAATTCCCCACGCCCTATTCTTCTAATCAGTATCAACAGAC
TCAAGATCATTGTTGCCAATACAGACGCTCACAACAGTTCGAGCAACGAAT
CGTCGTTGGTAGAGAACAGTATATTACCGCATCATCAGCAGATACAACAG
CAACAACAACAACAACAACAACAACAACAACAGCAAGCTCTAGGTTTC
ACTTGTACCTCCTGCTGTACAAGGACAGATACAAGTGAGACTTTGGACG
ATATCAACGTTCAACCTTCTTCTGTTTTGCAGTTCGGCAACTCTTTACCC
AGCGAATTTTTGGTTGCATCCCCAGAGCAATTCAAAGAATTTTTGTTGGA
CTCTCCGTCACCAATTTCAATTTCTTTTCAAAAACCTCCGGCAAAGACAC
CACTTCGATTTGTAACAGATTCTAACGGTGCTCAGCAAAGCACCACAGAG
AACCCAGGTCAACAACAGAATGTTTTTAGCAATGTCGATTTGAACAATCT
TTTGAAGAGTAATGGAAAAACACCCTCATCTTCATGCACCGGCGCATTTT
CAGCGACTCCTCTGAGTAAGATTGACATGAATCTCATGTTCAATCAACCG
CTGCCGACTCTCCATCAAAAAGGTTCTCCTCCCTGTCGTTGACACCATA
TGGAAGAAAAATTCTGAATGACGTCGGTACACCTTATGCAAAAGCATTGA
TATCGTCTAACAGCGCGTTAGTGGATTTTCAGAAGGCAAGAAAGGATATT
ACCACTAATGCAACATCCATAGGGCTGGAAAATGCCAACAACATCTTACA
GAGAACGCCGCTAAGATCTAACAATAAAAAATTATTTATTAACCCCCC
AGGATACCATCAATAGCACTAGCACACTAATAAGGACAACGAAAATAAA
CAGGACATATACGGCTCTTCACCGACTACCATCCAATTAAATTCATCAAT
AACTAAATCTATCTCAAATTGGATAACTCTAGAATTCCTTGTTAGCTT
CGAGATCAGATAACATTCTGGATTCCAATGTGGATGACCAATTGTTTGAT
TTGGGGTTGACAAGATTACCTTTATCACCAACACCAAAATTGTAATCTTT
GCATAGTACAACCACAGGTACATCTGCCTTACAAATTCCTGAGCTACCCA
AGATGGGGTCTTTTAGAAGTGATACGGGAATCAATCCAATTTCAAGTTCA
AACACAGTTTCTTTTAAGAGCAAATCAGGCAATAATAATTCAAAGGGTCG
AATCAAAAAAATGGGAAGAAACCTTCAAATTTCAAATTATTGTGGCAA
ATATTGATCAATTTAACCAGGATACATCATCGTCATCTTTATCATCATCA
TTGAATGCAAGTTCGAGTGCAGGGAATTCAAATTCAAACGTAACAAAGAA
AAGAGCAAGTAAACTCAAAAGATCACAGTCTTTACTTTCTGATTCCGGAT
CGAAATCACAAGCAAGGAAAAGCTGTAATCTAAATCTAATGGAAATTTA
TTCAATTCACAGTAA

YOR372C, 554 aa (SEQ ID NO 372)

MDRDISYQQNYTSTGATATSSRQPSTDNNADTNFLKVMSEFKYNFNSPLP
TTTQFPPTYSSNQYQQTQDHFANTDAHNSSNESSLVENSILPHHQIQQ
QQQQQQQQQQQALGSLVPPAVTRTDTSETLDDINVQPSSVLQFGNSLP
SEFLVASPEQFKEFLLDSPSTNFFHKTPAKTPLRFVTD SNGAQQSTTE

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NPGQQQNVFSNVDLNNLLKSNGKTPSSSCTGAFSRTPLSKIDMNLMFNQ
LPTSPSKRFSSLSLTPYGRKILNDVGTPYAKALISSNSALVDFQKARKDI
TTNATSIGLENANNILQRTPLRSNNKKLFIKTPQDTINSTSTLTNDENK
QDIYGSSPTTIQLNSSITKSISKLDNSRIPLLASRSDNILDSDNDDQLFD
LGLTRLPLSPTPNCNSLHSTTTGTSTALQIPELPMGSRSDTGINPISS
NTVSFKSKSGNNSKGRICKNGKKPSKFQIIVANIDQFNQDTSSSSLSS
LNASSAGNSNSNVTKKRASKLRSQLSDSGSKSQARKSCNSKSNLNL
FNSQ

YDR224C, 896 bp, CDS: 501-896 (SEQ ID NO 111)
TTTCTTCAACAACGACGAGTTAACTATTGTGCTCTTTTTTTGAGCCACCA
AATACACTCCATTCCAATAGCTTCGCACAGTGAGGCGAAAAATTTGGAAC
AGCGCTAATGAATTATTTGTGAGCTCGGCGAGTTCAAATTTGAAGAAAC
GCGGTGGGTTCGTTAACTATGGTTAGACGCTCAATGTGCGCCGAAAGGA
AGGCTGTTCTCACATTTTTTCGCGCGTTGCACCTTTCTTCCGCGAAAAAT
GAGAACGATGGATTAAAAATCAAGAGAATTGGCCTTAGTAGTGGCAAATA
CTACCTTGGTTGGTTATCTTGTAAACGATTGGTAAGAAAGGGGCATCTCTG
TTTTCTTGATGTATATAAACAACATGATTTGATCATCTCAGATGGTCAGA
TTTATTAAAGACGTTTCTCTTTCCGCATTTTCGATTATTGTTATATTAAA
TTTATCCTATATAGACAAGTCAAACCACAAATAAACCATACACACATACA
ATGTCTGCTAAAGCCGAAAAGAAACCAGCCTCCAAAGCCCCAGCTGAAAA
GAAACCAGCCGCTAAAAAGACTTCCACTTCCACTGATGGTAAGAAGAGAA
GCAAGGCTAGAAAGGAAACATACTCTTCTTACATTTACAAAGTTTGAAG
CAAACCTCACCTTGACACTGGTATTTCCCAAAGTCCATGTCTATCTTGAA
CTCTTTTCGTTAACGATATCTTTGAAAGAATCGCTACTGAAGCTTCTAAAT
TGGCTGCGTATAACAAGAAGTCTACTATCTCTGCTAGAGAAATTCAAACC
GCTGTTAGATTGATCTTACCAGGTGAATTGGCTAAGCATGCTGTCTCTGA
AGGTACTAGAGCTGTTACCAAGTACTCTTCTCTACTCAAGCATAA

YDR224C, 131 aa (SEQ ID NO 112)
MSAKAEKKPASKAPAEKKPAAKTSTSTDGKKRSKARKETYSSYIYKVLK
QTHPDTGISQKSMSILNSFVNDIFERIEASKLAAYNKKSTISAREIQT
AVRLILPGELAKHAVSEGTRAVTKYSSSTQA

YLR294C, 830 bp, CDS: 501-830 (SEQ ID NO 281)
ACCAACCAACTTCTTCCCTTTGTCTCAATATCAAAGAAAAAAAAAAAAAC
CCACTGCTCAGATGTTATAAGGAAGGGGTGTTAACTTATATACAGGTTCA
TCTACCAGTCACCAGTCCATACAACTTGAACCGTCTGCGTACCAGTCCT
AATCAAAATGTTCCCTATCGCTTCCAGAAGAATACTGCTCAATGCTTCAG
TTCTGCCATTGAGACTGTGCAATAGAAATTTCACTACCACAAGAATATCC
TACAACGTCAACAAGATTTGTATTTGAGGGAACATAAGACACCAAACCT
GGCTCCAAGTACCTTGCAAGATGCTGAAGGTAATGTTAAGCCTTGGAACC
CACCACAAAAACCAATCTACCAGAATTGGAACCTCAAGGCCAGAGGCT
TTAAAGGCTTACACCGAGCAAAATGTAGAACTGCTCATGTTGCTAAAGA
GTCTGAAGAGGGTGAGTCAGAGCCAATTGAAGAGGATTGGCTAGTTTGG
ATGATGCTGAGGAAACCAAGAAAGTCATTGAACTTTTCATAGCATCCTC
CTTGTCGAAGAAAAACAAACAGAACCACAAGCTGAACAAGATCATTATT
TTTGGCTTTCTTCTCTCATCTTTTATATTTCGAATCCAGTACAATAAAG
AAAAAGCAAAATACACTACGCACTCTTTGTAATCAGCCACACAAATGCA
GAATTTATTTTTTAAACAAAAAATACAATTGTACATAGACACGTCTTTAT
CTTCTCTATTACTACTATCTTTTATTTCAATAACTATTACTTTCTAAGT
ATGACCTACGCTTCTTTGGTAAATAAATAA

YLR294C, 109aa (SEQ ID NO 282)
MMLRKPKKVIELFIASSLSKKKQTEPQAEQDHYFWLSSSHLFIFESSTIK
KKQNTLRLTLCNQPHKMQLNFFKQKIQLYIDTSLSFLLLFFYFNYYFLS

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MTYASLVNK

YMR256C, 683 bp, CDS: 501-683 (SEQ ID NO 319)
CTTTTCAGTTATTTACCTTTCCTTTCTCTCACGTGTAAATATTTGTGTGTC
ATACACACCGCTAAAAACCTTTGCATCAACTTATACCTACATTTCTATA
GACGCTATTTGGAAACAAGATGTAACCCTTTTTTTCTTTTAGTTTTGAGA
TTTGTACTCGTAAAGAGTACGTTTATTTATTTATTCAAATTTTATTTCTC
ATACCATGTAAATATAAGCGCATATAATCACTACGATCTTAGTACAGCTA
GAATTGCTGACGCTTACAATTGCTTTTATTGTTTGATTATATGCACGTATA
CATATAGTGTCTAGCAAAAAAAAAAAGGCAGTACTTGATTGGCTACGCC
GCGCATCGTCCGAGAAATCCGGCCTGGTAGGGGCAGGTTTGAAAAGGCGG
ATAGAAATAAAAGATGATATTATTTATTCATCCCATGAATAGTAGAACTC
GATATAAGATTCTAAACCAACAAGTACAGAAAGCAAAACAATAATAAATA
ATGGCTAATAAAAGTTATTCAACTACAGAAATCTTCCAATCTTCCACTAA
ACCTCTATGGTGGAGACATCCAAGGTCAGCTTTATACCTGTATCCATTTT
ATGCTATTTTTGCGGTAGCCGTCGTTACACCACCTCTATACATTCCAAAT
GCTATTAGAGGTATCAAAGCCAAGAAGGCATAG

YMR256C, 60 aa (SEQ ID NO 320)
MANKVIQLQKIFQSSTKPLWWRHPRSAlylyPFYAIFAVAVVTPLLYIPN
AIRGIKAKKA

YLR327C, 761 bp, CDS: 501-761 (SEQ ID NO 287)
TTCTCATACGTATGTTTTTTTAGATTATGCACCTTCTTTGCCACAGTAAA
TGTTGGCGGGGAAGATGTTGAGCTAGCGCCGTGCACAGTGAAGAGACGGA
GGCGATTGTGGGGTTTCATCGGATTGTGCGGGAAGAAGGCCCTACACCGTG
TTGAGCCACCCCCCCTCAGGAGTAAATTTACACAAACAGTGGTGGTGCC
TATGGTGGTATACGAGATAGTGATAGAAGCTGCTGGATTGGGGTAGAAAT
TTTGTAGGCGTTTATGGATATGGTATGGATATGGTATGGCTTGAGGTAGG
TAATCCAGACACCACCTGGAATATATATAAGGAGAGAGTTCTGGCAGGTA
GATTTGTACTCCTCTCTACCACCTTCTTCTACTCCTTTTATTATGTAATG
TTTATTTATAAGCACAGCAAAAACGTTAAATAAATCTAATAAGATTTTCAAT
ATAACATAACATTAAGCACACAAATTTCTAACACAAACACAATTCAAAC
ATGACCAGAACTAGCAAATGGACAGTCCACGAAGCAAAGTCTAACCCAAA
GTATTTTACCCATAACGGCAACTTTGGGGAGTCTCCCAACCACGTCAAGA
GAGGAGGCTATGGGAAAGGCAATTGGGGCAAGCCTGGCGATGAGATTAAT
GACTTAATCGATTCTGGCGAAATTAAGACAGTCTTCAACAAGACCAGAAG
GGGCTCTAACTCCCAAAACAATGAAAGAAGGCTTTCTGATTTGCAACAAT
ACCACATCTAA

YLR327C, 86 aa (SEQ ID NO 288)
MTRTSKWTVHEAKSNPKYFTHNGNFGESPNHVKRGYgkgnwgkpgdein
DLIDSGEIKTVFNKTRRGSNSQNNERRLSDLQQYHI

YHR161C, 2414 bp, CDS: 501-2414 (SEQ ID NO 211)
GTCATGCGCGCAATAGGAAAGCGCACGAAACAAATGAGTAATTCGTAGGA
AACAAATGCAGCCCCAGGGTCAGCAACTGACGTGACTCAGCCTGGCTTTT
GTAGAAAAAGATGACGCCCCTGGCAGAGAGGTGGGGGAATTGAGGGGTCTT
CGCTACCCACCTTAAAGTATGGAAGAATATGATGAAGAATATGATGATAAC
TCTTGGAAGCGAGCGGGCGGGTTCCATCACTTTTTACGGATTGGTAACACA
GGGGCCTCAGTTGATACTTGGTATTCAGGCTTCCAGCGTTGGTGAGTTT
AGTTAGCGGTATGGTATGCACATGGTGTGATGCTTGGTGGTAATCATTC
GTTAGGTGAATTGAGCAGTAGCGATATTAGATATATTTAGTATTTTATAG
CGTCTTTTTTGGTGGGGGAGGAAGGACAAAACCTGTCTCGTAAATATAAAG
GGACTGTTTCGATATCGCAGATACTAGAGTATAAATTTTCGATTGAGGCGAG
ATGACAACATATTTCAAGTTGGTAAAAGGTGCTACCAAGATCAAGTCAGC

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CCCGCCCAAACAGAAGTATCTGGATCCGATACTGTTGGGGACCAGCAATG
AAGAGGATTTCTATGAGATCGTGAAGGGTTTGGATTTCCCGAATTAATGAC
ACGGCGTGGACTATTTGTGTATAAATCGCTGTTGGTGGTTCATTTGATGAT
AAGGGAGGGTTCCAAAGATGTTGCATTGCGGTACTACTCTAGGAACCTGG
AGTTTTTTTGACATTTGAAAACATACGTGGCTCCAATGGCAGTGCGTCTGGA
GACATGAGGGCACTTGATAGATACGATAATTATCTGAAGGTGAGATGCAG
GGAGTTTGGTAAAAATCAAAAAGGACTATGTGAGAGACGGCTATCGAACAC
TGAAGCTGAACAGTGGCAATTACGGAAGCTCCAGAAACAAGCAACACTCT
ATCAATATAAGCAC TAGATCATGTGGAGTCCC TAGAGGTACAAATACAAGC
CCTGATTAAAAACAAGTATACACAATATGATTTGAGTAACGAATTGATCA
TATTTGGTTTCAAGCTGCTTATTCAAGACCTGCTAGCGCTATATAATGCT
CTCAACGAAGGTATCATAACTCTGCTGGAGTCTTTTTTCGAACATATCTCA
TCATAATGCAGAGAGAACTCTAGACCTGTACAAGACGTTTGTGATTTGA
CCGAGCACGTTGTCAGGTACTTGAAGAGCGGGAAGACTGCGGGCTTGAAA
ATACCCGTCATCAAGCATATCACTACCAAAC TGGTCAGATCGCTAGAAGA
ACATCTGATAGAGGATGATAAGACGCACAACACTTTTGTGCCCCGTTGACA
GTTCTCAAGGAAGTGTGGGGCCGTAGTAGCCAAATCTACTGCACAGGAA
AGGTTGGAGCAAATCCGGGAACAAAAAGGATACTAGAGGCACAAATTGAA
AAACGAACAAGTAGCGATTTCCCTGCTCTAACTACTGTACGCGCGGCTC
AATCTTACAACCCGTTTGGAACAGACTCTTCTATGCATACTAACATTCCA
ATGGCTGTGGCTAATCAAACGCAACAGATCGCAAATAACCCATTTGTATC
TCAAACTCAGCCACAGGTGATGAATACACCAACCGCTCATACAGAGCCCG
CAAATTTAAACGTTCC TGAATATGCAGCGGTCCAACACACAGTGAAC TTC
AACCCGTGTACAAGATGCTGGCGTAAGTGCCCAACAAACGGGGTACTATTTC
GATTAACAACCATTTAACACCCACATTTACAGGTGCAGGGTTTGGAGGAT
ACTCCGTTTTCACAGGATACAAC TGGCGCTTCTAATCAACAAGTCTCTCAT
TCACAAACTGGTTCTAACAACCCGTTTCGATTCACAAACGCGCGACGAT
CGCAACAGGGAATCCTGCACACGAAAATGTCTTAAATAACCCATTTTCAC
GACCAAAC TTTGATGAACAAAATACCAATATGCCGCTACAACAACAGATA
ATAAGTAACCC TTTTCAAAACCAAACGTACAATCAACAACAATTTCAACA
ACAAAAATGCC TTTGAGCTCGATCAATAGCGTTATGACAACCCCTACTA
GCATGCAGGGATCGATGAATATTCCTCAGCGTTTGTATAAAATGGAATTT
CAGGCTCACTACACTCAGAATCATCTCCAACAACAGCAACAACAGCAACA
GCAACAACAGCAACAGCAACAACAGCAACCACAACAGGGTTATTATGTGC
CTGCAACTGCAGGAGCCAACCCGTGTACAAATATAACTGGGACAGTTCAA
CCTCAAAATTTCCCTTTCTATCCACAACAGCAACCACAACCGGAACAGTC
TCAAACACAGCAACCAGTTT TAGGAAACCAATATGCTAACAACCTCAATT
TAATTGATATGTAA

YHR161C, 637 aa (SEQ ID NO 212)

MTTYFKLVKGATKIKSAPPKQKYLDPIILLGTSNEEDFYEIVKGLDSRIND
TAWTIVYKSLLVHLMIREGSKDVALRYSRNLEFFDIENIRGSNGSASG
DMRALDRYDNYLKVRCREFGKIKKDYVRDGYRTLKLNSGNYGSSRNKQHS
INIALDHVESLEVQIQALIKNKYTQYDLSNELIIFGFKLLIQDLLALYNA
LNEGIIITLLESFFELSHHNAERTLDLYKTFVDLTHEVVRYLKSGKTAGLK
IPVIKHITTKLVRSL EEHLIEDDKTHNTFVPVDSSQGSAGAVVAKSTAQE
RLEQIREQKRILEAQLKNEQVAISPALT TVTAAQSYNPFGTDS SMHTNIP
MAVANQTQQIANNPFVSQTQPQVMNTPTAHTEPANLNVPEYAAVQHTVNF
NPVQDAGVSAQQTGYYSINNHLTPFTTGAGFGGYSVSQDTTAA SNQQVSH
SQTGSNNPFALHNAAT IATGNPAHENVLNNPFSRPNFDEQNTNMPLQQQI
ISNPFQNTYNQQQFQQQKMP LSSINSVMTTPTSMQGS MNIPQRFDKMEF
QAHYTQNH LQQQQQQQQQQQQQQQQQQPQQGYYPATAGANPVTNITGT VQ
PQNF PFYPQQQPQE QSQTQQPVLGNQYANNLNLIDM

YLR206W, 2342 bp, CDS: 501-2342 (SEQ ID NO 277)

TACACCCTGACTTTCCCATCATACGACGATGCTCTAGTAAACTTGCACC

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CGCACCTGTTAGATAAACAAGTGCGCCCAAGATCACAATACCGAAGGGGC
GATATCACCACCTCAGTATTCTACAGTCGAGCATAGCGTAGTCTGGCAGTA
TCCCGCACGATCCATTGTATTGTTTGTCCAAACCGCATTATGTGTAAAC
GATTAATCGTATATACATGGCCTACAAGAAATTACCCTGCGGCGAAGGGT
GAAAAAAAAGTAGTGGAAGCTAAAGAAAGAAGAGTTTAGTTACGGACCC
TTTCAAGGATTGACACACTCCCAATATTTTGCTACATTATTGACCTTTGT
TGAAGGAGGCGTTTCGTTTATTTAATTATTTTGTCTGTTTTGCTACAAC
TGCGAATACGCTCACATTCTAGTTTGACCTTCACAAATCTTATCATCTT
CTTTTGTATTATTTTGACACACCCCTATTAAGTGTATTTGTTTTGTAAGTA
ATGTCTAAGCAGTTTGTTCGTTCTGCAAAGAACATGATGAAGGGCTACTC
ATCCACACAAGTGCTTGTGAGAGATGCCACGGCGAAGCACTCGAGGACTC
CATCGATAGACACTCTCGACGATTTGGCACAGAGATCTTACGATTCCGGTG
GACTTCTTCGAGATTATGGATATGTTAGACAAGAGGCTGAACGATAAGGG
CAAATACTGGAGACACGTTGCCAAATCGCTGACCGTTTTGGACTATCTTG
TTCGTTTTCGGGAGTGAGAACTGTGTGCTATGGTGCAGAGAGAATTTTAC
GTAATTAAGACATTAAGGGAATTCAGACACGAAAATGAGTCCGGATTGTA
CGAGGGACAAATTATCAGAGTAAAGGCTAAAGAACTCGTCTCTTTGTTGA
ATGATGAAGAAAGGCTACGCGAAGAGAGGTCTATGAATACAAGAAACAGA
AGGGCGAAGCAGAGCTGCTAGGCCAAGGCCAAGAAGACAAAGAACAAGGAG
CAACCCACACGATTCTTCTCCCTCTTACCAGGACGATTTGGAAAAGGCC
TAGAGGAGAGCAGAATTACTGCTCAAGAAGATGAACAACGTAGAAGAGAA
CTGGCCAGTACGACGATGAAGATCCTGACTTCCAAGCTGCCTTACAAC
AAGTAAAGAAGAAGAGGAGTTGAAGCAATTGCAGGAACACAGAGATTAC
AGAAGCAACAACAGTCTCTGTCTCAATTTCAAGCTCCTTTACAACAACAA
CAACCACAACAACAACAGCGTACTACGACATTTTCGGTAATCCAATCTC
CCAAGATGAATACTTACAGTATCAGTACCAACAGGACCAGGAACAAGCAA
TGGCTCAGCAAAGATGGCTGGACCAGCAGCAAGAACAACAGCAGCTTGCT
GAACAACAATATTTTCAGCAGCAACAACAAGCTGCGGCCGCCGCTTCTGC
CTTGCAACAGCAACAACAACAGCCGCTAATATGCAACAACAACAACAACAGC
CCGCTGATTTTCAACAACCTTTGCCTACAGGTTCTAATAATCCGTTTTTCC
ATGGATAATCTTGAAAGACAAAAGCAGGAGCAACAGCATGCTCAATTGCA
AAGACAACAAGAAGAAGCTAGACAACAACAAGAACAATTGAAGCTACAAC
AATTGCAAAGACAACAACAAGAGGAAGCTCAATTACACCAGAAGAGGCAA
GAAGAAGCCCAATTACAACAGCAGCAAGCCCAATTGCTACAACAGCAAGC
CCAGTTCCAGCAACAACAACCTTGAAGCAAACAAGGACTGGGAACCACT
CTATATCGGATAAATACAGCGACTTGAATACCTTGTAGCAACTGGTACA
GGGATAGATACTTTTGGTAACACTGGAGAGGCACGTATTCTGCACAACA
TACAAAGACAGGCACATTTATAAATCTCAGGGTACAGGCTACAACAGG
TTACTAATGAACCCAAGAACAACCTTTCTTAAGCAACCAATACACTGGT
TTACCAAGCACAAATATCGTGCCACGCAACAGGGTACGGGTTTGGTAA
CCAACCTCAAAGTCTCTCTACTAATCTCTCTCAGCAAAATCTTACTGGTA
TAAGCTACTCTCAGCCACAACAGCAACAACAGCCACAGCAACAACCGCAA
TACATGCAAAATTTCCAACAACAGCAACCTCAATACGCCCAAAACTTCCA
ACAACAACCACAATACACTCAAATTTATCAACAACAACCACAATACATTC
AACCTCATCAACAACAACAGCAGCAGCAGCAGCAGCAACAGCAGCAACAG
GGATATACTCCTGACCAAGGTGTAAGCTTAATTGATCTTTGA

YLR206W, 613 aa (SEQ ID NO 278)

MSKQFVRS AKNMKGYSSTQVLVRDATANDSRTPSIDTLDDLAQRSYDSV
DFFEIMDMLDKRLNDKGKYWRHVAKSLTVLDYLVRFGSENCVLWCENFY
VIKTLREFRHNESGFDEGQIIIRVKAKELVSLNDEERLREERSMNTRNR
RANRAARPRPRRQTRSNPHDSSPSYQDDLEKALEESRITAQEDQRRRE
LAQYDDEDPDFQAALQLSKEEEEELKQLQELQRLQKQQQSLSQFQAPLQQQ
QPQQQPAYYDIFGNPISQDEYLQYQYQQDQEQAMAQQRWLDQQQEQQQLA
EQYFQQQQQAAAAASALQQQQTAANMQQQQQPADFQQPLPTGSNNPFS
MDNLERQKQEQQHAQLRQQEEARQQQEQLKLQQLRQQQEEAQLHQKRQ

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EEAQLQQQQAQLLQQQAQFQQQQPLKQTRTGNQSIDKYSIDLNTLLATGT
GIDTFGNTGEARIPAQHTKTGTFINSQGTGYKQVTNEPKNNPFLSNQYTG
LPSTNIVPTQTGYGFGNQPSPTNSPQQNPTGISYSQPQQQQPQQQPQ
YMQNFQQQQPQYAQNFQQQPQYTQNYQQQPQYIQPHQQQQQQQQQQQQ
GYTPDQGVSLIDL

YDR342C, 2213 bp, CDS: 501-2213 (SEQ ID NO 119)
CACTTCTCAGAAATGCATGCAGTGGCAGCACGCTAATTCGAAAAATTCT
CCAGAAAGGCAACGCAAAATTTTTTTTCCAGGGAATAAACTTTTTATGAC
CCACTACTTCTCGTAGGAACAATTTCTGGGCCCTGCGTGTTCTTCTGAGG
TTCATCTTTTACATTTGCTTCTGCTGGATAATTTTCAGAGGCAACAAGGA
AAAATTAGATGGCAAAAAGTCGTCTTTCAAGGAAAAATCCCCACCATCTT
TCGAGATCCCCGTGTAACCTTATTGGCAACTGAAAGAATGAAAAGGAGGAAA
ATACAAAATATACTAGAACTGAAAAAAAAAAAAAGTATAAATAGAGACGATA
TATGCCAATACTTCACAATGTTTGAATCTATTCTTCATTTGCAGCTATTG
TAAAATAATAAAACATCAAGAACAAACAAGCTCAACTTGTCTTTTCTAAG
AACAAAGAATAAAACACAAAAACAAAAAGTTTTTTTAATTTTAATCAAAAA
ATGTCACAAGACGCTGCTATTGCAGAGCAAACTCCTGTGGAGCATCTCTC
TGCTGTTGACTCAGCCTCCCACTCGGTTTTATCTACACCATCAAAACAAGG
CTGAAAGAGATGAAATAAAAGCTTATGGTGAAGGTGAAGAGCACGAACCT
GTCGTTGAAATTCCAAAGAGACCAGCTTCTGCCTATGTCAGTGTCTCTAT
TATGTGTATCATGATCGCCTTTGGTGGTTTTCGTTTTCGGTTGGGATACTG
GTACCATTTCTGGTTTCATCAATCAAACCGATTTTCATCAGAAGATTTGGT
ATGAAGCATAAAGATGGTACTAATTATTTGTCTAAGGTTAGAAGTGGTTT
GATTGTCTCCATTTTCAACATTGGTTGTGCCATTGGTGGTATTATTCTTT
CCAAATTGGGTGATATGTACGGTCTGAAGGTGGGTTTGATTGTGCTGTT
GTCATCTACATCATCGGTATTATTATTCAAATTGCATCTATCAACAAATG
GTACCAATATTTTCATCGGTAGAATTATTTCCGGTTTGGGTGTTGGTGGTA
TTGCCGTTTTATCTCCTATGTTGATTTCTGAAGTATCCCCAAAGCATTTA
AGGGGTACTTTAGTCTCTTGTCTACCAATTGATGATTACTGCCGGTATTTT
CTTGGGTTACTGTACCAACTTCGGTACTAAGAACTACTCCAACCTCTGTGC
AATGGAGAGTTCCATTAGGTTTGTGTTTTGCCTGGGCTTTGTTTATGATT
GGTGGTATGACATTTGTTCCAGAGTCTCCACGTTATTTGGCTGAAGTCGG
TAAGATCGAAGAAGCCAAACGTTCTATTGCCGTTTCTAACAAGGTTGCTG
TTGATGATCCATCTGTTTTGGCTGAAGTCAAGCTGTCTTGGCTGGTGTA
GAGGCAGAGAAATTAGCTGGTAATGCATCCTGGGGTGAATTGTTTAGTAG
CAAGACAAAGGTCCTTCAGCGTTTGATCATGGGTGCTATGATTCAATCTC
TACAACAATTGACAGGTGATAACTATTTCTTCTACTATGGTACTACTATT
TTCAAGGCTGTTGGTTTGAGTGACTCTTTCGAAACCTCTATTGTCTTGGG
TATTGTTAACTTTGCTTCCACCTTTGTTGGTATTTACGTTGTTGAGAGAT
ATGGTCGTCGTACTTGTGTTGCTATGGGGTGCTGCATCCATGACTGCTTGT
ATGGTTGTCTATGCTTCCGTGGGTGTCAACAGATTATGGCCAAATGGTCA
AGACCAACCATCTTCCAAGGGTGCTGGTAAGTGTATGATTGTCTTTGCCT
GTTTCTATATTTTCTGTTTTGCTACTACATGGGCTCCAATTCCTTATGTC
GTTGTTTCTGAACTTTCCCATTTGAGAGTCAAGTCTAAGGCTATGTCTAT
TGCTACAGCTGCTAATTGTTGTGGGGTTTCTTGATTGGTTTCTTCACTC
CATTTATTACTGGTGCTATTAACCTTCTACTACGGTTACGTTTTTCATGGGC
TGTTTGGTCTTCATGTTCTTCTATGTTTTGTTAGTTGTTCCAGAACTAA
GGGTTTGACTTTGGAAGAAGTCAACACCATGTGGGAAGAAGGTGTTCTAC
CATGGAAGTCTGCCTCATGGGTCCACCATCCAGAAGAGGTGCCAACTAC
GACGCTGAAGAAATGACTCACGATGACAAGCCATTGTACAAGAGAATGTT
CAGCACCAATAA

YDR342C, 570 aa (SEQ ID NO 120)
MSQDAAI AEQTPVEHLSAVDSASHSVLSTPSNKAERDEIKAYGEGEEHEP
VVEIPKRPASAYVTVS IMCIMI AFGGFVFGWDTGTISGFINTDFIRRF

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MKHKDGTNYLSKVRTGLIVSIFNIGCAIGGIILSKLGDMYGRKVGLIVVV
VIYIIGIIIIQIASINKWYQYFIGRIISGLGVGGIAVLSPMLISEVSPKHL
RGTLVSCYQLMITAGIFLGYCTNFGTKNYSNSVQWRVPLGLCFWALFMI
GGMTFVPESPRYLAEVGKIEEAKRSIAVSNKVAVDDPSVLAEEVAVLAGV
EAEKLAGNASWGELFSSKTKVLQRLIMGAMIQSLQOLTGDNYFFYYGTTI
FKAVGLSDSFETSIVLGIVNFASTFVGIYVVERYGRRTCLLWGAASMTAC
MVVYASVGVTRLWPNGQDQPSSKGAGNCMIVFACFYIFCFATTWAPIPYV
VVSETFPLRVKSKAMSIATAANWLWGFLIGFFTFFITGAINFYGYVFMG
CLVFMFFYVLLVVPETKGLTLEEVNTMWEEGVLPWKSASWVPPSRRGANY
DAEEMTHDDKPLYKRMFSTK

YDR343C, 2213 bp, CDS: 501-2213 (SEQ ID NO 121)

AAAAAATGTTTTTTTAGGCAACGGAGATTTCGTTTTATCCACGTTTACCCC
ACAAAAAGTGCAGGTACATTGTGGGGCCCCGGCATCGAAAACCAGTTTTT
TTCTTTAAACGCTGGAAAAAAGGAGAAATTATTGGAACTTTGCAGAGA
ATAGTCCGTAGGCAAATTGAAAATGTTCTTAAAAAATTTTCGTTTCTTAC
TCATTGAGATTATTTCAGATGCCCTCCGTGCCTTCATTGAAAAAATCCAA
GAGATGTCTCGGATCTGTATGCAGATTTTGGCTTGCAGACAATGGAGAGC
AAATGGGTATACAATATAGAAAGCACAGAAACATATAAAAAGAGCTCGAG
AAAAGACATATGGTTTGTAACTATCTTCTTCTTTTTTCCAATTTTCTGT
TTTAATAATAAAAAACAAGAACAAACAAGCTCAACTTGTCTTTTCTAAG
AACAAAGAATAAACACAAAAACAAAAAGTTTTTTTAATTTTAATCAAAAA
ATGTCACAAGACGCTGCTATTGCAGAGCAAACCTCTGTGGAGCATCTCTC
TGCTGTGTGACTCAGCCTCCCACTCGGTTTTATCTACACCATCAAACAAGG
CTGAAAGAGATGAAATAAAAGCTTATGGTGAAGGTGAAGAGCACGAACCT
GTCGTTGAAATTCCAAAGAGACCAGCTTCTGCCATATGTCACGTCTCTAT
TATGTGTATCATGATCGCCTTTGGTGGTTTCGTTTTTCGGTTGGGATACTG
GTACCATTTCTGGTTTCATCAATCAAACCGATTTCATCAGAAGATTGGT
ATGAAGCATAAAGATGGTACTAATTATTTGTCTAAGGTTAGAAGTGGTTT
GATTGTCTCCATTTTCAACATTGGTTGTGCCATTGGTGGTATTATTCTTT
CCAAATTGGGTGATATGTACGGTCGTAAGGTGGGTTTGATTGTCTGTGT
GTCATCTACATCATCGGTATTATTATTCAAATTGCATCTATCAACAAATG
GTACCAATATTTTCATCGGTAGAATTATTTCCGGTTTGGGTGTTGGTGGTA
TTGCCGTTTTATCTCCTATGTTGATTTCTGAAGTATCCCCAAAGCATTTA
AGGGGTACTTTAGTCTCTTGCTACCAATTGATGATTACTGCCGGTATTTT
CTTGGGTACTGTACCAACTTCGGTACTAAGAACTACTCCAACCTCTGTGC
AATGGAGAGTTCATTAGGTTTGTGTTTTGCCCTGGGCTTTGTTTTATGATT
GGTGGTATGACATTTGTTCCAGAGTCTCCACGTTATTTGGCTGAAGTCGG
TAAGATCGAAGAAGCCAAACGTTCTATTGCCGTTTCTAACAAGGTTGCTG
TTGATGATCCATCTGTTTTGGCTGAAGTCGAAGCTGCTTTGGCTGGTGTA
GAGGCAGAGAAATTAGCTGGTAATGCATCCTGGGGTGAATTGTTTAGTAG
CAAGACAAAGGTCCCTTCAGCGTTTGATCATGGGTGCTATGATTCAATCTC
TACAACAATTGACAGGTGATAACTATTTCTTCTACTATGGTACTACTATT
TTCAAGGCTGTTGGTTTGAGTGACTCTTTCGAAACCTCTATTGTCTTGGG
TATTGTTAACTTTGCTTCCACCTTTGTTGGTATTTACGTTGTTGAGAGAT
ATGGTTCGTCTGTTGTTGCTATGGGGTGCTGCATCCATGACTGCTTGT
ATGGTTGTCTATGCTTCCGTGGGTGTCACCAGATTATGGCCAAATGGTCA
AGACCAACCATCTTCCAAGGGTGCTGGTAACGTATGATTGTCTTTGCCCT
GTTTCTATATTTTCTGTTTTGCTACTACATGGGCTCCAATTCCCTTATGTC
GTTGTTTCTGAAACTTTCCCATTGAGAGTCAAGTCTAAGGCTATGTCTAT
TGCTACAGCTGCTAATTGGTTGTGGGGTTTCTTGATTGGTTTCTTCACTC
CATTTATTACTGGTGCTATTAACTTCTACTACGGTTACGTTTTTCATGGGC
TGTTTGGTCTTCATGTTCTTCTATGTTTTGTAGTTGTTCCAGAACTAA
GGGTTTGACTTTGGAAGAAGTCAACACCATGTGGGAAGAAGGTGTTCTAC
CATGGAAGTCTGCCCTCATGGGTTCCACCATCTAGAAGAGGTGCCAACTAC
GACGCTGAAGAAATGGCTCACGATGATAAGCCATTGTACAAGAGAAATGTT

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CAGCACCAAATAA

YDR343C, 570 aa (SEQ ID NO 122)

MSQDAIAIEQTPVEHLSAVDSASHSVLSTPSNKAERDEIKAYGEGEEHEP
VVEIPKRPASAYVTVSIMCIMIAFGGFVFGWDTGTISGFINQTDFFIRRFG
MKHKDGTNYLSKVRTGLIVSIFNIGCAIGGIILSKLGDYGRKVGLIVVV
VIYIIGIIIIQIASINKWYQYFIGRIISGLGVGGIAVLSPMLISEVSPKHL
RGTLVSCYQLMITAGIFLGYCTNFGTKNYSNSVQWRVPLGLCFAWALFMI
GGMTFVPESPRLAEVGKIEEAKRSIAVSNKVAVDDPSVLAEEVEAVLAGV
EAEKLAGNASWGELFSSKTKVLQRLIMGAMIQSLQQLTGDNYFFYYGTTI
FKAVGLSDSFETSIVLGIVNFASTFVGIYVVERYGRRTCLLWGAASMTAC
MVVYASVGVTRLWPNGQDQPSSKGAGNCMIVFACFYIFCFATTWAPIPYV
VVSETFPLRVKSKAMSIATAANWLWGFLIGFFTFFITGAINFYGYVFMG
CLVFMFFYVLLVVPETKGLTLEEVNTMWEEGVL PWKSASWVPPSRRGANY
DAEEMAHDDKPLYKRMFSTK

YGR192C, 1499 bp, CDS: 501-1499 (SEQ ID NO 183)

ACAGTTTATTCTCGCATCCACTAAATATAATGGAGCCCGCTTTTAAAGC
TGGCATCCAGAAAAAAGAATCCCAGCACCAAATATTGTTTTCTTCA
CCAACCATCAGTTCATAGGTCCATTCTCTTAGCGCAACTACAGAGAACAG
GGGCACAAACAGGCAAAAAACGGGCACAACCTCAATGGAGTGATGCAACC
TGCCTGGAGTAAATGATGACACAAGGCAATTGACCCACGCATGTATCTAT
CTCATTTTCTTACACCTTCTATTACCTTCTGCTCTCTCTGATTTGAAAA
AGCTGAAAAAAAGGTTGAAACCAGTTCCTGAAATTATTCCTTACTTG
ACTAATAAGTATATAAAGACGGTAGGTATTGATTGTAATTCTGTAAATCT
ATTTCTTAAACTTCTTAAATTCTACTTTTATAGTTAGTCTTTTTTTTAGT
TTTAAACACCAAGAACTTAGTTTCGAATAAACACACATAAACAAACAAA
ATGGTTAGAGTTGCTATTAAACGGTTTCGGTAGAATCGGTAGATTGGTCAT
GAGAATTGCTTTGTCTAGACCAAAACGTCGAAGTTGTTGCTTTGAACGACC
CATTCATCACCAACGACTACGCTGCTTACATGTTCAAGTACGACTCCACT
CACGGTAGATACGCTGGTGAAGTTTCCCACGATGACAAGCACATCATTGT
CGATGGTAAGAAGATTGCTACTTACCAAGAAAGAGACCCAGCTAACTTGC
CATGGGGTTCTTCCAACGTTGACATCGCCATTGACTCCACTGGTGTTTTTC
AAGGAATTAGACACTGCTCAAAAGCACATTGACGCTGGTGCCAAGAAGGT
TGTTATCACTGCTCCATCTTCCACCGCCCCAATGTTTCGTCATGGGTGTTA
ACGAAGAAAAATACACTTCTGACTTGAAGATTGTTTCCAACGCTTCTTGT
ACCACCAACTGTTTGGCTCCATTGGCCAAGGTTATCAACGATGCTTTCGG
TATTGAAGAAGGTTTGATGACCACTGTCCACTCTTTGACTGCTACTCAAA
AGACTGTTGACGGTCCATCCCACAAGGACTGGAGAGGTGGTAGAACCGCT
TCCGGTAACATCATCCCATCCTCCACCGGTGCTGCTAAGGCTGTGCGGTAA
GGTCTTGCCAGAATTGCAAGGTAAGTTGACCGGTATGGCTTTCAGAGTCC
CAACCGTCGATGTCTCCGTTGTTGACTTGACTGTCAAGTTGAACAAGGAA
ACCACCTACGATGAAATCAAGAAGGTTGTTAAGGCTGCCGCTGAAGGTAA
GTTGAAGGGTGTTTTGGGTTACACCGAAGACGCTGTTGTCTCCTCTGACT
TCTTGGGTGACTCTCACTCTTCCATCTTCGATGCTTCCGCTGGTATCCAA
TTGTCTCCAAAGTTTCGTCAAGTTGGTCTCCTGGTACGACAACGAATACGG
TTACTCTACCAGAGTTGTGCGACTTGGTTGAACACGTTGCCAAGGCTTAA

YGR192C, 332 aa (SEQ ID NO 184)

MVRVAINGFRIGRLVMRIALSRPNVEVVALNDPFITNDYAAVMFKYDST
HGRYAGEVSHDDKHIIVDGKKIATYQERDPANLPWGSSNVDIAIDSTGVF
KELDTAQKHIDAGAKKVITAPSSAPMFVMGVNEEKYTSCLKIVSNASC
TTNCLAPLAKVINDAFGIEEGLMTTVHSLTATQKTVDGPSHKDWRGGRTA
SGNIIIPSSGAAKAVGKVLPELQGKLTGMAFRVPTVDVSVVDLTVKLNKE
TTYDEIKKVVKAAAEGKLKGVLYTEDAVVSSDFLGDSHSSIFDASAGIQ
LSPKFVKLVSWYDNEYGYSTRVVDLVEHVAKA

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YOR374W, 2060 bp, CDS: 501-2060 (SEQ ID NO 373)
CGACCCCTCTGGTTAGATGACACTCCTGCCCCAACTGCCACGAATCTGTAA
CCCCATAACTATACCCGTACGCAGTACTAAAAATGTATGTAATTAGTAAA
TGTATGTAACAATTTACCGTTTTGTGTAACAATTCATTCATTCATTCTT
TTGATCCTTTTAGTACCGTCCGCACATGATGTCATTTCCCCCTCATTTTTG
TTTGCTGGTATGATTCCCCGCCCGGGCGACGGTACGGCTGTTATCCAGCG
ATGCGGGGACTTCCGTCCACAGGTATCTTTTTCTCCAACCTCCAACAGAGAT
GGAAAAATGAGGGGCGGGTGTAGGTAAGCAGAATGAGGAGAAATTTGTAAT
GAAAAATGGAAGTTCCGGCGGTATATAAAATGGGGGGGGTTTTGTCGGTGACA
ATTGACTTCACTCTCTTTCTCTCAAAAATCTTGGGTGTTAGGATTAGAA
GTATCTGGAAGCAACCAAGAACTACAATAACAAAAATAAATAAAGC
ATGTTTCAGTAGATCTACGCTCTGCTTAAAGACGTCTGCATCCTCCATTGG
GAGACTTCAATTGAGATATTTCTCACACCTTCTATGACAGTGCCTATCA
AGCTGCCCCAATGGGTTGGAATATGAGCAACCAACGGGGTTGTTTCATCAAC
AACAAGTTTTGTTTCTTCTAAACAGAACAGACCTTCGAAGTCATTAAACCC
TTCCACGGAAGAAGAAATATGTCATATTTATGAAGGTAGAGAGGACGATG
TGGAAGAGGCCGTGCAGGCCGCCGACCGTGCCTTCTCTAATGGGTCTTGG
AACGGTATCGACCTATTGACAGGGGTAAGGCTTTGTACAGGTTAGCCGA
ATTAATTGAACAGGACAAGGATGTCATTGCTTCCATCGAGACTTTGGATA
ACGGTAAAGCTATCTCTTCTCGAGAGGAGATGTTGATTTAGTCATCAAC
TATTTGAAATCTTCTGCTGGCTTTGCTGATAAAATTTGATGGTAGAATGAT
TGATACTGGTAGAACCCATTTTCTTACACTAAGAGACAGCCTTTGGGTG
TTTTGTGGGCAGATTATTCCTTGGGAATTTCCCACTGTTGATGTGGGCCTGG
AAGATTGCCCCCTGCTTTGGTCAACGGTAACACCGTCGTGTTGAAGACTGC
CGAATCCACCCCATTTGTCCGCTTTGTATGTGTCTAAATACATCCACAGG
CGGGTATTCACCTGGTGTGATCAACATTGTATCCGGGTTTGGTAAGATT
GTGGGTGAGGCCATTACAAACCATCAAAAATCAAAAAGGTTGCCTTCAC
AGGGTCCACGGCTACGGGTAGACACATTTACCAGTCCGCAGCCGAGGCT
TGAAAAAGTGACTTTGGAGCTGGGTGGTAAATCACCAAACATTGTCTTC
GCGGACGCCGAGTTGAAAAAGCCGTGCAAAACATTATCCTTGGTATCTA
CTACAATTCTGGTGAGGTCTGTTGTGCGGGTTCAAGGGTGTATGTTGAAG
AATCTATTTACGACAAATTCATTGAAGAGTTCAAAGCCGCTTCTGAATCC
ATCAAGGTGGGCGACCCATTTCGATGAATCTACTTTCCAAGGTGCACAAAC
CTCTCAAATGCAACTAAACAAAATCTTGAAATACGTTGACATTGGTAAGA
ATGAAGGTGCTACTTTGATTACCGGTGGTGAAAGATTAGGTAGCAAGGGT
TACTTCATTAAGCCAACTGTCTTTGGTGACGTTAAGGAAGACATGAGAAT
TGTCAAAGAGGAAATCTTTGGCCCTGTTGTCACTGTAACCAAATTCAAAT
CTGCCGACGAAGTCATTAACATGGCGAACGATTCTGAATACGGGTGGCT
GCTGGTATTACACCTCTAATATTAATACCGCCTTAAAAGTGGCTGATAG
AGTTAATGCGGGTACGGTCTGGATAAAACACTTATAACGATTTCCACCACG
CAGTTCTTTTCGGTGGGTCAATGCATCTGGTTTGGGCAGGGAAATGTCT
GTTGATGCTTTACAAAACACTTGCAAGTTAAAGCGGTCCGTGCCAAATT
GGACGAGTAA

YOR374W, 519 aa (SEQ ID NO 374)
MFSRSTLCLKTSASSIGRLQLRYFSLPMTVPKLPNGLEYEQPTGLFIN
NKFVPSKQNKTFEVINPSTEEIICHIEGREDDVEEAVQAADRAFSNGSW
NGIDPIDRGKALYRLAELIEQDKDVIASIEITLDNGKAISSSRGDVLVIN
YLKSSAGFADKIDGRMIDTGRTHFSYTKRQPLGVCGQIIPWNFPLLMWAW
KIAPALVTGNTVVLKTAESTPLSALYVSKYIPQAGIPPGVINIVSGFGKI
VGEAITNHPKIKKVAFTGSTATGRHIYQSAAAGLKKVTLELGGKSPNIVF
ADAELKKAVQNIILGIYNSGEVCCAGSRVYVEESIYDKFIEEFKAASES
IKVGDPEDESTFQGAQTSQMLNKILKYVDIGKNEGATLITGGERLGSKG
YFIKPTVFGDVKEDMRIVKEEIFGPVVTVTKFKSADEVINMANDSEYGLA
AGIHSTNINTALKVADRVNAGTVWINTYNDFFHHAVPFGGFNASGLGREMS
VDALQNYLQVKAVRAKLDE

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YER177W, 1304 bp, CDS: 501-1304 (SEQ ID NO 151)
AGATAGATAGATATAGATAGATAATGGACGTAGTTATAGAACAGAAAATC
GGTAGATCGAAAACACAGGGGAAAAAGGGGGGGGGGGGGGGGAGACAGCG
CAGCCACGTGACGGGCTTCCTCTTTGGAAAGTGGAGCGAAGTTTTGCGGA
AGCTACTTTTATTCGGGCTGGAGTCAAAGAGGAAGCTCGGTGGCAAATA
GCTTCCTCTTTGTGGCCGGGGCGCGGGGGGACGAGGCAAAAAGCAAAGAA
AAGCAAAAAAATAAAAAAACAACAAAAACAGGGGTATGAGAAAAAG
ACACGCTTTTCCACGCGCAGCAAAAAGGAAAAAGGAAAAGGAACTCTTT
ATTATTGGACCTTAAACCTGAAAACGAGACGAACCGTAACATAAAACCGT
GTAGTTTCTGCAAAAATAACTTAGTTTTCCTACTTTTCAAATTGAGAG
CGCAAGCAAGTGAGAAGAAAAAGCAAGTTAAAGATAAACTAAAGATAAAA
ATGTCAACCAGTCGTGAAGATTCTGTGTACCTAGCCAAGTTGGCTGAACA
GGCCGAACGTTATGAAGAAATGGTCGAAAACATGAAGACTGTTGCCTCCT
CTGGCCAAGAGTTGTCGGTCGAAGAGCGTAATTTGTTGTCTGTTGCTTAT
AGAAGCATTATTGGTGCTCGTTCGTGCTCTTGGAGAATTGTTTCTTCTAT
TGAGCAAAAGGAGGAGTCCAAGGAGAAGTCCGAACACCAGGTGAGATTGA
TTTGTTCTGACCGTTTGAAGATTGAGACCGAATACTAAGATCTCCGAC
GATATTTTGTCCGTGCTAGACTCCCACTTAATTCATCAGCCACCACTGG
CGAGTCCAAGGTTTTCTACTATAAGATGAAGGGTGACTACCACCGTTATT
TGGCTGAATTTTCTAGTGGCGATGCTAGAGAAAAGGCCACAAACGCCTCT
TTAGAAGCATACAAGACCGCTTCTGAAATTGCCACCACAGAGTTACCCCC
AACTCACCCAATCCGTCTAGGTTTGGCTCTTAACCTTCTCTGTCTTCTATT
ATGAAATTCAAACCTCTCCAGACAAAGCCTGCCATTTGGCCAAGCAAGCT
TTTGACGACGCTATTGCTGAGTTGGACACTCTGTCTGAAGAATCATACAA
AGATAGCACACTTATCATGCAACTGCTAAGGGACAATTTAACCTTATGGA
CTTCAGACATGTCCGAGTCCGGTCAAGCTGAAGACCAACAACAACAACAA
CAACATCAGCAACAGCAGCCACCTGCTGCCGCCGAAGGTGAAGCACCAAA
GTAA

YER177W, 267 aa (SEQ ID NO 152)
MSTSREDSVYLAKLAEQAERYEEMVENMKTVAASSGQELSVEERNLLSVAY
KNVIGARRASWRIVSSIEQKEESKEKSEHQVELICSYRSKIETELTKISD
DILSVLDSHLIPSATTGESKVFYKMGDYHRYLAEFSSGDAREKATNAS
LEAYKTASEIATTELPPTHPIRLGLALNFSVFYIEIQNSPDKACHLAKQA
FDDAIAELDTLSEESYKDSTLIMQLLRDNLTLWTSDMSESGQAEDQQQQQ
QHQQQQPPAAAEGEAPK

YOR267C, 2780 bp, CDS: 501-2780 (SEQ ID NO 363)
TAGTTCTATTTGGCTATATATTTTCAGAGTGACAAATCTTTAAGAGAGACA
AACTGAGAATTAGCATATAGAATCATTACATAACTGTTTACAAACAAGT
AAGCCCAAGACAGTTCCCAACCGCTTAAAGAAGTTTTTCTTAGAGGGAGC
AAAGTTCGTTTACATTTACACACACAGTTTTTTTTTCACTTTTTTGGGCC
TCTTCCTTTTCCCGTTTTTTTCAAAAAGCTTAGAAATCTTCTTACCTCC
TATTTTTCTAGAATCGTGAAGAATTTCCAGATTTAACAGTTTTCCACTTT
TTCAATAAGGAAATAGTAGGAATAATAAAAAAAGGATAGTAGTAACGATA
TACGTCGACTTTCCAGACTGGTCTCGAGCCGGAATTAAATACAATAGCAG
CGTTTGACTACTACCACATTGTAGCTCCGCTAGAATTGATCGAAAAACAAAAT
AATAACACTAATAATTATAATAATACGGTAGAATAATTTCTCGTATAAAG
ATGCCTAATCTATTGTGAGAAACCCATTCCATGGTCATCATAATGACCA
TCATCATGACCGTGAAAATTCGTCTAATAACCCGCCACAGTTGATCAGAA
GTTCTAAATCTTTCTTAAACTTCATTGGTAGAAAACAAAGTAATGACTCA
CTAAGAAGCGAGAAATCTACAGATTCCATGAAATCTACCACAACCACTAC
AAATTATACTACAACAACCTTAATAACAACACCCATAGCCATTCTAATG
CAACCAGTATCTCAACAACAACACTACAATAATAACTATGAAACAACAC
CACCATAATATTTCTCATGGGCTCCATGACTATACTTCTCCCGCCTCTCC

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AAAACAAACCCACTCCATGGCAGAATTGAAAAGGTTTTTCAGACCTTCTG
TAAATAAAAAACTATCTATGTCTCAACTTCGTTCCAAGAAACATAGCACC
CATTCCCCCCCCACCTTCAAAATCAACTTCTACAGTTAATTTAAATAATCA
CTATCGTGGCCAGCATCCTCATGGCTTTACAGACCACTATGCTCATACCC
AGTCTGCTATACCGCCAAGTACCGATTCTATCCTATCTTTGTCCAATAAT
ATTAATATATATCACGATGATTGTATTCTGGCTCAAAAATACGGGAAATT
GGGTAAGTTATTGGGTTCCGGTGCCGGTGGGTCCGTTAAAGTTCTTGTGA
GACCAACTGATGGTGCTACTTTTGCCGTCAAAGAATTTCAGACCAAGGAAA
CCGAATGAGAGTGTGAAAGAATATGCCAAGAAGTGCACCGCAGAATTTTG
TATTGGTTCGACTTTACATCACCCAAATGTTATCGAAACTGTTGACGTTT
TCTCTGATTCTAAACAAAATAAATACTATGAAGTTATGGAGTACTGTCCG
ATTGATTTTTTTGCTGTTGTTATGACAGGCAAGATGTCTCGTGGCGAGAT
CAACTGTTGCTTGAAGCAATTGACTGAAGGTGTTAAATATTACATTCTA
TGGGATTGGCCACATAGAGATTTGAAATTGGATAAATTGTGTCATGACTTCC
CAGGGTATTTTGAAATTAATTGATTTTGGTAGTGCTGTTGTGTTTCAGATA
TCCTTTTGAAAGATGGCGTAACGATGGCTCATGGAATCGTGGGTAGTGACC
CTTACTTAGCGCCGGAAGTGATTACCTCCACCAAATCTTATGATCCTCAG
TGCGTCGATATATGGTCTATTGGGATCATATATTGTTGTATGGTGCTTAA
AAGGTTTCCATGGAAAGCCCTAGAGATTCTGACGATAATTTTAGATTAT
ATTGTATGCCGGATGATATAGAACACGACTATGTTGAATCTGCCAGGCAT
CACGAAGAGTTACTGAAGGAAAGAAAAGAAAAGCGTCAAAGGTTTTTGAA
TCACAGTGACTGTTCCGCCATCAATCAGCAACAACCAGCTCATGAATCAA
ACTTGAAAACAGTTCAAAATCAAGTTCCAAATACTCCAGCATCTATACAG
GGTAAAAGCGATAACAAACCAGACATTGTGGAAGAAGAAACCGAAGAAAA
TAAAGAAGATGATAGCAATAATGATAAAGAAAGCACGCCAGATAATGACA
AGGAAAGTACCATCGATATTAATAAAGCAAAATGAGAATAAAAGCACG
GTAGTTTCAGCTAACCCAAAGAAAGTAGATGCCGATGCCGACGCTGATTG
CGATGCTAATGGTGACTCTAACGGCAGAGTGGATTGCAAGGCTAACAGTG
ACTGCAATGACAAAACGGATTGTAATGCTAACAAATGACTGCAGCAATGAA
TCGGATTGTAACGCTAAAGTTGATACTAACGTCAACACTGCTGCCAACGC
TAACCTTGATATGGTTCCCCAAAACAATCCACAACAACAACAACAAC
AACAACAACAACAACAACAACAACAACAACAACAACAACACCATCAT
CACCAGCATCAAAATCAAGACAAGGCCCATAGTATCGCTTCCGATAATAA
ATCGAGTCAACAGCACAGAGGACCTCACCATAAAAAAATTATTCATGGCC
CATACCGTCTATTACGTCTACTACCACATGCTTCAAGACCTATCATGTCC
CGTATACTGCAAGTAGATCCAAAGAAAAGAGCAACCTTAGATGATATTTT
TAATGATGAATGGTTTGCCGCCATTGCTGCCTGTACCATGGATTCAAAAA
ATAAAGTTATTAGAGCGCCTGGCCATCACCATACATTGGTTAGGGAGGAA
AATGCTCACTTAGAGACCTACAAGGTTTAA

YOR267C, 759 aa (SEQ ID NO 364)

MPNLLSRNPFHGHNDHHHDRENSSNNPPQLIRSSKSFLNFIGRKQSNDS
LRSEKSTDSMKSTTTTTNYTTTNLNNNTHSHSNATSISTNNYNNNYETNH
HHNISHGLHDYTSASPQKQTHSMAELKRFRPSVNKKLSMSQLRSKKHST
HSPPPSKSTSTVNLNNHYRAQHHPHGFTDHYAHTQSAIPPSTDLSLSNN
INIYHDDCILAQKYGKLGKLLGSGAGGSVKVLVRPTDGATFAVKEFRPRK
PNESVKEYAKKCTAEFCIGSTLHHPNVIETVDVFSKQNKYYEVMYCP
IDFFAVVMTGKMSRGEINCCCLKQLTEGVKYLHSMGLAHRDLKLDNCVMTS
QGILKLIDFGSAVVFRYPFEDGVTMAHGIVGSDPYLAPEVITSTKSYDPQ
CVDIWSIGIIYCCMVLKRFPWKAPRDSDDNFRLYCMPDDIEHDYVESARH
HEELKERKEKRQFLNHSDCSAINQQQPAHESNLKTVQNQVPNTPASIQ
GKSDNKPDIVEEETEENKEDDSNNDKESTPDNDKESTIDIKISKNENKST
VVSANPKKVDADADADCDANGDSNGRVDCKANSDCNDKTDNANNDCSNE
SDCNAKVDTNVNTAANANPDMVPQNNPQQQQQQQQQQQQQQQQQQHHH
HQHQNQDKAHSIASDNKSQQHRGPHHKIIHGYPYRLRLLPASRPIMS
RILQVDPKKRATLDDIFNDEWFAAIAACTMDSKNKVIRAPGHHTLVREE

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NAHLETYKV

YLR110C, 902 bp, CDS: 501-902 (SEQ ID NO 275)

TATTGGCGTCTGATTTCCGTTTTGGGAATCCTTTGCCGCGCGCCCTCTC
AAAACCTCCGCACAAGTCCCAGAAAGCGGGAAAGAAATAAAACGCCACCAA
AAAAAAAAAAAAATAAAAGCCAATCCTCGAAGCGTGGGTGGTAGGCCCTGGA
TTATCCCGTACAAGTATTTCTCAGGAGTAAAAAAACCGTTTGTTTTGGAA
TTCCCCATTTTCGCGGCCACCTACGCCGCTATCTTTGCAACAACCTATCTGC
GATAACTCAGCAAATTTTGCATATTCGTGTTGCAGTATTGCGATAATGGG
AGTCTTACTTTCCAACATAACGGCAGAAAGAAATGTGAGAAAAATTTGCAT
CCTTTGCCTCCGTTCAAGTATATAAAGTCGGCATGCTTGATAATCTTTCT
TTCCATCCTACATTGTTCTAATTATTCTTATTCTCCTTTATTCTTTCTTA
ACATAACCAAGAAATTAATCTTCTGTCATTTCGCTTAAACACTATATCAATA
ATGCAATTTTCTACTGTGCTTCTATCGCCGCTGTGCGCGCTGTGCTGCTTC
TGCCGCTTACAGTTACCACTGCTACTGTCAGCCAAGAATCTACCACTT
TGGTCACCATCACTTCTTGTGAAGACCACGTCTGTTCTGAAACTGTCTCC
CCAGCTTTGGTTTCCACCGCTACCGTCACCGTCGATGACGTTATCACTCA
ATACACCACCTGGTGCCCATTTGACCACTGAAGCCCCAAAGAACGGTACTT
CTACTGCTGCTCCAGTTACCTCTACTGAAGCTCCAAAGAACACCACCTCT
GCTGCTCCAACCTCACTCTGTACCTCTTACACTGGTGCTGCTGCTAAGGC
TTTGCCAGCTGCTGGTGCTTTGTTGGCTGGTGCCGCTGCTTTGTTGTTGT
AA

YLR110C, 133 aa (SEQ ID NO 276)

MQFSTVASIAVAVAASAAANVTTATVSQESTTLVTITSCEDHVCSETVS
PALVSTATVTVDVITQYTTWCPLTTEAPKNGTSTAAPVTSTEAPKNNTTS
AAPTHSVTSYTGAAAKALPAAGALLAGAAALLL

YLR109W, 1031 bp, CDS: 501-1031 (SEQ ID NO 273)

TGTCTATTAGTAATCAAGAAAAGAACCCTAAATCATCGGCGTCCCCTGTG
GGGCTCTCGGAAAAACCGGTCCTGACGTCAGTGAAGAAATTTTCGGCACAT
GGTCATGGGACCAGAGAAAAATTAATCCGACATGTGGAATATTTCCCTCC
GTTAAGGTAGTGAGCGCGGATTTTTTCTGATTTGTAATTATACGGGGAGC
TCTGGCCAAAAAGGTCAGTATTTGGTGATGAAGTTGAATATCATCTTTTG
ATTTTCTTCTGTATCATTCTTTTCTTTTCCACACCCCTTCCGGACGGT
ATTACATATTTGTTGAGAGGTTAAATGAAAAATAAAGGGGTGGAAAATTA
AGGACGAGATGTAAGGGAAAAGCATAAACGAAACATTATATAAAGGAGCA
CAATTTCCCTCTCCCTTGCCAATTGTGCATATACCGTTTCTTTATAACGAA
ATTTCAACAAACCAGAACAACACAAGTACTACCAATAACCACAACAAAAC
ATGTCTGACTTAGTTAACAAGAAATCCCAGCTGGCGACTACAAATTCCA
ATACATTGCTATCAGCCAAAGTGATGCTGACAGTGAATCTTGTAAGATGC
CACAAACAGTTGAATGGTCCAAATTAATTTCTGAAAACAAGAAGGTTATC
ATTACCGGTGCTCCAGCTGCTTTCTCCCCAACCTGTACTGTCAGCCATAT
TCCAGGTTACATCAACTACTTGGATGAATTAGTTAAGGAAAAGGAAGTTG
ACCAAGTGATCGTTGTTACTGTTGACAACCCGTTGCTAACCAAGCGTGG
GCTAAGAGTTTAGGTGTTAAGGACACCACACACATCAAGTTTGCTCCGA
CCCAGGCTGTGCTTTCACCAATCCATTGGTTTCGAATTAGCCGTCGGTG
ACGGTGTTTACTGGAGTGGTAGATGGGCCATGGTTGTTGAAAACGGTATC
GTTACTTACGCTGCCAAGGAAACCAACCCAGGTACCGATGTGACCGTTTC
CTCAGTCGAAAGTGCTTTGGCTCATTTGTAG

YLR109W, 176 aa (SEQ ID NO 274)

MSDLVNKKFPAGDYKFQYIAISQSDADSESKMPQTVESKLISENKKVI
ITGAPAAFSPTCTVSHIPGYINYLDLVKEKEVDQVIVVTVDNPFANQAW
AKSLGVKDTTHIKFASDPGCAFTKSI GFELAVGDGVYWSGRWAMVVENGI
VTYAAKETNPGTDVTVSSVESVLAHL

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YBL081W, 1607 bp, CDS: 501-1607 (SEQ ID NO 29)
TTGTTGCAACAATTTTGGGATGCTTCTGCGTCGTACGACCCTGTATTTAC
CTTCTCTAGCTCATCGCTTCCCAGGGTCCACGTTAATTTTCAATTTTTT
CTTGCGTGTGCAAGATTTCAGGTCTCGAGAAATTTGTCAAAAATTTTTCAC
TAGATATTAAGAACTATATACATCGAATAAGATGCCAGCACAGAAGAGAT
AGGCAATCAGTTTAGATACTACAGACACTATCCAATAGTGCAAAGCAAAA
GCAGCATAGAAAAAAGAGAATCCCGTTTCCAGCTTTTTCTCTTTTTCCCA
TTCGTTTTTTCCTGATCTTTTTTCTGCATCGTGGCACCTAGAACAAGAGG
TACCTTCCATCCTTCGCTTAATATTTGATACGACTTTTTTGATTTCATT
ATTATTATTTGTTACTATTATTATTTATCATTTGGGTTTCGGTTTTTTGT
AATAATTTTCTTTTTTTTTTTTGGCTCTATTTCACTAAGACATCGTATAT
ATGCCAGGCCAGATAATCAGCATTCCGTTTTTTGTGCGAGAACGAGGACAT
GGATAAATCCTTGTGGAGTACCGCAGTTTGAAGCTCCTTCATCAGTCCA
GTAATTCCTTCCAGTCTCACAATGCGCCCTCCACCAGTCGAACACCAC
CCCCATTACAATCAGTGAATACAACAACACTGGTAGCTATTACTATTA
CAACAACAACAATAACAGCAGTGTAACCCACATAACCAAGCTGGTCTAC
AATCCATTAAACAGATCTATTCCATCGGCCCGTACGGGGCTTACAACCAG
AACAGAGCTAATGACGTACCATATATGAATACCCAAAAGAAACACCACAG
ATTTAGCGCTAACAATAATTTGAACCAGCAAAAATACAAGCAATATCCCC
AGTATACGTCCAATCCAATGGTTACTGCACATCTGAAGCAAACGTACCCT
CAACTGTACTACAATAGCAACGTCAATGCTCACAACAACAACAACAG
CAACAACAACAACAACAACAACAACAGCAACAACAACAACAATCTTT
ACAACCAGACGCAGTTCTCCACGAGGTACTTCAACTCGAACTCCTCTCCC
TCGTTGACTTCTTCCACTTCTAACTCATCTCTCCATACAACCAAAGCAC
CTTCGAATACATTTTGCCGTCAACTTCGGCAGCTTCCACAAATTTATCGT
CGTCATCATCAAACAACCTCTATGCACACCAACCCAACTGCAACATCG
ACATCCGCCGATTTAATCAATGATTTACCCGTGGGCCCCACGTCCAGTTC
GCTTATCTCGGATCTACATTCTCCACCAACTGTATCTTTCTACCAGCAA
GCCAAACCCCTGCTCATGTCTCTCCACCACATCTAGCTCTATTGGCACCAC
ATAAACCACCGCAACATTCACCATCCCCATCGCAAAGGGAGGATTTTTC
GACGGCACCAAGTGAACATGTCTTCGTCCGCATCACTCTTGATGAATGATT
CTTCTTTAGGATGGGGGTCTAACCACATGAACGTATCTTCATCCTCTCAA
CCAGCATCATCAAGACCCTTTGGCATTGTGAATACTGACATGAGCGTTTG
GAGTTGA

YBL081W, 368 aa (SEQ ID NO 30)
MPGQIIISIPFLSQNEDMDKYLLEYRSLKLLHQSSNSFQSHNAPSHQSNYH
PHYNHMKYNNNTGSYYYNNNNNNSSVNPQNAGLQSIINRSIPSAFYGAYNQ
NRANDVPYMNQKKHHRFSANNNLNQKQYKQYPQYTSNPMVTAHLKQTYF
QLYNSNVNAHNNNNNNNNNNNNNNNNNNNNLYNQTFSTRYFNSNSSP
SLTSSTSNSSSPYNQSTFEYILPSTSAASTNLSSSSNSNMHTNPPTATS
TSADLINDLPVGPTSSSLISDLHSPPTVSFLPASQTLMSSTSSSIGTN
INPPQHSPSPSQREDFSTAPVNMSSSASLLMNDSSLGWGSNHMNVSSSSQ
PASSRPFGIWNTDMSVWS

YDR366C, 899 bp, CDS: 501-899 (SEQ ID NO 125)
CTGTCGATATTGGGTTACTTTGTAGTGCATTATTTCCATCAATATTAGCA
GTGTCTTCCAAGGTGAACCATTCGCTGGTAAACCATAGAGTAAAAAACA
AGTGGAATGGTATCGATTGTATAAAGTACGCAGATTTGCGAAAATACCA
GCAAGTTTGGCTTATGAATCAAATACAGCCCTTGTGAGAATACGATTAAT
GTAAATACCGACCAAAGATATGCTATCCATTGCATAAAATCCAACGGATG
ACCCGTGAACAATGCTAAATACCATAAGCACCCTGCATTTGTTTAGAA
TGGAATACCTAAGACAATCTCAACTGCAAGGTATAGCGGCATAAACCCC
AAAAAGACTATGAAAAAAAATATGTTTGAGAACAGGTTAGTAAATTG
TGCTTTGCTTCGAATCCTTACAAGTTAACAAAAATTTATAGCGTTTGCCG
GAAACATACTTTTGAAGGGTTAGAAGAGATGATCTCATAACTAAGGTTA

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ATGGTTACAATTGGTAGTTCCTCCCTGGTATTATTTCTTTTCTTCGTAGT
TTTTGTACAGATCACTTATACAGCTTTACACAGATTTTCCCGCTTGTGT
GCACTTTTTTTTCGAAGATTATTGAAGAGGGATGCGTTTGGTACAATAAA
AAACATAGGTTCCCAAACCTATATAAATATATATATGTATATGTATATAT
ACTACATATATGCTTTGAGAAATATGTGAATGTTGAGATAATTGTTGGGA
TTCCATTGTTGATAAAGGCTATAATATTAGGTATACAGAATATACTAGAA
GTTCTCCTCAAGGATTTAGGAATCCATAAAAGGGAATCTGCAATTCTACA
CAATTCTATAAATATTATTATCATCATTTTATATGTTTATATTCTATTGA

YDR366C, 132 aa (SEQ ID NO 126)
MVTIGSSSLVFLFFVVFVQITYTALHRFSRLCTFFSKIIEEGCVWYNK
KHRFPNLYKYIYVYVYILHICFEKYVNVEIIVGIPLLIKAILGIQNILE
VLLKDLGIHKRESAILHNSINIIIIILYVYIH

YDR154C, 851 bp, CDS: 501-851 (SEQ ID NO 101)
TAGACGGGCTTCCACGCGCTTCCACTCATTTCTGTCTCTGGTAATGGCCG
TGGCCCTTCTCACTTTGGTTGGGCTTACGCTGACAAGTGTCTGTTTCGATT
CCCTGTATAAATATAAACGTATTCTCTTGAGCCTTCTATCCTTTTGCCAC
TGTCGTCATCATTTGTTCTCTCTTTTTCGCTAGATAGGTTATATTAAGAT
TTGTCTTGAATTTAATATCTCAACTCAATCCAACTCAACCGCTAATACT
ACCATGTCCCAAGTCTATTTTGATGTGCAAGCTGATGGCCAACCAATTGG
CCGTGTCTGTTTTCAAGTTGTACAACGACATAGTCCCAAAGACTGCAGAAA
ACTTCAGAGCTCTATGTACCGGTGAAAAGGGATTTCGGCTACGCTGGCTCT
CCATTCCACAGAGTTATTCCAGACTTCATGTTGCAAGGTGGTGACTTCAC
TGCTGGTAACGGTACCGGCGGTAAGTCTATCTACGGTGGCAAATTCCCAG
ATGAAAACCTTCAAGAAGCACCACGACAGACCAGGTTTGTGTCCATGGCC
AACGCCGGTCCAAACACCAACGGTTCTCAATTCTTCATCACCACCGTTCC
ATGCCCATGGTTGGACGGTAAGCATGTTGTCTTTGGTGAAGTTGTTGACG
GTTACGACATCGTTAAGAAGGTTGAGTCCTTGGGTTCTCCTTCCGGTGCC
ACCAAGGCTAGAATTGTTGTTGCCAAGTCCGGTGAATTATAACCGCTCTG
CCTGGAACAATACAGCAAAAATTGAAACGAACTATTCTCTCTTAAATTAT
ATGTATATGTATAAGGTATGTGTATGTATGACAATCAATTCTTATAACTA
A

YDR154C, 116 aa (SEQ ID NO 102)
MKTSRSTTTDQVCCPWPTPVQTPVLNSSSPFHAHGWTVSMLS LVKLLT
VTTSLRRLSPWVLLPVPPRLELLLSPVNYNRSAWNNTAKIETNYSLLNY
MYMYKVCVCMTINSYN

YHR162W, 890 bp, CDS: 501-890 (SEQ ID NO 213)
CGCTCGCTTCCAAGAGTTATCATCATATTCTTCATCATATTCTTCCATAC
TTAAGGTGGGTAGCGAGGACCCCTCAATTCCCCCACCTCTCTGCCAGGGC
GTCATCTTTTTCTACAAAAGCCAGGCTGAGTCACGTCAGTTGCTGACCCT
GGGGGCTGCATTGTTTCTACGAATTACTCATTTGTTTCGTGCGCTTTCC
TATTGCGCGCATGACTAGGATGGAAAAAAGAAAGAAAAAGAAAGCGT
TGAGTATATAATAAGAAAGAAAGAAAGTCCGAGAGAAAAGAACACAAA
GGTTTTTCTCGAGGAAAACAGTAAAGTTTGATACGCACATCGTTGACAT
CGCTGACTGCAATAGGAACTGAAATAGACGGCAAACCATTAGTTCATT
GAAAGAACGTATTGTCGAGAATTATCACTCACTATATCAGAAAATTGACA
CACGAATTATATAAACGAAGTTATACAGAAAAAGATTAAAGAAAAAGAAA
ATGTCTACATCATCCGTACGTTTTGCATTTAGGCGGTTCTGGCAAAGTGA
GACAGGCCCAAGACGGTGCATTTCTGGGCTCCTACTTTGAAATGGGGTC
TGTTTTTTCGCTGGATTCAGCGATATGAAGAGACCGGTGAAAAAATTTCT
GGTGCTCAAATTTGTCGCTGCTATCTACTGCGCTGATTTGGACTCGTTG
GTCCTTTGTCAAGCAAGAAACATCTTGTTGGCTTCTGTCAACTCGT
TTCTTTGTCTGACCGCTGGCTATCAATTGGGTAGAATTGCCAACTACAGG

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ATACGGAATGGCGACTCTATATCGCAATTGTGTAGCTATATTCTCAGCGG
CGCCGACGAAAGCAAAAAGGAAATTACTACGGGCAGATAA

YHR162W, 129 aa (SEQ ID NO 214)
MSTSSVRFAFRFRWQSETGPKTVHFWAPTLKWGLVFAGFSDMKRPVEKIS
GAQNLSLLSTALIWTRWSFVIKPRNILLASVNSFLCLTAGYQLGRIANYR
IRNGDSISQLCSYILSGADESKKEITTGR

YGR243W, 941 bp, CDS: 501-941 (SEQ ID NO 189)
CCTCCACCAAAGCAAAATGAAAACAAAGCCATACTGGGAAAAATCTGAAA
AAAAAATGGTAGGAGTAAAAGAAAAGAAAAATAAAGGTTACCTGCAG
TTTGGATAGTCGGGTAACATTTGGCCCTTTTCCTCCTTGATTGGATATTA
TTACCCCGATTACCCCTCATCTTGGGAGTGCCCGCTTTTATTTCTCCCG
CCAATCGGCTATTAACGGCTTTACGTCATTCCGTGGGCGGGTCAAGCGAG
CCGCTCCCTGGTTTGGTCACGCAAAACCGAAAGGCTCAAACAAAATAAG
GCCATCATATATATATATGCGGCTGCGTGCGTGATTCTCCCGGATAATA
TGGTGCGTTGCAATTGGAGTATTGGAGAAAATTTCTTTTCCCTTTCATT
ACGGCGGAAATACTTCATATAAAAAAAGAATACAATCAGTCTTTAAGA
CTATACGCATAAGCATTCAAGACACATAGAAACACAAACCTATATTTTAA
ATGTCAGCATCAGCTTTTAATTTTGCCTTTAGAAGATTTTGGAATAGTGA
AACAGGCCCTAAACAGTACACTTCTGGGCCCCAACTTTGAAGTGGGGGC
TGGTCTTCGCAGGGCTAAATGATATTAAGAGGCCTGTTGAGAAGGTATCA
GGAGCACAAAATTTATCTTTATTAGCGACGGCACTGATTTGGACGCGTTG
GTCGTTTGTCAAGCCCAAGAACTATCTGTTAGCTTCCGTCAATTTTT
TCCTGGGTTGCACTGCAGGCTACCATCTAACAAGAATTGCTAACTTTAGG
ATACGGAACGGTGATTCTTTTAAACAGGTTATTCATACATAATAAAGG
GGAGACTCCTGCAGCCGTCGCAGCAAAGCAAACCTGCATCCACATCGATGA
ACAAAGGTGTGATCGGTACTAATCCGCCAATAACGCACTGA

YGR243W, 146 aa (SEQ ID NO 190)
MSASAFNFAFRFRWNSSETGPKTVHFWAPTLKWGLVFAGLNDIKRPVEKVS
GAQNLSLLATALIWTRWSFVIKPKNYLLASVNFFLGCTAGYHLTRIANFR
IRNGDSFKQVIHYIILKGETPAAVAAKQTASTSMNKGVIQTNPPITH

YBR050C, 1517 bp, CDS: 501-1517 (SEQ ID NO 43)
AAGTACGATATGGTATAACTGTAACATTGAAGGACTGAAGGACTGAAGGA
CTGAAGGACTATAGTCAAGGGCCAATGGGGAAGGTCCCTTCCAGGCCATT
TGCCCGATAGTTTGTCTTCTCTTGCTTTTCCGACGGCCCGATTGCATGT
GGCGGGGCAGCACTGGATAAAAAACGTGGGGGGAGTGATTAAATTTATA
CGCTTATTGTGTCAACACGGAAACCTTATAGTTATCATTACTAACATCGC
AACAAGCTGCTTTTTTACTCGTTTTTAGCCACACCATACCCCTTTAATT
AACTAATAATGCATAAAATAGTTATTGCTTCTTGAGTTGCAGCTTCTTCC
TGGACGTACTGTTATATATGGCATGTCTTCGCATGTCCGTCAAATTTAGC
GTTGTCTCGAAACTTAGGCTGTCGTTCTTGCTGTCTGTCTTCTGATAAAA
TAATATATTGGAATAAGAAAAAATAGGAACAAGAAAGTGTGTGAGA
ATGACTTTGAGTAATTGCGACTCTTTGGATAACTTATTCAGGACCTCC
AGAGGAAGAAGAAAGTAGTAAATTCGTTGAGGCGGTGAGAACTTTGATGA
ATAGAAACGATATGGGATATCCTCCCGCCGTGCAAAATGGTACGTATTGC
TTAAAAAAATCAAGTCTTTGAATGCCAAACAGTGGAAAAATAAACAAGAA
AAGAATGTGCATGTTGCCAGCAGTAAAGAAGAAAAATTCGACTTTCACG
AGCAAAGAAGTTAATCTTGAATTTAAATTTATGGAAATTCATCAAGTTT
ATCAATTGTAGTAGTAAAAACAATTACAATAAAAAATAAAGCATGTGAG
AAGCTCGAACAACACTGTAAAAAATGAAAATGTTTTACCGTTACAAAAAC
ACAAGAAAGTGGACAATGATCAAAGATTGGAGAACCTTTTTTGGAGAAGC
TGGTTTAAGGCACGCAAAAGGAGAGATATAATGGGCAAGCCACGAGAGAG
GCATATCAAATTTAACGATAACGTTGAACAGTGTATTATAACTGATGAGC

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ATTTTCATACAAAGGCTTCCTTCTACACGGTTGAATTCGACTGATGAACAG
CGCCCTTGTTCAAAGTCTGAACTAGATCCCTGTATTGGCAACGCAGCAAG
TAAGCGAAGTTTCTATGATTATAACAGCGTTTACGTCGCGAGTGACGCAA
TTATTACGACTGCCGCTGCCACTGCCATTATCAGTAGTAATAGTGGAGAC
TATCAGCGTGGGCACGATGTTCCGCGATGTTCCAAGAAATGTTTTGTTACA
GGCAGGAGAAACAGATTTTCAGTAGTGTGCTTCGGGTTGACTCCGATCTCA
AGTTATCCAACATAAGTCATCATTTCCCCCGTAAAACCTTCGTCAACTTCA
AGTCATTCGACCTTCATTTTCGAGTCGGAAACTGACACTGATACTGATAC
TGACGCTGAAACAGAAAATGACATTGACGCTTACATAGACACCAGTATAC
CCAACCTGCTCCTATAA

YBR050C, 338 aa (SEQ ID NO 44)

MTLSNCDSLDNLFDPPPEEESSKFVEAVRTLMMNRNDMGYPAAANGTYC
LKKIKSLNAKQWKINKKRMCM LPAVKKKNFDFHEQRLILNLNLWKFIKF
INCSSKNYNKNNKHVRSSNNTVKNENVLP LQKHKVDNDQRLLENLFWRS
WFKARKRRDIMGKPRERHIKFNDNVEQCIITDEHFIQRLPSTRLNSTDEQ
RPCSKSELDPCIGNAASKRSFYDYNVYVADAIITTAATAI I SSNSGD
YQRGHDVDRVPRNVLLQAGETDFSSVLRVDSDLKLSNISHSPVKPSSTS
SHSTFIFESETD TDTDTDAETENDIDAYIDTSIPNLLL

YEL071W, 1991 bp, CDS: 501-1991 (SEQ ID NO 143)

TAGCTTGACCTGGTCAGATTAATCAGCTTCCAACGTTACTTCCCTTTTCGC
AAGAATCTACCCAAATGTCTCGAGCATCTTGATAATTACAGTATCGTTC
GTCCCGACTTGGCATTGTGTTAAATTTCTAAGATGCTTCTATAGGAACA
TAATTGTCAAGAAAGCACAACAAATTGTCTGCAATGTCAACAGGAGTGGC
GCATTTTATGTTTTTTCATTTTTTTTTTTTTTGTGCGTGATCATTAAGCGG
GATATTGTCCACAGTCATCTAAAAGAATGACCATTTTCGACGACTTAGTTC
GGAAAATATTTCCAGCGGATGACACCACTTGCCACAGTTGGTGACCGCCA
AATCTAAGTCACGCGCGGAAACTGAAAGGTTGTGAGTATATAAGTGATCA
CTCGCTTATATAACTGACGAGGCAGAACAGGGTGCCAAAATGCTCCTCAA
TATTTTATTCATTTGAGATTC AAGGCTTAAAGACAGCATATATAAGAATT
ATGACGGCGGCACATCCTGTGTGCTCAGTTAACTGCCGAGGCATACCTTAA
AGTCAAGAGAAAACCCAAATTTCAAAGTTCTCGACTCGGAAGATTTGGCGT
ACTTTTCGTTTCGATTTTGTGCAAAATGATGAAATCTTAAACTCTCAAGCTCCA
GAAGAGCTTGCTTTCGTTTFAACCAGGACTGGATGAAAAAATATAGAGGCCA
GTCCAATTTAATTCTCTTGCCAAACTCCACTGATAAAGTGTTCAAGATTA
TGAAATACTGTAAACGATAAAAAGTTGGCAGTAGTACCACAAGGTGGTAAC
ACCGACTTGGTCGGAGCCTCTGTTCCGGTATTTGATGAGATTGTTCTTTC
TCTAAGAAATATGAACAAAGTCAGAGATTTTGATCCAGTTAGCGGGACTT
TCAAGTGTGACGCGGGTGTGCTTATGCGTGATGCGCATCAATTTTACAC
GACCATGACCATATCTTCCCATTGGATCTGCCCTCTAGAAACAACGTGCA
AGTGGGCGGTGTAGTTTCAACAAATGCAGGTGGTTTGAACTTTTTAAGAT
ATGGGTCTCTACACGGTAATGTTTTGGGTTTGGAAAGTGGTGCTACCCAAC
GGTGAGATTATCAGCAATATCAATGCCCTAAGGAAGGACAATACTGGTTA
TGACTTGAAACAATTATTCATCGGTGCAGAGGGTACTATCGGTGTGCTTA
CTGGTGTATCCATAGTTGCAGCAGCAAAGCCAAAAGCCTTGAATGCCGTA
TTTTTTGGTATTGAGAAATTCGATACCGTTCAGAAATTATTTGTCAAGGC
TAAAAGTGAATTATCTGAGATTTTATCTGCTTTTGAATTCATGGACCGTG
GCTCCATTGAATTGATACGATAGAATACTTGAAGGACTTGCCTTTCCCTCTG
GAGAACCAACACAACTTTTATGTTCTTATTGAAACGTCAGGGTCCAATAA
GAGACACGACGATGAGAAGCTGACTGCTTTCCCTCAAAGATACCACAGATT
CTAAATTAATTTTCGGAGGGTATGATGGCTAAGGACAAAAGCCGATTTTGAT
AGACTTTGGACCTGGAGAAAAATCTGTTCCAACAGCTTGTAATCTTACGG
TGGTATGTACAAGTATGACATGTCACTTCAATTGAAAGATTTATATTCCG
TATCTGCGGCTGTGACGGAGAGATTAAACGCAGCCGGTTTGATTGGTGAT
GCACCAAAACCAGTTGTTAAATCATGTGCTTATGGTCATGTCCGTGACGG

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AAACATCCATTTAAATATCGCGGTAAGAGAATTTACAAAACAGATTGAGG
ACTTACTAGAACCATTTGTTTATGAATATATTGCATCAAAGAAAGGTTCC
ATCAGTGCTGAGCATGGGATCGGTTTCCATAAGAAAGGTAAGTTACACTA
CACCAGAAGTGATATTGAAATTAGATTTATGAAGGATATCAAAAATCACT
ACGATCCAAATGGAATCTTAAACCCATACAAGTACATTTGA

YEL071W, 496 aa (SEQ ID NO 144)

MTAAHPVAQLTAEAYPKVKRNPVFKVLDSEDLAYFRSILSNDEILNSQAP
EELASFNQDWMKKYRGQSNLILLPNSTDVKVSKIMKYCNDKKLAVVPQGGN
TDLVGASVPVFDEIVLSLRNMNKVRDFDPVSGTFKCDAGVVMRDAHQFLH
DHDHIFPLDLPSRNNCQVGGVSTNAGGLNFLRYGSLHGNVLGLEVLPN
GEIISNINALRKDNTGYDLKQLFIGAEGTIGVVTGVSIVAAAKPKALNAV
FFGIENFDTVQKLFVKAKESEILSAFEFMDRGSIECTIEYLKDLFPPL
ENQHNFYVLIETSGSNKRHDDEKLTAFLKDTTDSKLISEGMMAKDKADFD
RLWTWRKSVPTACNSYGGMYKYDMSLQKLDLYSVSAAVTERLNAAGLIGD
APKPVVKSCGYGHVGDGNIHLNIAVREFTKQIEDLLEPFVVEYIASKKGS
ISAEHGIGFHKKGKLHYTRSDIEIRFMKDIKNHYDPNGILNPFYKYI

YDR133C, 836 bp, CDS: 501-836 (SEQ ID NO 95)

GTGCAGAGGGTGAATCAACGGCCCCCTTCACAGAAACCGCGCAGGAATTTT
TCTGGTGTTTGTATTTTTTTTTTTCCTTGTACTTATCTCACTTTTCTTTT
CTAACTATTTTTTTTGCAATTTTTTTGTGTACACTTTCCACAACATATAG
GATGGTTTAGTCATCTCTCGAAGTATATAAACCGTTGCTGGATCGTGGTT
GTTCTTCATCGACTTCTCTCTGCTAGACTCTCTTTTTTAAAATTTTTTCA
TAGAATAAAAAACCAAGGATAACAAACATCTTCTTTCGTTTCGCTTCAAAA
TAACTACAAATTAATAATGCAATTTCTTACCGTCGCTTCTATCGCTGCTA
TTGCCGCTGTGTCCTCCGCCGCTTCTAACATTACCACTGCTACTGTCACA
GAAGAATCTACCACTTTGGTCACATCACTTCTTGTGAGGACCACGTTTG
TTCTGAAACAGTTTCCCCAGCTTTGGTTTCCACTGCTACCGTCACCGTAA
ATGACGTTATCACTTAATACACCACCTGGTGTCCATTGCCAACCCTGAA
GCACCAAGAATACCACTTCTCCAGCTCCAAGTAAAAGCCAAACCGAAAA
GCCAAGTAAAAGCCAAACCAACAAGGTTCTAGCACTCAAACGTTTACCT
CCTACACTGGTGCCGCTGTTAAGGCTTTGCCAGCTGCCGGTGCTTTGTG
GCTGGTGCTGCCGCTTTATTGTTGTAATTTACTCAACCTTTTCTTTAATA
TATTTTTTAGAAAAATGGTTAAGTACTTTTCCGTCATACAGCTTCCACAA
AATCGTTTTTATTTCAATTAATAAGATATTCTGGTAA

YDR133C, 111 aa (SEQ ID NO 96)

MTLSLNTPPGVHCQPLKHQRIPLLQLQLKSQPKSQLKSQPNKVLALKLLP
PTLVPLRLRCQLPVLCWLVLPLYCCNLLNLFNIFLEKWLSTFPSIQLPQ
NRFISINKIFW

YHL021C, 1898 bp, CDS: 501-1898 (SEQ ID NO 193)

GGTAAAAGAAATGATCAGGGAGCGTTTCTTGCAACAGCAGCAACAGTACA
GGCAGCAACAGCAGAAGGATGGCAATTACGTAAAGCCCTCTCAGGACAAC
GTGGATAGCAAGGACTAACCAGACAGATTGAGGTCTTTTCATGCATTACC
ACCAGTAATAATATTATACGGAATAATATAGTTTATATAATATCCATAAT
CATAATCATAATCATAATCATAATCGTGATATTGTACCAGCCCC
GCTTCTCCCTTTTGAACACCATTATTATCGGACCCTCTTTACCTTTGA
ATGGCTCAGTAAGGACCTTTGCGCAGCCGTAAGGGGGTCGGGAATACATT
TCCGGGGTTGATCCTCGAGGAAAAGTGCTATCTATATAAGGAGAAGCCCT
TCTAGATCCAAATATCAGGGGTAACCTTTCACAACCTGGCCAGGAACATAT
TCCAAGTTAAAAGAAAAATAATTATTAGAAACCAATTACCAACACAAG
ATGCTAAGATCAAATTTATGCAGAGGATCTCGAATCCTTGCAAGACTGAC
CACTACACCAAGGACATACACATCTGCGGCGACAGCTGCGGCTGCGAATC
GGGACATATCATCAAAACATACTTCAATAGAGATTCTACGACAATTACG

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TTCTCCATGGAGGAGTCCAGCAAGCCGGTTTCCGTTTGCTTTAACAACGT
TTTTCTTAGAGATGCCTCCCATAGTGCCAAGCTGGTGACCACGGGAGAAC
TGTATCATAACGAGAAATTGACCGCTCCTCAGGACATTCAAATTTCTGAG
GACGGAAAATCTCTAGTGGTGAAATGAAAAGATGGCGGTATCACCAGTT
CCCTTTACAATTCTTTATCGACTATAAAGGTTCCAGTTTGTTCGCCAG
CAACAAGAAAACAAGAATCCAGATATAGACCCAGTTATGGAATAAGCGC
ATCCTGAAAGATAACGTCAAGGACTTACTTTCTGTGAGCTACAACGAGTT
TATTGATCCTAAGGATGACTCCAAGCTTTTCCAAACGCTGGTCAACCTAC
AAAAGTTTGGTATCGCTTTCATTTCCGGTACTCCTTCATCCTCCTCTGAA
GGCCTTACCATACAAAAGATCTGTGAAAAGGATCGGACCCATAAGATCGAC
TGTACATGGTGAAGGTACATTTGACGTGAATGCATCCCAAGCGACAAGTG
TTAATGCCATTATGCCAATAAAGACTTGCCGCTACATACGGATTTACCA
TTTTTAGAAAATGTGCCAGGTTTCCAGATTCTACAATCTCTACCTGCTAC
AGAAGGGGAAGATCCCAATACTAGACCCATGAATTACTTCGTGGACGCAT
TTTATGCTACCCGTAATGTTAGAGAATCGGATTTTGAGGCTTATGAGGCT
TTACAAATTGTTCTCTGTAAATTATATATATGAAAACGGCGATAAGAGGTA
CTACCAATCCAAACCTTTAATCGAACATCACGACATTAACGAGGACAATA
CTCTTCTGGGTAATTATGAGGCCCTTGATTAAATGCATTAACTACTCTCCA
CCATACCAAGCACCTTTCACCTTCGGAATTTATGATAAGCCCTCAGATCT
AAATAATAATCTGGACTTGAATTTAATTACCACCCAGCAAACTAACAG
AGAGATTTTGTTTAAGTCTTTCATTAGGGGGTTGAACTTGTTCGAGAGT
CATATCAATGACTTCAACAATCAATTTAGATTGCAGTTGCCCGAAAACCTG
TTGTGTTATCTTTAACAACAGGAGAATTTTGCATGCTAACTCTTTAACAA
GCTCAAACCAGCAATGGTTAAAGGGTTGCTATTTTCGATTCTGATACTTTC
AAGAGTAAATTAAAGTCTTGGGAAGAGAAGTTTCCTCATGACAAATAA

YHL021C, 465 aa (SEQ ID NO 194)

MLRSNLCRGSRLARLTTPRPTYTSAATAAAANRGHIIKTYFNRDSTTIT
FSMEESSKPVSVCFNNVFLRDASHSAKLVTGELYHNEKLTAPQDIQISE
DGKSLVVKWKDGGHHQFPLQFFIDYKGSSFVSPATRKQESRYRPQLWNKR
ILKDNVVDLLSVSYNEFIDPKDDSKLFQTLVNLQKFGIAFISGTPSSSSE
GLTIQKICERIGPIRSTVHGEFTFDVNASQATSVNAHYANKDLPLHTDLP
FLENVPGFQILQSLPATEGEDPNTRPMNYFVDAFYATRNVRSDFEAYEA
LQIVPVNYIYENGDKRYQSKPLIEHHDINEDNTLLGNYEALIKCINYS
PYQAPFTFGIYDKPSDLNNLDLNLITTPAKLTERFLFKSFIRGLNLFES
HINDFNNQFRLQLPENCCVIFNNRRILHANSLTSSNQWLKGCYFDSDTF
KSKLKFLLEKFPPhDK

YKL054C, 2717 bp, CDS: 501-2717 (SEQ ID NO 237)

CCTGCTCTAGACGAAGCTAGGGAGGAGGCGCCGTTTGAAAATGGCGGCAA
ACTAAAAGAAGTTGACAAATGAAGTATATATTTTAGCACAGAATGTGCAT
TATTCAACATGTAAATACTAATACTGCAATATCGACTTATAATAATGTAT
AGTGATCCGTATATTAATAGATCTGTTTCAATTCTTTACCTTTTTAGGAT
ATCCGTCACCCGTGATTCCGTCGGAGGTGAGCACTCGCCCAAATAAAATAA
CGGGAAATGGTGGCAAAAAGTAGTGGCGGGAAAAGGAAAAATTTTCGTTT
TCTCCCATATAAACGTTTCATTCCTTTTCCTAAGTCTTTTACAGTAATTT
CAGAAACATTCGTATTTTATATTTGATCTTTTGAAGCTACAAGAAAACT
CTTACCAATTACCCCAAAAAATCACCATCATAAAGTACTTACATATTTA
TTTTTGTGTTGGTTCGTTTCTCAATATAATCTACATCATCATATATATA
ATGTCTACACAATTTAGGAAGTCTAATCATATAGTCATAGTAGTAAAAA
ACTAAATCCTGCGCTAAAGTCCAAAATAGATACGCTTACAGAATTGTTCC
CTGACTGGACGAGTGATGATTTAATTGATATAGTTCAAGAATATGATGAT
TTGGAACTATAATTGATAAAATTACTTCCGGCGCAGTGACAAGATGGGA
TGAAGTAAAGAAACCTGCTAAGAAGGAAAAATATGAAAAAAGGAGCAAC
AACACTCATATGTCCCTCAACAACATTTGCCAAATCCAGAAGATGATATT
ACATATAAGAGTTCTAATAATAGCAATTCTTTTACTTCTACAAAGCATAA

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CAGTAGTAACAATTATACTCAAGCCAGAAATAAGAAGAAGGTACAAACAC
CACGAGCTCATACAACCGGGAACATGTTAATCTCGACAAGGGGAAGCAC
GTACCATCCAAGCCTGTTTCAAACACTACATCGTGGGCAGCAGCTGTTTC
TGTAATACTAAACATGACGTTCTCAAGATTCAAATGATAACAATAATG
AAGAATTAGAAGCACAAGGGCAACAAGCGCAGGAGAAAAATCAAGAAAA
GAGCAAGAAGAGCAACAACAGCAGGAAGGGCATAATAACAAAGAAGAACA
CAAACAAATAGAGCAACCTTCTTTATCTTCAAAGAAAACAACTTCTAGGA
CATCTGCTTCACAACCAAAGAAAATGTCGTGGGCTGCAATTGCTACACCA
AAGCCAAAGGCTGTTAAAAAGACCGAGTCTCTCTTGAAAACGTTGCTGA
ATTGAAGAAAGAAATAAGCGATATTAAGAAGGATGACCAAAAGTCTGAAG
CTAGTGAAGAAAAAGTTAATGAACAAGAAACATCTGCACAAGAACAAGAG
GAGGAGACTGCTGAACCTTCTGAAGAAAATGAAGACAGAGTCCCTGAAGT
GGACGGAGAAGAAGTCCAAGAAGAAGCTGAAAAAAGGAACAAGTAAAG
AAGAGGAACAGACAGCGGAAGAGCTGGAACAAGAACAAGATAATGTTGCT
GCTCCAGAAGAAGAAGTTACAGTTGTTGAAGAAAAGGTTGAAATTAGTGC
TGTTATTTTCAGAGCCTCCAGAAGATCAAGCTAATACTGTACCTCAACCAC
AACAACAATCCCAACAACCACAGCAACCACAGCAACCACAGCAACCACAG
CAACCACAGCAACCACAGCAACAACAACAACCACAGCAACCACAACAACC
ACAACAACAACACTACAACAGCAACAGCAACAGCAACAACAACCAGTACAAG
CTCAAGCTCAAGCCCAAGAAGAACAATTATCTCAAACTACTATACTCAA
CAACAGCAGCAACAATACGCTCAACAACAGCATCAGTTACAGCAACAGTA
TTTGTCCCAACAACAACAATATGCTCAGCAACAGCAACAGCATCCACAAC
CTCAATCACAACAACCTCAATCACAGCAAAGTCCACAAAGTCAAAAACAA
GGGAACAACGTGGCTGCCCAACAGTACTACATGTATCAAAACCAATTTCC
TGGATATTCTTATCCAGGTATGTTTGATTACAAAGGATACGCTTACGGTC
AACAATATCAGCAACTTGCTCAAAACAACGCTCAAACTAGTGGTAATGCT
AACCAATATAATTTCCAACAAGGTTATGGTCAAGCAGGCGCGAACACTGC
TGCTGCTAATTTGACTAGTGCTGCCGCTGCTGCTGCCGCTTCTCCAGCTA
CAGCTCAGGCCCAACCTCAACAACAACAGCCATACGGTGGCTCATTTCATG
CCATACTACGCCCACTTTTACCAACAGTCATTTCCATATGGTCAACCTCA
ATACGGTGTAGCTGGTCAATATCCATACCAGTTACCAAGAACAATTACA
ACTATTACCAAACTCAAAACGGTCAGGAACAGCAAAGTCCAAATCAAGGT
GTTGCCCAGCATTCTGAAGACTCTCAACAGAAGCAATCACAACAGCAACA
GCAACAGCAACCTCAAGGTCAACCCCAACCTGAAGTTCAAATGCAAAATG
GCCAACCTGTTAACCCACAACAACAATGCAGTTCCAACAATACTATCAA
TTCCAACAACAACAGCAACAAGCTGCTGCCGCTGCCGCTGCTGCTGCCCA
ACAAGGTGTACCATATGGCTACAACGGTTATGATTACAATTCTAAAAATT
CAAGAGGTTTCTACTAA

YKL054C, 738 aa (SEQ ID NO 238)

MSTQFRKSNHNSHSSKKLNPALKSKIDLTLELFPDWTSDDLIDIVQEYDD
LETIIDKITSGAVTRWDEVKKPAKKEKEYEKKEQHSYVPQQHLPNPEDDI
TYKSSNNSNSFTSTKHNSNNTQARNKKKVQTPRAHTTGKHNLDKGKH
VPSKPVSNNTSWAAVSVDTKHDVPQDSNDNNNELEAQGQQAQEKNEK
EQEEQQQEGHNNKEEHKQIEQPSLSSKKTTSRTSASQPKMSWAAIATP
KPKAVKKTESPLENVAELKKEISDIKKDDQKSEASEEKVNEQETSAQEQE
EETAEPSEENEDRVPEVDGEEVQEEAEKKEQVKEEEQTAELEQEEDNVA
APEEEVTVVEEKVEISAVISEPPEDQANTVPQPQQQSQQPQQPQQPQ
QPQQPQQQQPQQPQQPQQQLQQQQQQQQPQVQAQAQAQEEQLSQNYTQ
QQQQQYAQQQHQLQQQYLSQQQQYAQQQQQHPQPQSQQPQSQQSPQSQKQ
GNNVAAQQYYMYQNQFPGYSPGMFDSQGYAYGQQYQQLAQNNAQTSNA
NQYNFQQGYGQAGANTAAANLTSAAAAAASPATAHAQPQQQPYGGSFM
PYYAHFYQQSFYGPQYGVAGQYPYQLPKNNYNYQTQNGQEQQSPNQG
VAQHSEDSQQKQSQQQQQQQPQGPQPEVQMONGQPVNPQQMQFQQYYQ
FQQQQQAAAAAQAQGVYPYNGYDYNKNSRGFY

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YLR311C, 848 bp, CDS: 501-848 (SEQ ID NO 283)

ACAAAACAGACTTAGTTATTTTATGGTATACAACAAAAGCTCGAATGAAA
GACGGTTGGCACAAGAGAATTAACAAAATAAACGGAGGAAGAATAAAGTT
ACACCTATTTCTCAAGAATTCTTTTAAATCCGCTCAAGAAAGTTTAAGGG
TATTGCATAAAGAACAGAAACGCCGCTGGAAAAGGCTCTTTGTGCTACTT
CATAATAAATACAGGCAATTTTCTCCACATATTAAGGTTATTTTCGATCA
TTCTTGCCAAAAAGCAAAACAATGTTGGTCGGGATCCAGATTGCAGTTGC
GCAAGCTTCGTTTCAAGTCAATGAAACCATTCCGAGTTTTCAGTTTAAG
GTTTCGCAAAGATACCAACTGGTTTGTAAGCAGCTGAAACGGTTCGGATT
GAAATTACAGCATTTCGAGGATGTATAAGCGATGTCAGAATGCAGGAAAA
AAAATTATTTTAAAGTGCAACACTAGATCATCCAAAACCCAGCATGAAGA
ATGAATTAACAAAAGAAAAAAAACGACTGCTTAGTAGGAGTGTCATA
TATCCCTCCTTTAAATTTTACACTTACTTTCCTTTTATTGAGAA
TAGAAAAGGTGCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTAAGG
TTTTATTACTTTTATAACGTATGCTATCCATCTCTTTTCTTTTTTTTTTG
TTTTGTTATTCCCTTTTTTACTCAGTTAGATTCACTACTATATTTAC
ATATTCTTCGAAGCTTTTATGAGTTAAATATTTTGTGTGCTTTATGGGGCA
GAAAATAGTCGACGTCAGTCACCTCCAGGTTATTATGTAATTCGCTAA

YLR311C, 115 aa (SEQ ID NO 284)

MKLTKEKKNDCLVGVSYPPLNFFTLTFLFLLRIEKVHLSLSLSLSLR
FYFHNVCYPSLFLFFCFVIPFFYSVRFILLYLHILRSFYELNILLLYGA
ENSRRQSPPGYYVIR

YMR107W, 848 bp, CDS: 501-848 (SEQ ID NO 309)

AGAGCAGAAATGATGAAGGGTGTAGCGCCGTCCACTGATGTGCCTGGTA
GTCATGATTTACGTATAACTAACACATCATGAGGACGGCGGCGTCACCCC
AACGCAAAAGAGTGACTTCCCTGCGCTTTGCCAAAACCCCATACATCGCC
ATCTGGCTCCTGGCAGGGCGGTTGATGGACATCAGCCGCTCCCTTAATT
GCTAAAGCCTCCACAAGGCACAATTAAGCAATATTTTCGGGAAAGTACACC
AGTCAGTTTGCGCTTTTATGACTGGGTTCTAAGGTACTAGATGTGAAGTA
GTGGTGACAGAATCAGGGAGATAAGAGGGAGCAGGGTGGGGTAATGATGT
GCGATAACAATCTTGCTTGCTAATCACCCCATATCTTGTAAGTAT
ATAAATAGGAGCCTCCCTTCCTATTGCAACTCCATAAAATTTTTTTTGT
AGCCACTTCTGTAAACAAGATAAATAAAACCACTAATCGAGATATCAAAT
ATGGGTAGTTTTTGGGACGCATTTCGCAGTATACGACAAGAAAAAGCACGC
AGATCCAAGTGTATATGGAGGAAACCATAACAACACAGGAGACAGTAAAA
CGCAGGTTATGTTTTCGAAAGAGTACCGTCAACCTAGGACACATCAGCAA
GAGAACTTGCAGAGCATGAGAAGATCTTCCATAGGATCACAGGACAGTTC
CGATGTTGAGGACGTTAAGGAAGGGAGATTACCCGCAGAAGTAGAAATAC
CAAAGAATGTTGACATCTCTAACATGTGCGCAAGGTGAGTTTTTAAGACTT
TACGAAAGTTTGAGGAGGGGGGAACCCGACAATAAAGTAAATAGATAA

YMR107W, 115 aa (SEQ ID NO 310)

MGSFWDFAFVYDKKKHADPSVYGGNHMNTGDSKTQVMFSKEYRQPRTHQQ
ENLQSMRRSSIGSQDSSDVEDVKEGRLPAEVEIPKNVDISNMSQGEFLRL
YESLRRGEPDNKVNR

YKL066W, 944 bp, CDS: 501-944 (SEQ ID NO 243)

GAAAAACATCTCATAAATCATCCCTGGAAAAATGTCTAGTCAAACAGAAA
GAACTTTTATTGCGGTAAAACCAGATGGTGTCCAGAGGGGCTTAGTATCT
CAAATTCTATCTCGTTTTGAAAAAAAAGGTTACAACTAGTTGCTATTAA
ATTAGTTAAAGCGGATGATAAATTACTAGAGCAACATTACGCAGAGCATG
TTGGTAAACATTTTTCCCAAAGATGGTATCCTTTATGAAGTCTGGTCCC
ATTTTGGCCACGGTCTGGGAGGGAAAAGATGTGGTTAGACAAGGAAGAAC
TATTCTTGGTGCTACTAATCCTTTGGGCAGTGCACCAGGTACCATTAGAG

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GTGATTTTCGGTATTGACCTAGGCAGAAACGTCTGTACGGCAGTGATTCT
GTTGATAGCGCTGAACGTGAAATCAATTTGTGGTTTAAGAAGGAAGAGTT
AGTTGATTGGGAATCTAATCAAGCTAAGTGGATTTATGAATGAATAACTT
ATGGCATGGGAGGGTACATATGAGCGCCTTTTTTTTCTCGCTTTGGGCAG
CTCATATCATGTTCCCTCACTAGCTAATAATATAATGAATTTTTTAGAAG
GAGCACGATTATATAAAAAAATACCACTTATGTTGCTACCCTTATATAC
GAATTTATAATACTTAATGACGCTTCAATGACGCCTGATGTCAAATGCTT
TTGGCTCCCAGTGAAATTGCCACACTTCCTTCTTCTTTCCGAACCTTTATA
GTATCATCGAAAAATACAAGTTGGCAAAGGTCTATTACAATCGCGGAACG
TACGATGTTTCATACGGTTTCAGCGAATAGTCTTGTAATATCCGGAAGCAT
GCCTACCGGCATTATTATAGGTAGTTCATCGCCCTTGGACTATGTAGGGG
TACAAGTAAATAGGCAACTTGAAATGGATCTCCCTATTGAATGA

YKL066W, 147 aa (SEQ ID NO 244)
MAWEGTYERLFFLAGSSYHVPSLANNIMNFLEGARLYKKNNTTYVATLIY
EFIILNDASMTDPVKCFWLPVKLPHPHLLSELYSIIIEKYKLAKVYYNRGT
YDVHTVSANSLVISGSMPTGIIIGSSSPLDYVGVQVNRQLEMDLPIE

YML053C, 1139 bp, CDS: 501-1139 (SEQ ID NO 295)
GAGGCGACACCTGCTAATGTTTACAATTTTCCCGATTGGGGTGCTAGAGG
CATACAGTGGGCTACATGGCACAGCACGGCAGTGCAGAGTGAGAAAATAT
GACTTCACGCTCGAGGCGAGGCCACGCTTTCGAAGCTTCGAATGCCACTA
CCTAGACCATTGCTGTTTTGTACCTTCACGGTCCCATTAGAGACATTTTA
CTTAATGCAAGATTGCCATATCCGTTGTCATGGTACCAAACAGGGTAATA
ATTTCTAGAAATCATGATACACGTATGACATCTGGGTAACCTAATCCATC
TGGGTAACCGATTTTTCTCTCCCTTTGCTTTCTCTTTACCACTCAGCTGA
CTTTATTATTTTTTTTATATTTTTCATTTTGACAAAATTATATAGTTAGG
AAGAATACAATAGGACTGCGACAGAAACAGATAAGGGCTCTTTTTTCTTG
GGGTGGCTGCTTTTATTCATTAATTTAAGACTCAAGTGTGCTGCGTGAA
ATGCTCTCATACTATGAACACAATACTGCGTTCCAAACAAACAATTGCAA
TTCCGGTAGCAATGCCGCCACTACATAACAACAGCGACGCCAATAATGATA
CGATCATGAATAAAAGAAAAAATGACCATTTTCGAGTTTGATACACACACT
TTCTACCAAAGATCGAAGAGAAACAAAACGAGATTCTGTAAGTACAAAGTT
TTCGGTTCGGTTCCGGGTGTGCTAATCTTAATAACAACAACAACATCA
TCATCAACAACAACAACAACAATAATAATAATAAACCATAATCAT
AATAACAGCAATAATACTGCAACCTACAATAATATTATTATAAAAAAAA
TATCGAAATATGTCCCCTGAAACCGGTTAGTATGCACCACACTATGAACA
GCCGCTTACTGAACGAATCTGAATTTTATTCTGAAACAGAAGAGTACATG
ATTTCATGGTTATTTTCGGTAACACTAATCGCGACATAACAGGCACGAGTCC
TACTGGAAGTGCTAGTATTATACAACACCAGTATCATCTTCTACCATCCC
AAAGTATAATTGCATCACAAGCACCCGGTACTGCCATGGCCGCGTTGACT
AACAACAATATCGCTAACGATTACATGGATATAGATTAA

YML053C, 212 aa (SEQ ID NO 296)
MLSYYEHNTAFQTNNCNSGSNAATTYNDSANNDTIMNKRKNDHFEFDTHY
FYQRSKRTRKDSVSTKFSVSGCANLNNNNNNNIIINNNNNNNNNNNNNHNH
NNSNNTATYNNIHYKKNIEICPLKPVSMHHTMNSRLNNESEFYSETTEEYM
IHGYFGNTNRDITGTSPTGSASIIHQHYHLLPSQSIIASQAPGTAMAALT
NNNIANDYMDID

YOR121C, 806 bp, CDS: 501-806 (SEQ ID NO 355)
GGTGACGCTGTTTGGGCTACTTCTGGTGGCCTATCTTTGCAACCAAACGA
AATTGGTGAAATTGTTCAAGGCTTCGACAATCCAGCTGGTTTGCAAAGCA
ATGGTTTGATATTCAAGGCCAAAAGTTCATGTTGTTGAGAGCTGACGAT
AGAAGTATCTACGGTAGACATGATGCTGAGGGTGTGTTTGTGTAAGAAC
TAAGCAAACCGTTATTATTGCTCATTATCCACCAACCGTACAAGCCGGTG

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AGGCCACCAAGATTGTCGAGCAATTGGCTGACTTGTGATTGGTGTTCAA
TACTAATTTATGCAGGTAAAGTTTTCTTGCCTTATACACCACCTATTCG
GCATCTGCGGGATTTTCGCTTCCATTTTACAAATATTTTATTGATTGACG
CTAATTATCAGTGTAAAAGGCGCACTTTTTATATGTAGTCACATCCGGTA
TTTAACATATTTACGAAACAGTCTTAAGAATATCGACATTTGATATAC'TT
ATGTTTAATTTATCTACATATTACAATCATACGAGAAACACGCAAAAACA
ATTACTTGAATACTTCGAAAGGAGACCAATTTGGATGTACAACCC'TTTT
TCGCCCTTTTCC'TTCGATATGTTATTGATAGCTTCAAAGTCCTCAGTAGA
CAAAGTAAATATTTTCC'TGTTTCGTTTGTGATTTCGATCGGGATTACAGATT
TTGGCAAGACAACATAACCTCTTTGGACGTGCCAGCTAATAACAACGTGT
CCGGGTGAACGTTATTTTCTTCGCAATTTCAAGGATAACCGGTTCC'TT
CAATAG

YOR121C, 101 aa (SEQ ID NO 356)

MFNLSTYYNHTRNTQKQLLEYFERRPIWMYNPFFALFLRYVIDSFKVLRSR
QSKYFPVRFD SIGIHRFWQDNITSLDVPANNNVSGLNVI FLRNFKDNRFL
Q

YOL106W, 854 bp, CDS: 501-854 (SEQ ID NO 341)

ATATGGTTTTCATCATTTTGTCTCAATTGTTCTCCATTTGGGTTACCTTTTT
TGCCAGTTGGTCGTACTTGGAGTTTTCAGAACTTGCACCCTTGAATT
GTCCCTCTTTTGCCAACAAC'TAATCTCAAGGTGGTCAGGAAATATTGGTC
GGCGATGCATCTGATAC'TTTCAATTGATTTACTTCTTTCC'TGATCTAAT
TAAGCCGATTTTGGAGCCGATTTTCAATTTCAATTTATAATGTAGTTGTTG
TAAATTTTAAAGTCATTAACCTTTTCATGATATTGATATAGATATTGGG
AACACCATCGCAGAAAGTAGAGGCGCCAAAAAATTTATGACTGTAGAAGA
AAGACGAAGACAGTTAGCTTTACAAGTTTGGGAAGAGCGTATGGTAAACC
CTTGATATATGGATCTATATAACTTGAAATATGCTCTATTATATCGTGAT
TTAATGACGGCTGTTGGCATTTCGGTCTTTACCAAGGTAGTAGGATTTGT
ATGCTGAATGTGCGCCAGTACTATCGAACCATAGAAACCCATATATTCCC
CAATATTAATAATTCTACTGAGAAATGGGTGAATTTTGAAATAATTGTTG
GGATTCCATCGTTGATAAAGGCTATAATATTAGGTATACAGAATGTACTA
GAAGTTCCTCCGATGATATAGGAATCCCATAATGGAATCTATATTTCT
ATGTACCAATATTACGATTATTCCTCATTCATTTTCATATGTTTCATTAT
CCTATTACATTATCGATCCTTGCAATTCAGCTTCTCTAACTTCGGTGAC
AGCTTCTATAATAACTTATGTCACTATCTAACACCGTATATGATAATATA
TTGA

YOL106W, 117 aa (SEQ ID NO 342)

MLNVRQYYRTIETHIFPNINNSTKWNFEIIVGIPSLIKAILGIQNVL
EVLDDIGIPIMESIFLCNTIIPHISISVLSLYIIDPCISASSNFGD
SFYNNLCHYLTPYMIY

>YAL003W, 1487 bp, exon1: 501-580, intron1: 581-946, exon2:
947-1487 (SEQ ID NO 17)

CCGATGGAACGTTCTGGAAAAAGAAGAATAATTTAATTACTTTCTCAACTAAAATCTGGA
GAAAAACGCAAATGACAGCTTCTAAACGTTCCGTGTGCTTTCTTTCTAGAATGTTCTGG
AAAGTTTACAACAATCCACAAGAACGAAATGCCGTTGACAATGATGAAACCATCATCCA
CACACCGCGCACACGTGCTTTATTTCTTTTTCTGAATTTTTTTTTTCCGCCATTTTCAAC
CAAGGAAATTTTTTTCTTAGGGCTCAGAACCTGCAGGTGAAGAAGCGCTTTAGAAATCA
AAGCACACGTAACAATTTGTCGACAACCGAGCCTTTGAAGAAAAAATTTTTCACATTGT
CGCCTCTAAATAAATAGTTTAAGGTTATCTACCCACTATATTTAGTTGGTTCTTTTTTTTT
TTCCCTCTACTCTTTATCTTTTTTACCTCATGCTTTCTACCTTTCAGCACTGAAGAGTCCA
ACCGAATATATACACACATAATGGCATCCACCGATTTCTCCAAGATTGAAACTTTGAAAC
AATTAACCGCTTCTTTGGCTGACAAGTCATACATTGAAGGGTATGTTCCGATTTAGTTTA

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CTTTATAGATCGTTGTTTTCTTTCTTTTTTTTTTTTCTCTATGGTTACATGTAAAGGGAA
GTTAACTAATAATGATTACTTTTTTTTCGCTTATGTGAATGATGAATTTAATTCCTTGGTC
CGTGTATTATGATGGGAAGTAAGACCCCCGATATGAGTGACAAAAGAGATGTGGTTGACTA
TCACAGTATCTGACGATAGCACAGAGCAGAGTATCATTATTAGTTATCTGTTATTTTTTTT
TTCCTTTTTTGTTCAAAAAAGAAAGACAGAGTCTAAAGATTGCATTACAAGAAAAAAGT
TCTCATTACTAACAAGCAAAATGTTTTGTTTCTCCTTTTAAAATAGTACTGCTGTTTCTC
AAGCTGACGTCACGTCTTCAAGGCTTTCCAATCTGCTTACCCAGAATTCTCCAGATGGT
TCAACCACATCGCTTCCAAGGCCGATGAATTCGACTCTTTCCAGCTGCCTCTGCTGCCG
CTGCCGAAGAAGAAGAAGATGACGATGTCGATTTATTCCGGTCCGACGATGAAGAAGCTG
ACGCTGAAGCTGAAAAGTTGAAGGCTGAAAGAATTGCCGCATACAACGCTAAGAAGGCTG
CTAAGCCAGCTAAGCCAGCTGCTAAGTCCATTGTCACTCTAGATGTCAAGCCATGGGATG
ATGAAACCAATTTGGAAGAAATGGTTGCTAACGTCAAGGCCATCGAAATGGAAGGTTTGA
CCTGGGGTGCTCACCAATTTATCCCAATTGGTTTCGGTATCAAGAAGTTGCAATTAAC
GTGTTGTGCGAAGATGACAAGGTTTCTTGGATGACTTGCAACAAAGCATTGAAGAAGACG
AAGACCACGTCCAATCTACCGATATTGCTGCTATGCAAAAATTATAA

>YAL003W, 206 aa (SEQ ID NO 18)

MASTDFSKIETLKQLNASLADKSYIEGTAVSQADVTVFKAFQSAYPEFSRWFNHIASKAD
EFDSFPAASAAAAEEEEDDVDLFGSDDEEADAEAEKLKAERIAAYNAKKAAPAKPAK
SIVTL DVKPWDETNLEEMVANVKAIEMEGLTWGAHQFIPIGFGIKKLQINCVVEDDKVS
LDDLQQSIEEDEDHVQSTDIAAMQKL

>YAL060W, 1649 bp, CDS: 501-1649 (SEQ ID NO 19)

AAAGACTACGAGAATCAATAAACGAGGCTAAACTGCGTCACACATGATTGTGATTGAGTA
CTCACGTTCTCGTGTTAATCCCGCGGTCTTCTTGTTTTACTAACTTTTCTTTCTCTCATA
GCATTCTCTTGACAGTGTTTTATATACATCATATGTACATTTATCGAGCCAATCGAGGGC
AGCAGTTTAACATCAAGCCGGATTTGCTCAGCTACTTTGACCCCTTTTCGTTTCGACGG
AGAGAAGAAACCGGTGTTTTCTATCCTTGCCCTATTCTTCTCCTTACGGGGTCCCTAGC
CTGTTTCTCTTGATATGATAATAGGTGGAACGTAGAAAAAAAATCGACATATAAAAGT
GGGCGAGATACTTCGTGTGACAATGGCCAATTCAAGCCCTTTGGGCAGATGTTGCCCTTC
TTCTTTCTTAAAAAGTCTTAGTACGATTGACCAAGTCAGAAAAAAAAGGAAGT
AAAAAAAGTTTTAATTAATTATGAGAGCTTTGGCATATTTCAAGAAGGGTGATATTCAC
TCACTAATGATATCCCTAGGCCAGAAATCCAAACCGACGATGAGGTTATTATCGACGTCT
CTTGGTGTGGGATTTGTGGCTCGGATCTTCACGAGTACTTGGATGGTCCAATCTTCATGC
CTAAAGATGGAGAGTGCCATAAATTATCCAACGCTGCTTTACCTCTGGCAATGGGCCATG
AGATGTCAGGAATTGTTTCCAAGGTTGGTCCTAAAGTGACAAAGGTGAAGGTTGGCGACC
ACGTGGTGGTTGATGCTGCCAGCAGTTGTGCGGACCTGCATTGCTGGCCACACTCCAAAT
TTTACAATTCCAAACCATGTGATGCTTGTGAGAGGGGAGTGAATCTATGTACCCACG
CCGGTTTTGTAGGACTAGGTGTGATCAGTGGTGGCTTTGCTGAACAAGTCGTAGTCTCTC
AACATCACATTATCCCGGTTCCAAAGGAAATTCCTCTAGATGTGGCTGCTTTAGTTGAGC
CTCTTTCTGTACCTGGCATGCTGTTAAGATTTCTGGTTTCAAAAAGGCAGTTCAGCCT
TGGTTCTTGGTGCAGGTCCCATTGGGTTGTGTACCATTTTGGTACTTAAGGGAATGGGGG
CTAGTAAAATTGTAGTGTCTGAAATTGCAGAGAGAAGAATAGAAATGGCCAAGAACTGG
GCGTTGAGGTGTTCAATCCCTCCAAGCACGGTCATAAATCTATAGAGATACTACGTGGTT
TGACCAAGAGCCATGATGGGTTTGATTACAGTTATGATTGTTCTGGTATTCAAGTTACTT
TCGAAACCTCTTTGAAGGCATTAACATTCAAGGGGACAGCCACCAACATTGCAGTTTGGG
GTCCAAACCTGTCCCATTCCAACCAATGGATGTGACTCTCCAAGAGAAAGTTATGACTG
GTTGATCGGCTATGTTGTGCAAGCCTTCGAAGAAGTTGTTTCGTGCCATCCACAACGGAG
ACATCGCCATGGAAGATTGTAAGCAACTAATCACTGGTAAGCAAAGGATTGAGGACGGTT
GGGAAAAGGGATTCCAAGAGTTGATGGATCACAAGGAATCCAACGTTAAGATTCTATTGA
CGCCTAACAAATCACGGTGAAATGAAGTAA

>YAL060W, 382 aa (SEQ ID NO 20)

MRALAYFKKGDIIHFTNDIPRPEIQTDDVEIIDVSWCGICGSDLHEYLDGPIFMPKDGEC
KLSNAALPLAMGHEMSGIVSKVGPVKVTKVVGHDVVDAASSCADLHCWPHSKFYNSKPC
DACQRGSENLC THAGFVGLGVISGGFAEQVVVSQHHIIPVPKEIPLDVAALVEPLSVTWH

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AVKISGFKKGSSALVLGAGPIGLCTILVLKMGASKIVVSEIAERRIEMAKKLGVEVFNP
SKHGHKSIEILRGLTKSHDGFDSYDCSGIQVTFETSLKALTFKGTATNIAVWGPVKPVF
QPMQVTLQEKVMTGSIGYVVEAFEEVVRaihngDIAMEDCKQLITGKQRIEDGWEKGFQE
LMDHKESNVKILLTPNNHGEMK

>YBL058W, 1772 bp, CDS: 501-1772 (SEQ ID NO 23)

TTATTTACATAGTGCCATTGAACACTTTTCAAGCAAACCTACGCCAGCCGGACGCAGACAA
TAACACACACACAAAAGAGTCTTGCAGGTTCTCTTTTAGCGGCAACGGGCATGACACTAG
GTATATTTGGTATGGGCATCACAGGGACATGTTGGAGCTGGGATGTTTCATCATTTCAGG
AACTAAAGCAACGTCTGGAAGGCGTGCCAACAACGAATTTGTAGTGACAAACATGCCTC
TGGATAAAAGAAGCCAGCAAGTAGTGGACAGCTTAGTTAAGACACACAATTCATCTCTTT
GTAAATAGTGTATACCATAGTAGTAGTTTCAATAATATATCCACTACTTATATGTGTT
ACCCGCATTAGAACTCTTATTGGTGGCGAAAATCGATGGCAATAAAGAACGGAAGGGGTT
TAATAGTTGTATGCTTAACATATTTTCGATTTAAATATATAAGAAACGTCGGTAGCACAA
AATTAAGTTCATTATTTAGGTATGGCGGAAATACCTGATGAAACCATCCAGCAGTTTCATGG
CATTGACCAATGTGTGCGATAACATAGCCGTTCAATATCTCTCTGAATTTGGAGATTTAA
ATGAAGCACTAAATTCCTATTATGCTTCTCAAACGGATGACCAAAGGATAGAAGAGAGG
AAGCACATTGGAACAGACAGCAGGAGAAGGCCCTCAAGCAAGAAGCCTTCTCCACCAACT
CTTCAATAAAGCCATAAATACGGAGCACGTTGGTGGGTATGTCCAAAACAGGATCCT
CACAAGGTAGCAACGAGTACTTGAAGGAAAGGTTCTACCTCTCCTGAACCAACCAAGG
GTAGTAGCCGCTCTGGAAGTGGTAACAACCTCCAGGTTTATGAGCTTTTCGGATATGGTAA
GAGGTCAAGCTGATGATGACGATGAAGATCAACCGAGAAATACTTTTGCTGGTGGTGA
CATCCGGCTTAGAGGTTACAGATCCTTCAGATCCTAATTCATTACTGAAGGATTTGCTGG
AAAAAGCGAGAAGGGGTGGTCAAATGGGCGCTGAAAACGGATTCCGTGATGACGAAGACC
ATGAAATGGGTGCCAATAGGTTTACTGGAAGAGGTTTTAGATTAGGGTCAACCATCGACG
CAGCAGATGAAGTCGTAGAAGACAACACTTCACAATCACAACGTAGACCAGAAAAAGTCA
CAAGAGAAATTACATTTTGAAGGAAGGTTTTCAAGTGGCCGATGGTCCGCTTTATCGCT
ATGATGATCCTGCGAACAGTTTCTATTTGAGCGAGTTAAATCAAGGGAGGGCTCCATTAA
AGCTCTTAGATGTGCAATTTGGACAAGAAGTTGAAGTTAATGTATATAAAAAATTAGATG
AGTCTTATAAAGCTCCGACGAGAAAACTGGGCGGTTTTTCAGGCCAGGGCCAAAGACTAG
GATCTCCTATCCCGGGTGAATCGTCACCTGCGGAGGTTCCAAAGAATGAGACACCCGCTG
CTCAGGAACAACCCATGCCGGAATGAGCCAAAACAAGGCGACACCTCCATCCAAATTA
GATACGCAAATGGCAAAAGAGAAAGTTTTGCACTGCAATTCCACAGATACAGTAAAGTTTT
TGTATGAGCATGTGACATCAAATGCGAACACTGACCCATCGAGGAATTTACCTTGAATT
ATGCCTTTCTATCAAACCAATAAGCAACGATGAGACAACATTGAAGGACGCTGATCTGC
TGAACCTCCGTTGTCTGCGTCAAAGATGGGCATGA

>YBL058W, 423 aa (SEQ ID NO 24)

MAEIPDETIQQFMALTNVSHNIAVQYLSEFGDLNEALNSYYASQTDDQKDRREEAHWNRQ
QEKALKQEAFTSNSSNKAINTEHVGGCLPKPGSSQGSNEYLRKKGSTSPPTKSSRSRGS
GNNSRFMSFSDMVRGQADDDDEDQPRNTFAGGETSGLEVTDPSDPNSLLKDLLEKARRGG
QMGAEENGFRDDEHHEMGAANRFTGRGFRLGSTIDAADDEVVEDNTSQSQRRPEKVTREITFW
KEGFQVADGPLYRYDDPANSFYLSLNQGRAPLKLDDVQFGQEVENVYKKLDESYKAPT
RKLGGFSGQGQRLGSPIPGESSPAEVPKNETPAAQEQPMPDNEPKQGDTSIQIRYANGKR
EVLHCNSTDTVKFLYEHVTSNANTDPSRNFNLNYAFPIKPISNDETTLKDADLLNSVVVQ
RWA

>YBR039W, 1436 bp, CDS: 501-1436 (SEQ ID NO 41)

TTGAGATTTTCCAAGTAGTAACCTCATCTTCTGAGTGTGCTATCAAATACATACTAAGGA
GAATAAACTCTTGTTATTACGTATTCTTCATCCTTATGGGTAGAGAGCGCACTGTTTATG
TACATTTTCTAGACGTCGAAACGTAGAGCAATTTGTCGATAAAACAAAAAAGTAAGAA
GATATATGAATAGGACGTGTCGCTAGAACTAGTAAGTATATGATGGAGATATAATAAGTG
AATTATTGATATTTAATGAACGTTCTCATTATTTTGAAGAAATGTTTATCACGTGATG
GAGAACCAATGAGCGGCGAGTAACCTACGCGAGGAACCCGACCGCAATAACGATTAAAGA
AGGCCCGGAAGGGAGATGCTTAAATGATTATCACTCAGTTAAAAAGACAAATAAGAAAC
TATTGAGACTGAACCGTTTTGGTTAATTTACAGGTGGAACAATTGAAGACGAGCAGTAAA

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CATTATTTTATTTAGTAGTCATGTTGTCAAGAATTGTATCAAACAATGCAACACGCTCCG
TAATGTGCCACCAAGCGCAAGTGGGTATTCTTTATAAGACTAACCAGTGAGAACTTATG
CTACTTTGAAAGAAGTGGAAATGCGTTTGAAATCTATCAAAAATATTGAGAAGATCACAA
AAACTATGAAGATTGTTGCATCTACAAGATTGAGTAAAGCTGAAAAGGCTAAAAATTTCCG
CAAAGAAGATGGATGAAGCAGAGCAGTTGTTTTACAAGAACGCCGAAACCAAAAATTTGG
ATGTTGAGGCTACTGAAACAGGTGCTCCTAAAGAGTTGATTGTTGCTATCACCTCTGATA
AGGGGTTGTGTGGTTCTATCCACTCTCAAATTGGCTAAAGCTGTGAGAAGACATTTGAATG
ATCAACCAAACGCCGATATAGTCACATATTGGTGATAAAATTTAAATGCAGCTATTGAGAA
CCCATCCTAACAACATTAAATTTGTCTATTAAATGGAATTGGTAAAGATGCCCAACTTTTCC
AAGAATCTGCTTTGATTGCCGATAAGTTATTGAGTGTCTATGAAGGCCGGCACTTACCCTAA
AGATTTCCATTTTCTACAATGACCCAGTGTCTTCCCTATCTTTTGAACCATCTGAAAAAC
CGATCTTTAACGCCAAGACCATTTGAACAATCCCCATCATTCGGCAAAATTTGAGATCGACA
CGGACGCAAACGTTCCAAGAGATTTGTTTGAATATACTTTGGCTAACCAAATGTTGACAG
CAATGGCTCAAGGTTATGCTGCTGAAATTTCCGCCAGAAGAAACGCTATGGATAACGCTTT
CCAAGAATGCCGGTGATATGATCAATCGTTACTCTATCTTGTACAACAGAACAAGACAAG
CTGTCTACTACTAATGAAC TGGTTGATATTATTACTTGGTGCTTCCTCTTTGGGATGA

>YBR039W, 311 aa (SEQ ID NO 42)

MLSRIVSNNATRSVMCHQAQVGILYKTNPVRTYATLKEVEMRLKSIKNIEKITKTMKIVA
STRLSKA EKAKISAKKMDEAEQLFYKNAETKNLDVEATETGAPKELIVAITSDKGLCGSI
HSQLAKAVRRHLNDQPNADIVTIGDKIKMQLLRTHPNNIKLSINGIGKDAPTFQESALIA
DKLLSVMKAGTYPKISIFYNDPVSSLSFEPSEKPIFNAKTIEQSPSFGKFEIDTDANVPR
DLFEYTLANQMLTAMAQGYAAEISARRNAMDNASKNAGDMINRYSILYNRTRQAVITNEL
VDIITGASSLG

>YBR062C, 848 bp, CDS: 501-848 (SEQ ID NO 45)

CCATTTTGGTGACCAACTCTCCTACCCGAATTACTGTGATGATATATACTCTTCGTTTTC
TAGTAATGGCTTCATTTTGCCTAAGTTGGTCAAATTTGTTGTGGGCGGCTTTTGTTTGCA
CCGAGGAGCGCTCAGTTCGTTATAATACCAGTTTGGCCACTCCTAAACTACTAAAGAAAT
AATAGAAAAGATATATTCATCAAACATAATCACAATCAAAAAATGTCTACATATGAAGGT
ATGTAATGATATATATGAAGTAAGTTCCCCAAAGCCAAATTAACCTAACCGAATTTTAATC
TGCACCTCATCATTAGATTAGAGGAACATGGAAATACAACAAAACCTCAAGGGATTACCAAGA
AGTAGGAGGAACCTTACAGGAGGAGCAGAGAAGACAGGTCAAGATCCCAACTGCAAGGTC
TATTTCAAACCTTTGGTAACACCAGTGGTGAGGGTGATGCACATTCAGATTCAACACTAC
TTTACGATTATATCGCAAATGCTTCCAGAATCATTCAGGAAGAATGGTTGCAAGAAA
TGGATAAAGGCAAGAGTGCAGGCTGTCTTGATACTTTTGCAGCCTCTTTACCACGAATCA
ATAAAAAAAGCTCAAAGCAACTGACAACGTCTCCATTTGTTACACTAATTATTTAGAAG
ATGAGTACCCCTTAGTAGTTGAATTACCTCATTCGCATCATAAGTTCGACTTAGAGTGT
TGTCTGTCTGGCTATCTCGAAGTACAACATGTCCATTATGCAGAGATAATGTTATGGGCC
ACCGAATCATTAATGAGATTGATACAACCTGAAGCAGAACTGGAAGAAGATTGGGGTATGT
ACGGTTAA

>YBR062C, 115 aa (SEQ ID NO 46)

MLPESLQEEWLQEMDKGSAGCPDTFAASLPRINKKKLKATDNC SICYTNYLEDEYPLVV
ELPHCHHKFDLECLSVWLSRSTTCPLCRDNVMGHRINEIDTTEAELEEDWGMYG

>YBR101C, 1373 bp, CDS: 501-1373 (SEQ ID NO 49)

AATGATGAAATGTTATCCCCAGGGTCCATTAAAGTCATCCAGAAAACAGATAGATGGATTG
AAGGCCGTAGGTTTGGATTTTGTCTACAAATTTGGACGAGTTTATCAAAAAGAACAGTGAT
AAAATTCGCTAAACAAGATCACAGAAAATAAACCTCACTTCAATATATATGATGTGTAGG
TAGGGTATATACTTATACCACTGCTGTGACAGTGTACTAACCTATTTCTATTTTGTAG
GTAAGCTTTTTCAGCTACTGGTTGGTCAAGTTGGGCCCTATTAAGGTTGTAATCAGCTTAT
TCGTTTGAATGATATACCTCTTGGACTGGAATCTTCTGGAAGTTTTTTGGAGGTTAGAA
AAGAGGAAGGCATCTCGCGCTGACAGAAATTTGCTTATAAACCAGCGATTGGCTATATCT
AAAAGAGCACTCATCGTCAGTCAGAAAGCCATTACCTTTCAACGAAAGAGTAAAATAGAA
AAAAAACACATACATAACTATGGAAAAGCTATTACAGTGGTCTATTGCGAATTCTCAAG

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GGGACAAAGAAGCTATGGCTAGGGCCGGCCAACTGATCCTAAATTGCTACAGCAGTTAT
TCGGTGGTGGTGGTCTGACGATCCAACCTTAATGAAAGAATCCATGGCTGTTATTATGA
ATCCGGAGGTTGACTTAGAAACAAAACCTCGTTGCATTTGACAACTTTGAAATGTTGATTG
AGAACTTAGATAATGCTAATAATATCGAAAATTTAAACTGTGGGAGCCATTGTTGGATG
TTCTTGTTTCAGACGAAGGATGAAGAACTACGTGCTGCTGCTTTATCCATTATTGGAACGG
CTGTGCAAAACAACTTGGATTTCGCAAAATAATTTTCATGAAATACGACAATGGTCTGCGAA
GCCTTATCGAAATAGCTAGTGACAAGACAAAGCCACTCGACGTGAGAACAAAAGCTTTTT
ACGCACTATCTAATCTAATAAGAAACCACAAAGATATCTCAGAAAAGTTTTTCAAATTAA
ATGGGCTCGACTGCATAGCACCTGTATTAAAGTGATAACACCGCCAAACCAAACTGAAAA
TGAGAGCCATTGCCTTATTGACCGCATATTTGTCATCTGTTAAGATTGATGAAAATATAA
TCAGTGTGCTGAGAAAGGATGGAGTAATTGAAAGTACGATTGAGTGCCTGTCTGACGAGA
GTAACCTGAACATCATAGATAGAGTTCTGTCTTTTCTCTCTCACCTGATATCTTCCGGAA
TAAAATTTAATGAACAGGAATTGCACAAATTGAACGAAGGTTACAAACATATCGAGCCTC
TAAAGGACAGACTTAATGAAGACGATTATTTAGCCGTAAAGTATGTATTATGA

>YBR101C, 290 aa (SEQ ID NO 50)

MEKLLQWSIANSQGDKEAMARAGQPDPKLLQQLFGGGPDDPTLMKESMAVIMNPEVDLE
TKLVAFDNFEMLIENLDNANNIENLKLWEPLLDVLVQTKDEELRAAALSIIIGTAVQNNLD
SQNNFMKYDNGLRSLIEIASDKTKPLDVRTKAFYALSNLIRNHKDISEKFFKLNLGLDCIA
PVLSDNTAKPKLMRAIALLTAYLSSVKIDENIISVLRKDGVIESTIECLSDENLNIID
RVLSFLSHLISSGIKFNEQELHKLNEGYKHIEPLKDRLNEDDYLA VKYVL

>YBR139W, 2027 bp, CDS: 501-2027 (SEQ ID NO 55)

GGAGGAGTCAAGGGCCTGGAAGTACGGATCCTGTAGAAATATCACTGGCAATTATACTG
AGTTTATTGTTGGTGTGTGCTATTTCATATTTGAGCTGGTATTGGACGAAAGCAAGGATAAT
GAGTTTGTGTCTACTGACTCCAACACCCTAGGCTGGATTTGATCTTTCTCCATCCTTTAA
TTTTAACCTTTTAATTAGTGGTTGGATCAAGTTTTTCGAGACTATTCCAATCTGTGACTTG
TTGGATAAATAGTTTTTGACTCGTTTAGTATAATCCTTTTTTCTAAAAGTGCTTAGAGTT
CTCTAAGATGTTCTTGTTTACAATGTGAGCGATTTAGGAAATTTCTAAAATGGCCGAG
GCGGCGCTAGCATTCTACGAAAGGTGAGATAACGCTTCGTTATCGAAAATGTCAGGGGA
CAGGGGTTATATAAGAACGAAAATTGTCATCCTGCATTTTTTCTTTAAAACAGCTATACA
AAAAGTGATACCGACATACAATGAAGTATCTAAACTTAGTTTTCTGTGCTTCAGCTTCTTA
TTAGCATCAAATACGCCTCATTTCGGCCGAGCCTTTTTCTCTTTTTGAAGATGATACCACCT
TTGCCAATTTGGATAAACAGCTAAAGCTTCCACAGAATACACAGCAAACCTTAAATTGG
ACCGTTTGAATCACGATGATCCGCTGTTTACAACCTTTTATTCTTCTGTGGACACAGATT
ACAGTTTGAGACTTAGAACAGTAGATCCTTCTAAACTAGGAATTGACACCGTAAAACAAT
GGTCGGGTTACATGGACTATAAGGATTCCAAACACTTTTTTTACTGGTTTTTTGAAAGTA
GGAACGATCCTGCTAACGACCCAATTATTCTTTGGTTAAATGGTGGACCTGGTTGTTCTCCT
CGTTTACTGGGTTGCTATTTGAACTAGGCCCTCATCAATTGGCGCCGATATGAAACCAA
TCCACAATCCCTATTCTTGAATAATAACGCTTCAATGATCTTCTTAGAACAGCCACTCG
GAGTCGGCTTTTTCTATGGTGATGAAAAAGTCTCCTCTACAAAATTAGCAGGCAAAGATG
CGTACATTTTCTGGAATTGTTTTTTGAAGCTTTTCTCATTTACGCTCCAACGATTTCC
ACATTGCAGGCGAATCCTATGCAGGACATTATATCCCTCAAATTGCACATGAGATCGTTG
TCAAGAACCCTGAAAGAACGTTCAATTTAACTTCAGTTATGATTGGTAATGGTATCACAG
ACCCTTTGATTCAAGCAGATTATTATGAACCAATGGCATGCGGGAAGGGGCTATCACC
CTGTTCTCTCATCAGAAGAATGTGAGAAAATGAGTAAAGCTGCAGGTCGTTGTCGTAGGT
TGAACAAGTTATGTTATGCTTCTAAATCAAGTTTACCATGCATAGTCGCCACTGCTTACT
GTGACTCTGCACTTTTGAACCGTACATTAACACAGGACTCAACGTCTATGACATTAGAG
GGCCCTGTGAAGATAATAGTACTGATGGTATGTGTTATACAGGTCTCCGCTATGTGCGACC
AGTATATGAATTTTCTGAAGTTCAAGAAACGCTAGGGTCCGACGTGCATAATTATTCTG
GCTGTGATAATGACGTGTTACCGGATTTTTGTTTACGGGCGATGGAAGTAAACCATTTTC
AACAATATATTGCTGAATTATTAATCAACAATCCGGTATTAATATATGCGGGTGATA
AGGATTATATTTGTAATTGGCTGGGAAACCATGCTTGGTCCAATGAGTTGGAATGGATCA
ATAAACGTAGGTATCAGAGAAGGATGTTAAGACCATGGGTGAGTAAAGAAACAGGTGAAG
AGTTGGGACAAGTCAAGAACTATGGCCCTTTTACCTTTTTGAGAATATACGATGCCGGTC
ATATGGTGCCCTATGATCAACCGGAGGCAAGTTTGGAAATGGTCAACAGTTGGATTTCGG

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GTAATCGTGCTTTTTTCGGATCTTCCACCTTGAAAATGCTAGTTAG

>YBR139W, 508 aa (SEQ ID NO 56)

MKYLNLVFLVQLLLISIKYASFGRAFSLFEDDTTFANLDKQLKLPQNTQQTLKLDRLNHDD
PLFTTFISSVDTDYSLRLRTVDPSKLGIDTVKQWSGYMDYKDSKHFFYWFFESRNDPAND
PIILWLNGGPGCSSFTGLLFELGPSSIGADMKPIHNPYSWNNNASMIFLEQLGVGFSYG
DEKVSSTKLAKDAYIFLELFFFAFPHLRSNDFHIAGESYAGHYIPQIAHEIVVKNPERT
FNLTSVMIGNGITDPLIQADYYEPMACGKGGYHPVLSSEECEKMSKAAGRCRRLNKL CYA
SKSSLPCIVATAYCDSALLEPYINTGLNVYDIRGPCEDNSTDGMCTGLRYVDQYMNFP
VQETLGSVDVHNYSGCDNDVFTGFLFTGDGSKPQQYIAELLNHNIPVLIYAGDKDYICNW
LGNHAWSNELEWINKRRYQRRMLRPWVSKETGEELGQVKNYGPFTFLRIYDAGHMPYDQ
PEASLEMVNSWISGNRAFSDLSTLENAS

>YCL052C, 1751 bp, CDS: 501-1751 (SEQ ID NO 67)

TGCACATGTTGAGTATGCGTATTGGGCATTTTCCTATTCTGAGAAGGAGTATGAAATAAT
TGCCGAGGGTTTCAGAAATGCTCTTTTAGAAATAAAAAATGAATGTAAATAGTTGGAATGTAT
CTTTAAGTAGACAAATGCAGGTAAGTTTTAGTGGCCTTTGCGGATTAACAGTATGCTCTT
AGTGCAAAACACGAAAAGAGCTCCCAATCTTTGAACACAATCGACCACGGAGGAACAATA
CACGTAGAAGGGGATAACTAAAACCTTTGTCGTGCAAGAGTATTGGAGGACACACTAACAG
CAGAACTTTGCCTTCTTAACTCTTGTATTGATTGCTTGAAGTATTACACATGTAATAAA
AGATGATTATTTTTTTTTTCTTAAAAAAGTTCTTTCTTTGAAGATCCCCCTGATAAAA
AAGATCAAATAATGGAAACGCTAATCATAATCAAATCGGGAGGAGAATAAACGCAAGAAG
TGTGCGTTTTCTAGCTGAGTAATGGTGACAAGACATAGAGTGACTGTACTCTACAATGCCC
CTGAGGATATCGGTAATCATATGCGCCAAAATGACACTCATTGACTGTTCGTGGAGGTT
CTGGTGTGGTTTTACAACAAAGGTGGCTATTAGAGAGGACTGGAAGCTTGGATAAATCCT
TTACGAGAATCACTTGGAGGCCCAGAGCGGACTTGGCTAGAAGTTTAAGCGTTATAGAAA
ATGAACTGAGTGTCTGGCTTTTTCAGTTTACTCAAATTCCTTCGGATGTGCCGAAAGGTTTA
TTACTAACCCAGTCTACAATTCATTTACAGTGAGAAGTTTGACATAGAGCAGTACTTGC
CTCCCGAAGTAGATTGAATCTGTCATGGAATCCAGAAGATTTTACATATGATATATCAG
TGGAGCCACACAAATCCAAATGTTGAATATCGTCTGTTGAAACAGGGTGAAGAATTTA
CAATTGCAAGAGTGAAAGATGAGAACTCGAAGTAGGTGTATTCTTTGTGGATGCAAGTG
ATGAAAGTGATGTCGATATTGGTGGAATACGTTGTAATTGGAGGATGGACGATGGTAAAA
TGGAAAGATGTCAGAAAACATCCTTATTGTATATAAACAGGGCCATATCGCATACAATCACT
CGACGACTACGACATCACTATATCTGAATGAACCTATCGGTTTGCATCCAAAAATCATGA
TTGATCTCACAGATTTTGAAGAACGCCCTAAATGCATGTATCTAATGCACCTGCAATTGC
CGTTAGAATTATTTATCGATAAATCCAATCCTCTCCCTTACTACTTTTTTGGAGAAGACG
ACTTAGAATTACCAGAATACTCTCTTCGAGATAAGGCATGGGGTTCTGAAAGTATCTTTG
AATTGAAAGCCGGCACAAATGAATGAAGTGACATTGCATACTAGATATATTGAGCCTTCTA
ATAATAAAGGGGATAAATTAGAAGTTTCATTTGATCCAGAAGTTATATTAGCCTGCGACA
CAGGTGACAATAAAGTTTCCCGTAATCCATTTTATAAAAAAGGCTTAGGATATGAATCTC
TCTTTACAGACGATACTACATTCGCCCATTTGAACTCGACAACCTTCTAGTACCAATTC
CAAGGCCTGACACAAAGGATTATTCGAAGATCAAAAATGGTACGTTACTATGCTTACTCA
TCTCCATCATATACATTTTCTCCAAGGTATTTGGTAACAACAAGAAGAAAAGATCAGTAA
AACGGGAATAA

>YCL052C, 416 aa (SEQ ID NO 68)

MVTRHRVTVLYNAPEDIGNHMRQNDTHLTVRGGSGVVLQQRWLLERTGSLDKSFTRITWR
PRADLARSLSVIENELSGFSVYSNSSDVPERFITNPVNSFHSEKFDIEQYLPPEVDLN
LSWNPEDFTYDISVEPTQIQIVEYRLLKQGEFTIARVKDEKLEVGVFVDASDESVDVI
GGIRCNRWMDGKMERCQKTSLLYKQGHIAYNHSTTTTSLYLNNEPIGLHPKIMIDLDFE
ERPCKMYLMHLQLPLELFDKFQSSPLLLFGEDDLELPEYSLRDKAWGSEIFELKAGTM
NEVTLHTRYIEPSNNKGDKLEVSFDPEVILACDTGDNKVS RNPFYKKG LGYESLFTDDTT
FRHLNSTLLVPIRPDTPDKYSIKNGTLLCLLSIIYIFSKVFGNNKKKRSVKRE

>YCR009C, 1298 bp, CDS: 501-1298 (SEQ ID NO 73)

GTACAAAAATGATTACGAAAATATAGATGATGTAAGCAAGGTACGGTTATAAACAGTTAA

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CATATAAGTTTACTTCACTTTTTTGTGACTCCTTTACTTGTCTTCCCTGCACTTTGATT
TTACTTCAGAAAAAATAAGATATATGTTTCTGATAAAACTTTATAGGTTAGCGGAGAAGAT
GTTGCCACGAATATCATGTAATTGAAAGGCAACGAAAGGCTATCGTTTGCATTTCATAA
TGTGATTTCGACTTGTCTTTTTTCATTGTAACAGACATGAAACGTTTCCTTTACGTCCCTAT
GAATTTTTTGTGGCTGAACTGGGCGCTGCAGGGGCTGGACGATCCAAATGCGCGGATTTT
GAACAATTATGAGAATCCGAATTAAAAGAAAGGGAAAACAAATTTAATAACAGGCAGACG
TGAGAGAAGAAAAGGAAACGCTGTGATATAGAAAACATACAAATCCTATTATAAGAAGC
CAGAAGAAAGCTGATACAAGATGAGTTGGGAAGGTTTTAAGAAAGCTATCAACAGAGCTG
GTCACAGTGTGATAATTAAGAATGTCGACAAGACCATTGATAAAGAGTATGACATGGAAG
AACGTCGTTATAAAGTTCTTCAAAGAGCAGGTGAGGCATTACAAAAGGAAGCCAAAGGTT
TCTTGGACTCATTTGAGAGCTGTGACAGCATCACAGACTACCATTGCCGAGGTCATCTCTA
ACCTCTATGACGATTCAAATATGTTGCTGGTGGTGGTTACAACGTTGGTAACATATTATT
TGCAATGTGTTCAAGATTTTGATAGCGAACTGTTAAGCAATTAGACGGGCCCTTAAGAG
AAACCGTACTAGATCCAATAACAAAGTTTTTCGACGTATTTCAAAGAAATTGAGGAGGCCA
TAAAAAAGAGAGACCATAAGAAACAAGACTTCGATGCTGCGAAGGCAAAAGTTTCGTAGAT
TAGTGGACAAACCTGCTAAAGATGCCTCTAAACTGCCAAGGGCTGAAAAAGAATTGAGCT
TAGCTAAAGATATTTTCGAAAATCTTAATAACCAATTGAAAACCTGAACACCACAGTTAG
TTTCATTAAGAGTACCTTACTTTGACCCAAGTTTTGAAGCTTTAATCAAGATTCAGCTAA
GGTCTGTACTGATGGTTACACTCGTTTAGCGCAGATTCAACAATATTTGGACCAACAAT
CAAGAGACGACTATGCCAATGGGTATTAGACACTAAAATCGAAGAATATTAGGACAAA
TGACAAGCCTAGATATTTGTGCGCTCGGGATAAAATAA

>YCR009C, 265 aa (SEQ ID NO 74)

MSWEGFKKAINRAGHSVIIKNVDKIDKEYDMEERRYKVLQRAGEALQKEAKGFLDSLRA
VTASQTTIAEVI SNLYDDSKYVAGGGYNVGNYYLQCVQDFDSETVKQLDGPLRETVLDPI
TKFSTYFKEIEEAIKKRDHKKQDFDAKAKVRRRLVDKPAKDASKLPRAEKELSLAKDIFE
NLNNQLKTELPQLVSLRPYFDPSEALIKIQLRFCTDGYTRLAQIQYLDQQSRDDYAN
GLLDTKIEELLGQMTSLDICALGIK

>YCR010C, 1352 bp, CDS: 501-1352 (SEQ ID NO 75)

GAGCTCCGTGGAATAGGCGAGCGGCTGAGTGGTTCTCCAAGCTACGGTTTTTACGTGTAG
CCCCATGTGAGCAAGCCAAACAAGGGCCCTTAAAGGCGTGACTACAAAAGGGGCGGGTT
GGAAGGTCATCTGCAGCGAGATACGAAAAGATTTTTTGCCAGATTTGCGGTTGGGCGGCT
ATTTCCGGTATTGTTGGGGTAACAAACGTTGGGGAAGACTGCATTTTCTTACAGCTTTTTT
TCGTTATCGCGGGTTGGGCGGCTATGGCGCCTTCTCCTCTGTACTCCAACCTGTCAGAGA
CACCAAGCTGTATATAAAGCACCTTGGTTGGATCGTATTTCCCTGAGATCTTGCTATAGG
TTCATTTTATATATCGTCCAATAGCAATAACAATACAACAGAACTACTAGCATCTGTTT
ATAAGAAAAAGGCAATAGTCGACAGCTAACACAGATATAACTAAACAACCACAAAACAA
CTCATATACAAACAAATAATATGTCTGACAAGGAACAAACGAGCGGAAACACAGATTTGG
AGAATGCACCAGCAGGATACTATAGTTCCCATGATAACGACGTTAATGGCGTTGCAGAAG
ATGAACGTCCATCTCATGATTGTTGGGCAAGATTTACACTGGAGGTGATAACAATGAAT
ATATCTATATTGGGCGTCAAAAGTTTTTGAAGAGCGACTTATACCAAGCCTTTGGTGGTA
CCTTGAATCCAGGGTTAGCTCCTGCTCCAGTGCACAAATTTGCTAATCCTGCGCCCTTAG
GTCCTTCAGCCTTCGCGTTGACGACATTTGTGCTGTCCATGTTCAATGCGAGAGCGCAAG
GGATCACTGTTCCCTAATGTTGTGCTCGGTTGTGCTATGTTTTATGGTGGTTTGGTGCAAT
TGATTGCTGGTATTTGGGAGATAGCTTTGGAAAATACTTTTGGTGGTACCGCATTATGTT
CTTACGGTGGGTTTTGGTTGAGTTTCGCTGCAATTTACATTCCCTGGTTTGGTATCTTGG
AAGCTTACGAAAGACAATGAATCTGATTTGAATAATGCTTTAGGATTTTATTTGGGGT
GGCCCATCTTTACGTTTGGTTTAAACCGTTGTACCATGAAATCCACTGTTATGTTCTTTT
TGTTGTTCTTCTTACTAGCATTAACTTTCCTACTGTTGTCTATTGGTCACTTTGCTAATA
GACTTGGTGTCAACAAGAGCTGGTGGTGTCTGGGAGTTGTTGTTGCTTTCATTGCTTGGT
ACAACGCATATGCAGGTGTTGCTACAAAGCAGAATTCATATGTACTGGCTCGTCCATTCC
CATTAACATCTACTGAAAGGGTAATCTTTTAA

>YCR010C, 283 aa (SEQ ID NO 76)

MSDKEQTSNNTDLENAPAGYYSSHDNDVNGVAEDERPSHDSLGIYTGDNNEYIYIGRQ

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KFLKSDLYQAFGGTLNPGLAPAPVHKFANPAPLGLSAFALTTFVLSMFNARAQGITVPNV
VVGCMFYGGVLVQLIAGIWEIALENTFGGTALCSYGGFWLSFAAIYIPWFGILEAYEDNE
SDLNNALGFYLLGWAIFTFGLTVCTMKSTVMFLLFLLALTFLLLSIGHFANRLGVTRA
GGVLGVVVAFIWYNAYAGVATKQNSYVLARPFPLPSTERVIF

>YCR021C, 1499 bp, CDS: 501-1499 (SEQ ID NO 79)

ATCGAAAGCGTGCTTTGTAAAGATATTTGGTATGGCTAAAGTAAGCAAAGCCATATCCCG
ATCCCGATCCCGACTCTTATTCGATCCCTTCCGCCACATCCTGCATGTTTATTCGAATA
CCAAATTAGCTCATCTTCGTTATTTTCATCATCCCTTTCTGCTATGGCAAGGACAAGTTTT
TTTCTAGCATCTCATCGAAAACCTTCTCTCCCTAATTGGCCAAAGTTTTTCATATTCATC
ATCAGTTAGAAAGTATAATATCAATCCCTTACCTCATTACAAGTTGTATCACACTAAAAA
AATCATATATAAGTCTGTGAGAGTCTTCAATTATTTAGCGTAACACCTATTCACTTTCTA
ATCTTGTCTTCTGTTTTTACATTCTGCAATACAACACAACAACAAATATTAACTCAATTA
TTATTATTTATAATTACAAAAACAAAACAACAAGTTTGAGACTTTAATATCTTTTGATTA
CTAAAAACAACAATTTCAAATGAACGATACGCTATCAAGCTTTTTTAAATCGTAACGAGG
CTTTAGGGCTTAATCCACCACATGGCCTGGATATGCACATTACCAAGAGAGGTTCCGGATT
GGTTATGGGCAGTGTTTGCAGTCTTTGGCTTTATATTGCTATGCTATGTTGTGATGTTCT
TCATTGCGGAGAACAAAGGGCTCCAGATTGACTAGATATGCCTTAGCTCCTGCATTTTGA
TCACTTTCTTTGAATTTTTTGCTTTCTTCACTTATGCTTCTGATTTAGGTTGGACTGGTG
TTCAAGCTGAATTTAACCACGTCAAGGTTAGCAAGTCTATCACAGGTGAAGTTCCCGGTA
TTAGACAAATCTTTTACTCGAAATATATTGCCTGGTTCTTGTCTGCGCCATGCCTTTTAT
TTTTAATCGAGTTAGCCGCTAGTACTACTGGTGAGAATGACGACATTTCCGCCTTGGATA
TGGTACATTTCGCTGTTAATTCAAATCGTGGGTACCTTATTCTGGGTTGTTTCGCTATTAG
TTGGTTCAATTGATCAAGTCCACCTACAAGTGGGGTTATTACACCATTGGTGCTGTGCGTA
TGTTGGTTACCCAAGGTGTGATATGCCAACGTCAATTCTTCAATTTGAAAACCTAGAGGGT
TCAATGCACCTTATGCTGTGTACCTGCATGGTAATCGTTTGGTTGTACTTTATCTGTTGGG
GTCTAAGTGATGGTGGTAACCGTATTCAACCAGACGGTGAGGCTATCTTTTATGGTGT
TGGATTTATGTGATTTTGCCATTTATCCATGTTACTTGCTAATTGCAGTCAGCCGTGATG
GCAAATGGCCAAAGGCTATCTTTGACAGGAGGATTCTCTCATCACCATGCTACGGACGATG
TGGAAGATGCGGCTCCTGAAACAAAAGAAGCTGTTCCAGAGAGCCCAAGAGCATCTGGAG
AGACTGCAATCCACGAACCCGAACCTGAAGCAGAGCAAGCTGTCTGAAGATACTGCTTAG

>YCR021C, 332 aa (SEQ ID NO 80)

MNDTLSSFLNRNEALGLNPPHGLDMHITKRGSDWLWAVFAVFGFILLCYVVMFFIAENKG
SRLTRYALAPAFLLITFFEFFAFFTYASDLGWTGVQAEFNHVKVSISITGEVPGIRQIFYS
KYIAWFLSWPCLLFLIELAASTTGENDDISALDMVHSLLIQIVGTLFWVVSLLVGLIKS
TYKWGYTTIGAVAMLVQGVICQRQFFNLKTRGFNALMLCTCMVIVWLYFICWGLSDGGN
RIQPDGEAIFYGVLDLCVFAIYPCYLLIAVSRDGLPRLSLTGGFSSHHTATDDVEDAAPE
TKEAVPESPRASGETAIHEPEPEAEQAVEDTA

>YDR073W, 1010 bp, CDS: 501-1010 (SEQ ID NO 91)

GTTAGCTTGCCCTGCATTTCCCATGCGTCTCGAATAGGAATTATTCAAGATGGATTATT
GGCATTTACGAGTAACCAAGGATAACCCCGCTGTGCGTGAAACCACCTCTTTTCACGTT
TCTTCAAGGCCAGTGCAAACGCGAATAAACATATCTACGCTATATATAGATATGACGTTT
CTCAAGCCAACAGAAGTAGATAAAGCAGCCAGGAGGTTAGAGAGTGTTCAAATTATAGCA
AGCCTTCTTCTACCTGTTTTTTTTTGATGATTGTTTTGCCGGGTAACAATCGACTTTCGG
GCAAATTTTTTTTCTCTTTTCTCCTAACAGTATATACGGAGTGAGAAACAGACTTCCCA
TAAAAGCATATTACGTGGGGTCGTAGTAAGATTGCCGTTTATGATACCTCTATTACAGG
CTCAGAGCGCATCACGATCGGGAGTGTAATTCATGTGCATATAAGCAAAACACACAGA
TTTCTTTTTTTTCCAGAAAATGAGCAGTGAAATTGCCTACTCGAATACGAACACCAACA
CTGAAAACGAGAACCGCAATACTGGCGCTGGCGTAGATGTAAATACAAATGCAAATGCAA
ATGCAAATGCAACTGCAAATGCAACTGCAAATGCAACTGCAAATGCAACTGCAGAGCTGA
ACCTCCCCACGGTCGATGAGCAAAGACAGTATAAGGTACAAGTCTATTGCATATCAACA
GCATATTACTTGCTAGAGTTATTACAGATGAATAATAGTTTACAAAACAATCTACAGAACA
ATATAAATAATAGCAATAACAATAACATCATCAGGATACAGCAACTTATATCTCAGTTCC
TTAAAAGGGTTCATGCCAATCTTCAATGCATATCTCAGATAAACCAAGGAGTGCCCTCAG

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CGAAACCACTGATCCTCACGCCTCCTCAGCTAGCCAACCAGCAGCAACCTCCACAGGATA
TTCTTTCTAAACTCTATCTTCTCTTGGCAAGAGTGTTGAGATATGGTAG

>YDR073W, 169 aa (SEQ ID NO 92)

MSSEIAYSNTNTNTENENRNTGAGVDVNTNANANANATANATANANATAELNLPVDE
QRQYKVQLLLHINSILLARVIQMNNSLQNNLQNNINNSNNNNIIRIQQLISQFLKRVHAN
LQCISQINQGVPSAKPLILTPPQLANQQPPQDILSKLYLLLARVFEIW

>YDR178W, 1046 bp, CDS: 501-1046 (SEQ ID NO 105)

ACGATTAGGCGTCAAGTCCCTTAGACCCCAATGACAACAACACAGCCAACCGTATCATCGA
GGAATTGTTGAAGTGAATAGATAAAAAAAAAAACGCACCAAGTAAGTAAGTAAATAAAGAA
TAAATAAAC'TATATGAGTAAACACCAAGCGAGGATGTTTCATGTGTCATCCGTGTTCTT
GATGATCACATAACTGTAAAGAATAATACGGCACGTAAATGTTATTTTAGAATATATA
AACACCTTATGTGCCATAAGCATTTAGCCAAATCGCTGCTGTTTTTTTATTCCGGGGCAC
CTTCGGAAGAACACAGGCGCAATTTAGTTATATAAGGAGAAGCCCTCGAGCGATCAGGGG
ACCGACTGCGGATCGCTTTAAGGCAAAGATAGAAGGATAAAATATCTGCTTTTGGGAAGATAG
TCGTATCTAAATTTCCCATTTCTGTTGTTTTCTTGATCTTTCCCTACGCTTTTCGACTTTCTTC
CTACGCGCTTTTATAATAGCTATGATGTTGCCAAGATCCATGAAATTTATGACTGGAAGGA
GAATTTTCCATACGCCACAGTAAGGGCCTTCCAGTCTACCGCTAAGAAGAGCTTAACCTA
TCCCATTTTTGGCCGTATTACCCCAGAAACCAGGTGGTGTTAGGGGCAC'TCCCAATGATG
CCTACGTCCCCCCCCCTGAGAATAAATTAGAGGGCTCATACCCTGGTATATGGAAAAAA
TCTTTGCCCTTGTCGCTCGTTCCATTGGCTACGACGGCTATGCTGACAACCGGTCCGTAT
CCACTGCAGCTGATTCTTTCTTTCTGTCATGCTTTTGGGATATTGTTACATGGAATTTA
ACTCTTGTATCACCGATTATATTTCTGAAAGAGTTTATGGTGT'TTGGCACAAGTACGCCA
TGTATATGTTGGGCC'TTGGTTCTGCGGTCTCCCTTTT'TGGAATCTATAAACTAGAAACCG
AGAATGATGGTGT'TGTTGGTTTAGTAAAAAGTCTATGGGATTCTTCCGAGAAAGACAACA
GTCAAAAGATTGAAGCCAAGAAGTAG

>YDR178W, 181 aa (SEQ ID NO 106)

MMLPRSMKFMGTGRRIFHTATVRAFQSTAKKSLTIPFLPVLQKPGGVVRGTPNDAYVPPPE
NKLEGSYHWYMEKIFALSVVPLATTAMLTGPLSTAADSFVSVMLLGICYMEFNSCITDY
ISERVYGVWHKYAMYMLGLGSAVSLFGIYKLETENDGVVGLVKSLWDSSEKDNSQKIEAK
K

>YDR202C, 1556 bp, CDS: 501-1556 (SEQ ID NO 107)

GAAT'TCCAACCGGAAAT'TGCAAACAGCAGCAAT'TTCTCGTACCGATGAAGGGGAACATGG
CCGT'TGTACCGAGGT'TCCATTGGCCGAGTATTAGCCAGGGCCCTAATACGTAAC'TCGGTA
CGCTCTT'CAGCTTCTTTTCGCATAATCAACGTTCTTGT'TATGTAAC'TCACACGTTCCATG
GCATCCGCCAACCTTGCTTCC'TTACCAAATATTAATGAGCCTAAGGTGTACATTGCCGCC
GCAGGTAATATTAGCCACGACGTTGGCATTTCAC'TGGCAAAGTAGCTGTTGATCTCAGT
AAAGATAACCTCAACATACTCTTTTACTTGTCTTTTTTGTAGCTAATTGCTTTTCTCCC
CTTCTTTTCCACAAACCGCAACTATTTTTCTCTCAAAAGTTATATGAAGTATATATACTG
AATGGAGCAATTCGGGGTTGAGTGAATTACAAAAT'TATAGTATCTGATCAAGCACACAGT
GGAAGTGCTCGAAAAGCAATATGAGTGT'TGATT'TGTTTCCAAATGATAGATTTGGTGCAG
AAGATAAATACGACAAC'TTAAGGATGCCGTAAAAGAATGCTCCTGGCTCATCGAAGAAA
TCGTCAAACCGCAAT'TACCCAACATTATTGACAAC'TTTCTAAATGCCTAGAGATGCTAG
AGAGTGACCAAATATTCAAATGCCTGTATCTAATGGTATTCCCAACGAAAGTAACAAAC
AAAACGACTCTCCGACGGTAAAGGGTGTTATCACAAAGACAAGGCCAATACATTGTTGACT
TTCACATTGTTGTGATGATTTCCACAATTTCAAAGGGGTAAACAAGTTATGTTCCGAATGA
ATACGGGACTGAATTTCTTACTTATTCAATTCAGTAAGATAATGACGCACTTGAAAAATA
TTTTGGAAATACTGAATCAACTTCAAGTAGCTACAGATGTCAGCGAATTCGTATCCAAAT
TTGGCGTGGCCATGGAAC'TTTGAACCATTCTCTAATACTTTTACAAAATCCTCCTAGAG
ACCTGGTATTCCCAAGATAACAAC'TTTGCTATGAAGGAAATGTTCCAGGATTGTTACT
CAGTCTGCGAATCCACAGCTCACATCCTAGGACTGGAAC'TTACGCTTTGTAGGAATGAGC
TTTGATAGAACTACGAAATCTAATTAAGGTGACTAAAAAACCTTGGTGCGAGATTGATA
GTAAACTGGCAGGTCATTTTGGCACCATAAGAAATCAAGTGACAAATGAAAGAAACA

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AAACTTTATCTAAGATCCTCTCAGAAAACGGTGTACAAGTCCAGGATTCACATTACTTA
ACCACATAATTTCTTCTTTTCAAAGTGAAGCTATAACACTTCCAGAAGCTCAGGAATTAT
TAAGAAGGGGCGTTACTTTTCGATAATAGGGTAGTCATGGAATGTGAAAAGTTAATAGTAT
CTACAAGTGATCCAACCTTTGATCAGTATAAGCGCCAAATTGAACAGTCTCAAAGCTTCGA
TGGCGAACCATCAAGCAAATTTGGTAGCTAGCAAACAGTTAAGTACATATAAGTAA

>YDR202C, 351 aa (SEQ ID NO 108)

MSVDLFPNDRFGAEDKYDNFKDAVKECSWLIIEIVKPLPNIIDNFSKCLEMLESQIFK
MPVSNIGIPNESNKQNDSPVKGVITRQGYIVDFHIVVRFQFQRGKQVMFRMNTGLNFL
LIQFSKIMTHLKNILEILNQLOVATDVSEFVSKFGVAMELLNLSLILLQNPRLVFPED
NNFAMKEMFQDCYSVCESTAHLGLELTLRNLCELRNLIKVTKKPWCEIDSKTGRSF
CDQIRNQVTNERNKTL SKILSENGVQVQDSTLLNHIISFQSEAITLPEAQELLRRGVTF
DNRVMECEKLIVSTSDPTLISISAKLNSLKASMANHQANLVASKQLSTYK

>YDR256C, 2048 bp, CDS: 501-2048 (SEQ ID NO 115)

GGGAAGAACTAAGAGATGTTATGGCTCGGAGAGTTTTGAAAAGCGAAATAGATTCGCTGC
AAGTTTGTGAAGAAACCATCGACAAGAATTACAAGGTTATTCTTGATGAAAAGCTGCTAA
CTAATATTTTAAAGAGAAAGTTGACAGAGGAAGAAAAAGCTCTGTCAAACGTCCTTGCG
TGAAGAAGTGAGCGGTTGTTCTAACCCTATTTAAAGCCGCAATTAGTAATGCAAAAAGT
TGGCCGGAATTAGCCGCGCAAGTTGGTGGGGTCCCTTAATCCGAAAAAGGACGGCTTTAA
CAAATATAAACTCCGAAAATCCCCACAGTGACAGAATTGGAGAAACAACAGTTTGTGATA
TCGCCATACATATAAAGAGATGTAGAAAGCATTCTTCACTGTAATGTCAAATCGTACAT
TTGAATTTCTTGAGGTTTATTTAAAAGGTAAGTTAAATAAATATAATAGTACTTACAAA
TAAATTTGGAACCTTAGAAGATGTCGAAATTGGGACAAGAAAAAATGAAGTAAATTACT
CTGATGTAAGAGAGGATAGAGTTGTGACAACTCCACTGGTAATCCAATCAATGAACCAT
TTGTCAACCAACGTATTGGGGAACATGGCCCTTTGCTTTTGCAAGATTATAACTTAATTG
ATTCTTTGGCTCATTTCAACAGGGAAAATATTCCTCAAAGGAATCCACATGCTCATGGTT
CTGGTGCCTTCGGCTATTTTGAAGTAACCGATGACATTACTGATATCTGCGGGTCTGCTA
TGTTTAGTAAATTTGGGAAAAGAACGAAATGTCTAACAAGATTTTCGACTGTGGGTGGTG
ATAAAGGTAGTGCCGACACGGTTCTGATATCCAAAGGGGGTTTGCCACCAAATTCACACTG
AAGAAGGTAATTTAGATTGGGTCTACAATAATACACCGGTATTCTTTATCAGAGACCCTT
CCAAGTTCCTCACTTTATCCACACACAGAAGAGAAACCCACAAACCAACCTAAGGGATG
CTGACATGTTTTGGGATTTCTCACCCTCTGAAAATCAGGTGGCCATTATCAAGTAA
TGATCCTTTTTTCAGACCGTGGTACCCCTGCCAACTACCGTAGTATGCATGGTTATTCTG
GTCATACCTATAAATGGTCCAATAAAAACGGAGATTGGCATTATGTGCAAGTTTCATATCA
AAACCGATCAAGGAATAAAGAATTTGACCATAGAAGAGGCTACCAAATTTGCGGGATCCA
ATCCAGATTACTGCCAGCAGGATTTATTTGAGGCTATTTCAGAAATGGAACTATCCTTCCT
GGACAGTTTATATTCAAACAATGACCGAACGCGATGCCAAAAAATTACCATTTTCAGTCT
TTGATTTGACTAAAGTATGGCCTCAGGGGCAATTCCTTTACGGCGTGTGGGTAAGATTG
TTTTGAACGAGAATCCACTGAACTTCTTCGCACAGGTGGAACAAGCTGCCTTCGCCCCCA
GTACCACGGTTTCCTTACCAAGAAGCAAGCGCTGATCCAGTATTACAGGCCCGTTTGT
CATATGCGGATGCTCATAGATACAGGCTAGGTCCCTAACTTCCATCAAATACCCGTAACT
GTCCATATGCATCTAAATTTTCAATCCCGCTATCAGAGATGGACCGATGAATGTTAACG
GCAACTTCGGCTCAGAACCTACATATTTGGCCAACGATAAATCGTACACGTATATCCAAC
AGGACAGACCCATTCAACAACACCAAGAGGTATGGAATGGGCCAGCTATCCCTTATCATT
GGGCAACATCCCCAGGTGATGTAGATTTCTGCAAGCAAGAAATCTCTACCGGTTTTGG
GTAAACAACCTGGACAGCAAAAGAACTTGGCATATAACATCGGCATTATGTAGAAGGCG
CCTGTCCTCAAATACAGCAGCGGTTTATGATATGTTTGCTCGTGTGATAAGGGACTAT
CTGAGGCAATTAAGAAAGTAGCTGAGGCAAAACATGCTTCTGAGCTTTTCGAGTAACTCCA
AATTTTGA

>YDR256C, 515 aa (SEQ ID NO 116)

MSKLGQEKNEVNYSDVREDRVVTNSTGNPINEPFVTRIGEHPDLLQDYNLIDSLAHFN
RENI PQRNPHAHGSGAFGYFEVTDITDICGSAMFSKIGKRTKCLTRFSTVGGDKGSADT
VRDPRGFATKPHYTEEGNLDWVYNNTPVFFIRDPSKFPHFHTQKRNPQTNLRDADMFWDF
LTPPENQVAIHQVMILFSDRGTPANYRSMHGYSGHTYKWSNKNGDWHYVQVHIKTDQGIK

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NLTIEEATKIAGSNPDYCCQDLFEAIQNGNYPSTVYIQTMTERDAKKLPFSVFDLTKVW
PQQGFPLRRVGKIVLNENPLNFFAQVEQAAFAPSTTVPYQEASADPVLQARLFSYADAH
YRLGPNFHQIPVNCPYASKFFNPAIRDGPMNVNGNFGSEPTYLANDKSYTYIQQDRPIQQ
HQEVWNGPAIPYHWATSPGDVDFVQARNLYRVLGKQPGQQKNLAYNIGIHVEGACPQIQQ
RVYDMFARVDKGLSEAIKKVAEAKHASELSSNSKF

>YER103W, 2429 bp, CDS: 501-2429 (SEQ ID NO 145)

ACTATTGTCACTTCTCCATTGAGATTCGAAAAACCCCTCGGGTCTTGTTAGAACTAAATT
ACGTTTCATAGGGGTGGGATTTATATTGTAATTCGCGAGGTTTACACGAAAGATATCTCA
ACTCTAGCCGCACATCCATTCCGGTATGTACTCTCCACCATTTGGGTATTATAGAATGTA
ATAGGTTTCAAAGCGGATATCTTTTGGCCGGTGAGTTGTTACTTTTTCATTTCGAGCAATG
AAGTACATTCTAGAAGTTCTTAGAACCTTATGGAAGCACCAAGAAAAAGGAAGTTAAAC
AAAACACTGATTCAATAAGCAAGGGGGGAAGCTCCTTAGTTTGACGACAGTAACAAAAATG
TTCGTATAAATTGAACGAACTCAAGCCAATAAAGGACTTTTCAGAGGCCATCTCTTCT
TTCCTCCACAACCTTTCGAATAAAAAACCCTAATAAAAAAGTAAATAACAAAAACAAGAAAA
AAATAAACAAAAACAATAATCATGTCAAAAGCTGTTGGTATTGATTTAGGTACAACCTATT
CATGTGTTGCTCATTTTGCAAACGATAGGGTTGAAATTATCGCTAACGATCAAGGTAATA
GAACGACGCCCTTCTTATGTGGCTTTTACTGACACAGAAAGGCTAATTGGTGACGCTGCGA
AGAATCAAGCTGCGATGAACCCACATAATACAGTATTCGATGCTAAGCGTCTGATCGGAC
GTAAATTCGATGATCCAGAAGTGACGAACGATGCTAAGCATTACCCATTCAAAGTGATTG
ACAAGGGAGGTAAACCGGTAGTGCAAGTGGAATATAAAGGCGAGACAAAGACATTTACTC
CAGAAGAAATTTCTCAATGATCTTGACAAAGATGAAGGAGACTGCTGAGAACTTTTTAG
GAACAGAAGTGAAAGATGCTGTAGTAACGGTTCAGCCTATTTCAACGATTACAAAAGGC
AAGCAACAAAAGATGCCGGTACAATCGCGGGCTTGAACGTTCTTCGTATCATTAATGAAC
CTACAGCTGCCGCTATTGCGTATGGGCTGGACAAGAAATCGCAGAAGGAGCACAAACGTCT
TGATCTTTGATTTAGGTGGTGGTACTTTTGTATGTCCTCTGCTATCCATAGATGAAGGTG
TCTTTGAGGTTAAGGCTACTGCTGGTGACACTCACTTGGGTGGTGAAGATTTTCGATAGTA
GGCTGGTTAACTTTCTAGCCGAGGAGTTCAAAGAAAAAATAAAAAAGGATCTAACAAC
ACCAAAGGTTCCCTAAGGAGGTTAAGGACCGCCGCTGAAAGGGCCAAGAGAACCTCTGTCTT
CGTCTGCTCAGACATCTATAGAAATAGATTCAATTATTGAGGGTATCGATTTCTATACCTT
CCATTACAAGGGCAAGATTTGAAGAATTATGTGCTGATTTGTTTAGATCTACATTGGAGC
CAGTGGAAAAAGTTTGGCTGATTCAAAATTAGATAAGTCACAAATTGATGAAATTGTAC
TTGTTGGTGGTTCAACAAGAATTCCAAAAGTACAAAACTGGTTTCTGATTTTTCATG
GTAAAGAACCAAAACCGTTCGATTAACCTGATGAGGCCGTCGCTTATGGTGTGCGGTAC
AGGCTGCCATCTTAACGGGTGACCAAGTCGTCGACGCCAAGATTTACTGTTGCTGGATG
TTGCACCATTATCTCTAGGTATTGAACTGCAGGTGGTATTATGACAAAGTTGATCCCAA
GAAATTCGACTATCCCAACAAAAAAATCGGAAGTGTTTTCCACCTACGCTGACAACCAAC
CTGGTGTGTTGATACAAGTTTTTGGGGTGAAAGGACAAGGACAAAAGACAACAATCTAC
TGGGTAAATTTGAGTTGAGCGGTATTCACCCGCTCCAAGAGGCGTACCACAAATTGAAG
TTACATTTGATATCGATGCAATGGTATTCTGAACGTATCTGCCGTTGAAAAAGGTACTG
GTAATCTAACAAGATTACAATTACTAACGATAAGGGAAGATTATCGAAGGAAGATATCG
ATAAAATGGTTGCTGAGGCAGAAAAGTTCAAGGCCAAGATGAACAAGAAGCTCAACGTG
TTCAAGCTAAGAATCAGCTAGAATCGTACGCGTTTACTTTGAAAAATTC'TGTGAGCGAAA
ATAACTTCAAGGAGAAGGTGGGTGAAGAGGATGCCAGGAAATTGGAAGCCGCCGCCCAAG
ATGCTATAAATTGGTTAGATGCTTCGCAAGCGGCCCTCACCAGGAATACAAGGAAAGGC
AAAAGGAAC TAGAAGGTGTTGCAAAACCCCATTTAGTAAATTTTACGGAGCTGCAGGTG
GTGCCCCAGGAGCAGGCCAGTTCCGGGTGCTGGAGCAGGCCCCACTGGAGCACCAGACA
ACGGCCCAACGGTTGAAGAGGTTGATTAG

>YER103W, 642 aa (SEQ ID NO 146)

MSKAVGIDLGTTYSCVAHFANDRVEIIANDQGNRTTPSYVAFDTERLIGDAAKNQAAMN
PHNTVFDKRLIGRKFDDEPVTNDKHYPFKVIDKGGKPVVQVEYKGETKTFTPEEISSM
ILTKMKETAENFLGTEVKDAVTVPAYFNDSQRQATKDAGTIAGLNLVRIINEPTAAAI
YGLDKKSQKEHNVLI FDLGGGTFDVSLLSIDEVFEVKATAGDTHLGGEDFDSRLVNF
LAEFFKRKNKKDLTTNQRSRLRLRTAAERAKRTLSSAQTSIEIDSLFEGIDFYTSITR
ARFEELCADLFRSTLEPVEKVLADSKLDSQIDEIVLVGGSTRIPKVQKLVSDFFN
GKEPNRS

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INPDEAVAYGAAVQAAILTGDSSTTQDLLLLDVAPLSLGIETAGGIMTKLI PRNSTIPT
KKSEVFSTYADNQPGVLIQVFEGERTRTKDNLLGKFELSGIPPAPRGVPQIEVTFDIDA
NGILNVSAVEKGTGKSNKITITNDKGRLSKEDIDKMVAEAEKFKAEDEQEAQRVQAKNQL
ESYAFTLKNVSENNFKEKVGEEDARKLEAAAQDAINWLDASQAASTEYKERQKELEGV
ANPIMSKFYGAAGGAPGAGPVPAGAGPTGAPDNGPTVEEVD

>YER150W, 947 bp, CDS: 501-947 (SEQ ID NO 149)

ATACGGGGGAAGAAGAAATATCATATTCAAAGCTAATTCATTGAAATTAGTGCTTGTCTC
ATCTAGCCTTTAGTGCTTAATCTCTGGAGGAGCACATATGGGGTTAAAGCCATGCCGGGA
CTGGGGGCCCCCTATCGGGGCTCGAACCCGAATCCCGCGAGTATTTATTTGAAGGTCCGGG
ACGCAAGTTACCTAATCTGGTTAATTGATATCCCATTTAGGCGATGACGTTCCCTTCCCCT
CACCCCTCGGCTTGTTAGAAGATCTATTGTTATAGCCTCCTCTGGAAGAATTTATGCCAG
ATGAAGAAAAAACTTCTCGAAGTTCCCAGATGCCCAAATGAGGGCTTTCCATCCCTGTT
AGCTGGAAGAGTGTAAGTATATCTATATAAAAAGTCGGCCTACTTTTGCCAGGTTTCGTCT
TTCACCTGCACTCTCTTGATCTTACTTTCTACTCAAAAAGAATCCAATACACAAAAATAA
AATCAGTACTATTACTAATAATGTTGTCTAACGCTAAGCTCCTTCTATCATTGGCCATGG
CCTCTACGGCTCTCGGATTGGTATCTAATTCTAGTTCCCTCTGTAATCGTGGTACCATCAA
GCGATGTCTACTATTGCCGGTAACGATACAGCCACGCCAGCACCAGAGCCATCATCCGCCG
CTCCAATATTCTACAACCTCGACTGCTACTGCAACACAGTACGAAGTTGTCAGTGAATTCA
CTACTTACTGCCCAGAACCAACGACTTTCGTAACGAATGGCGCTACATTCACTGTTACTG
CCCCAATACGTTAACAATTACCAACTGTCCTTGCACTATCGAGAAGCCTACTTCAGAAA
CATCGGTTTCTTCTACACATGATGTGGAGACAAATTCTAATGCTGCTAACGCAAGAGCAA
TCCCAGGAGCCCTAGGTTTGGCTGGTGCAGTTATGATGCTTTTATGA

>YER150W, 148 aa (SEQ ID NO 150)

MLSNAKLLLSLAMASTALGLVSNSSSSVIVVPSSDATIAGNDTATPAPEPSSAAPIFYNS
TATATQYEVVSEFTTYCPEPTTFVTNGATFTVTAPTTLTITNCPCTIEKPTSETSVSSSTH
DVETNSNAANARAIPGALGLAGAVMMLL

>YFR033C, 944 bp, CDS: 501-944 (SEQ ID NO 155)

ATCGAGCCATTTCGGGTCGCTGAGTAAGCGACGGTCATCGGGCGCGCTCGTGGACGATGA
CAAGCGCGAATCACACAAGCATGCAGAGCAAGCACGGCGTAATCGATTAGCGGTCGCGCT
GCACGAACCTGGCGTCTTTAATCCCCCGGGAGTGGAACAGCAAAATGTGTGCGCCGCGCC
GTCCAAAGCGACACCGTGAGGCGCGCTGCGGTACATCCGTCACCTACAGCAGAACGT
GAGCACGTGACCGTGACCAATGGGAAGCACGTTCCGGGCATATCGGACTGGGGCGCGCC
TCCCCTGCGCGGTGCTTGTTATAAGAGGCGCTTTGCTGGAAGTGCGCCACACCGGGTTT
TCGAGATTAGGACCTACTCAGTCTTAAGGCGAGTATTGGTTGGCGCTTATTTGCACATAT
TGTATACACGCACTCACATTAACAGAAGCACACATATACACTTACACCTACACACACGGA
TAAAGAAAAAGAAATAGAAAATGGGCATGTTGGAAGTAGTTGGTGAGTACTGGGAACAAC
TAAAGATAACCGTTGTGCCTGTTGTGGCCGCGGCCGAAGATGACGATAACGAGCAGCATG
AAGAAAAGGCAGCAGAAGGAGAAGAAAAAGAAGAAAATGGGGATGAAGATGAGGATG
AAGACGAAGACGAAGATGATGATGATGATGACGACGAAGATGAGGAAGAAGAGGAAGAAG
TCACTGATCAGTTGGAAGATTTGAGAGAACATTTCAAGAACACGGAGGAGGGTAAGGCCC
TTGTGCACCACTACGAGGAGTGTGCTGAGAGAGTCAAGATACAGCAACAACACCCGGCT
ACGCGGATCTTGAACACAAGGAGGACTGTGTGGAGGAGTTTTTCCATCTACAGCACTATT
TGGACACTGCCACGGCACCTAGATTATTTGACAAATTAAAGTAG

>YFR033C, 147 aa (SEQ ID NO 156)

MGMLELVGEYWEQLKITVVPVVAEAEDDDNEQHEEKAAEGEEKEEENGDEDEDEDEDEDD
DDDDDEDEEEEEVTDQLEDLREHFKNTEEGKALVHHYEECAERVKIQQQQPGYADLEHK
EDCVVEFFHLQHLYLDTATAPRLFDKLL

>YGR086C, 1520 bp, CDS: 501-1520 (SEQ ID NO 175)

GTTGAATATTTACCAATTGGGAAAAAGAACTCGTATTTTCATTCCCTTTTTTGGAAGGGG
TGGGGAGAGACTGTTGTTACGCCACGTCAATTATTATTTTTTCTTTGGCCCTGCGCTTGT
CTTATAAAATTCCGCAGCCGCTCTATTTTTTTTTTTTCGATTTTTTGCCACAGGTC

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ATATTGCAAAAACCGAATGGCCGCGCCCCCTCACGCACGGGACGGAAGAAGGGCGGCGT
CCCCTGTTTTTCTGCTTTGGCTCATCTCTTTGGCTCCGACGGACGAAAGACGGGATTCCC
CCTCCCGTGTCTTTTATAAATAACAAGTGCTCATTCTGCATCCTTCCTTGTTTCCCGTC
GTTTGGGTACAATGCGTTGATTATCCCAACCAAGAAAGAAAATTTGTCTCACATCTGCA
TCTGCACATTTATTTACCTATACTTTTCCATTGTTAGCAGTATTGCAAAGTGAAGAATAT
ATCAGCATCAAGTATATAGTATGCACAGAACTTACTCTTTAAGAAATTCAGGGCACCTA
CCGCCTCTCAATTACAGAACCCACCGCCACCACCATCTACAACCAAAGGTAGATTCTTTG
GGAAGGGTGGTCTAGCTTACAGCTTTAGGAGAAGTGCTGCTGGAGCTTTTGGCCCAGAAT
TATCCAGAAAGTTGTCTCAATTGGTTAAGATTGAAAAGAATGTTTGGAGTCCATGGAAT
TGACAGCCAACGAAAGACGTGACGCTGCTAAGCAATTGTCTATTTGGGGGTTGGAACG
ATGACGATGTTTCCGACATCACTGATAAATTAGGTGTCTTGATCTATGAAGTTAGTGAAT
TAGACGACCAATTTATCGATCGTTATGACCAATACAGATTGACTCTAAAGTCCATCAGAG
ATATCGAAGGTTCTGTTCAACCATCTAGAGACCGTAAGGACAAGATCACCGACAAAATCG
CCTACTTGAAATACAAAGATCCTCAATCACCTAAGATTGAGGTCTTGGAACAAGAATTGG
TGCGTGCTGAGGCTGAATCTTTGGTCGCTGAAGCTCAATTATCTAATATCACAAGGTCAA
AGTTGAGAGCTGCTTTCAACTACCAATTTGACTCCATCATCGAACATTCAGAGAAAATTG
CTTTAATCGCTGGTTACGGTAAGGCTCTCTTGGAATATTGGACGACTCTCCTGTCACTC
CAGGTGAAACCAGGCCTGCTTACGATGGGTATGAAGCCTCTAAACAAATCATTATTGATG
CTGAAAGCGCACTGAATGAATGGACACTAGACTCTGCCAAGTCAAGCCTACTTTAAGTT
TCAAGCAGGATTACGAAGACTTCGAACCTGAAGAAGGCGAAGAAGAGGAAGAGGAAGACG
GTCAAGGCAGGTGGTCCGAAGACGAACAAGAAGATGGACAAATTGAAGAACCTGAACAAG
AAGAAGAAGGTGCTGTTGAAGAACATGAACAAGTCGGACACCAGCAAAGTGAGTCTCTTC
CCCAACAAACAACAGCTTAA

>YGR086C, 339 aa (SEQ ID NO 176)

MHRTYSLRNSRAPTASQLQNPPPPSTTKGRFFGKGLAYSFRRSAAGAFGPESLRKLSQ
LVKIEKNVLRSMELTANERRDAAKQLSIWGLENDDDVSDITDKLGLVIYEVSELDDQFID
LYDQYRLTLKSIIRDIEGSVQPSRDRDKDKITDKIAYLKYKDPQSPKIEVLEQELVRAEAS
LVAEQLSLNITRSKLRAAFNYQFDSIIHSEKIALIAGYKALLELLDDSPVTPGETRPA
YDGYEASKQIIIDAESALNEWTLDSAQVKPTLSFKQDYEDFEPEEEEEEEEDGQGRWSE
DEQEDGQIEEPEQEEEGAVEEHEQVGHQQSES LPQQT TA

>YGR197C, 2144 bp, CDS: 501-2144 (SEQ ID NO 185)

TCCAGTATGCCACACATTATGCCTTGACACCTAAAGCACATATTTTCGTTATTTTTCAC
CACAATAGGTGGATCTCGAAAAGGATGGAATCAGGAAAAAGAAATGTTGAGAAAAAAA
TAAACCGATTCCCGTTTAGTTTTCTCCTATTTCCGTGTATATGCGTGGTTATTCGTTTTC
GAATCCTTTTATGAATGTCCGAGGAGGTGGTACAATCCGAAATAGACTAAAGAAAAGCGA
AAGCCGTGAGTTTGTGTTGATGATAGATGACTCGCAGCTTTGTCATCAACGGGCCACCCTA
TTCGAAGAAGGGAATGGAACGGACTGGCGTAGTCAATAAGCGTCTTCATATCTTAGCA
TTGTTGAGAGATACATAGTGTACTCCATATCGTTCCTTTTTTTTTTGATATATCAAGCCAC
ATATCCTGTTTCTTTAATCTTTTATACGCCGTAAGAATCGGGTACTGACATAAGTGAAG
TAGCCGTACAGAGAACAAATATGACTAAATCGGTTGGTGATGAAGAGTCACAGTACATTG
AGGACCCTAGTTTTGTCAGCAGCAGCTGCATTTACTGGCGGCAGGGACGGGGTTTCGTACA
GTAATCAGCGATTTGCTGAGGGTTCCGGCCATTCTTCTGACTTAGCAAAGTCATTAGAAG
ACTATCGGCCTCCTGATGAAAAGCCGTCCTCATTGTCATCTGTGGGGGAAGGTGGCGCTA
ATGAGGAAGAGAAGGGCGGTAACGACGGCGGTCCCTTGGCAAGAATTCAAACAGGGCTTT
TTTCTCCAAGACTGCGAAATCATAGGAAAAAGATTCTCTCGAAGTTTGTTTTGAACAAT
TCTTCATTGCTTGTGTGTGTATCGCTCATATCGATTTACTGGGGTGCCTGTTACGGAA
CAGATCGTTACTTTTTCAAAGTGAAAAATATTGTTGTATTGCAGGATGCGCCATCTAATA
CTTCAGTTCAATCTATTTCCGCGATCATACCCTCATTGTTAGCGTCTGTCCCCGGGACAT
GGCATATATACAACGCAACATCATTTTCATAGGAAATTTGGTACGACGAACTCCACCGAAA
TTGACAGAAAGATAGTCGATTTAATTTACGATGAGAGATACTGGCTGGCGTTAAACGTTA
AACCTAATGCTACAGACACTTTGTATAATTCTTTGATTAGCCAAGACGCAAACCTCGGAGT
TCAATTCATCAATTTTTTTTTGAATCCGTGTTTGAAAGTGGTCGTGACCCATCGAGTGTTA
AATCGACCATTCTACCACTCATGCAACAATTGGAGGTCCGCCTTCAGAAATATTACGTCA
AGGAATATCTTCCCTCATTGATGAGCAACATCACTTCTAATGACAGAGATCTTAATATAA

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ACATGGAGAACTGGGCGATTGCAGGACAGTTGTTGTTCACCTACAACGATTATCGTCCCT
TTGCTGATCGTATTCTAATGGCCCCCTGCGAGGTCGGTCTGATTTATTGTATTTTGTAA
CCGTTTTACAACGTCAATTATATGGTAAGTTGCACGGAGAAATGGCCAGAGTTCTGAAGC
CAAAGCATATTTTAACTACAGGCTTCTAATTTCTGGGCAACTATTTTCTTCTTTCCA
TTGGATTCTGTACCGTATCTGCAATTTTATAGGATCGATTTACCCCCGCCCTTTGGCAGAG
GAGGATTTCGTAGTATATTGGATGCTACGTGGTTGGTAATGATGGCTGTTGGTGGTGCCA
ATGAAAACGTTCTCAGCTTAGTTATAGCTTACTGCCCTCCATACCTGAGTATTTGGTTGA
TGACGTGGATCATATTAATATTTCTGCTTCATTCTACCCAATGGTTTTGAACAACGAAT
TTTACAGGTACGGCTACATAATGCCAATCCATAATGCCGTGGATATCTATAAAGTGATTT
TTTTGAATTTAACCAAAAGAAAAATGGGAAGAAATTACGGTATTCTCGTGGCATGGGTTG
CCCTCAATACATCCTTGATGCCATTTTGTATGAAGTTTGCAGGTAAAAAATGCAAAAA
ATGCTATGCAAGCAGCAGAAGCCGCTGTCGACGAGCTACCCAGCGTGCTAGCCGCCCGG
CAGAGGCCAATACTGATAAAAAATAACAACCCGCCCGGAAATTAA

>YGR197C, 547 aa (SEQ ID NO 186)

MTKSVGDEESQYIEDPSFAAAAAFTGGRDGVSYSNQRFAGSGHSSDLAKSLEDYRPPDE
KPSSLSSVGEGBANEEKGGNDGGPLARIQTGLFSPRLRNHRKKILSKFVLNNFFIACVC
VSLISIWGACYGTDYFFKVKNIIVLQDAPSNSTSVQISAIIPSLASVPGTWHIYNAT
SFHRKFGTTNSTEIDRKIVDLIYDERYWLALNVKPNATDTLYNSLISQDANSEFNSSIFF
ESVFESGRDPSSVKSTILPLMQQLEVRLOKYYVKEYLPSLMSNITSNDRDLNINMENWAI
AGQLLFYNDYRPFADRI LMAPLQVGLIYCILLTVLQLSLYGKLHGEMARVLKPKHILY
RLISWATYFLLSIGFCTVSAIFRIDFTPAFGRGGFVVYWMSTWLVMMAVGGANENVLSL
VIAYCPPYLSIWLMTWIILNISASFYPMVLNNEFYRYGYIMPIHNAVDIYKVI FLNLTKR
KMGRNYGILVAWVALNTSLMPFCMKFAGKKMQKNAMQAAEAAVAAATQRASRP AEANTDK
NNNPPGN

>YGR250C, 2846 bp, CDS: 501-2846 (SEQ ID NO 191)

TCTTGTGTACGTACGATGTTTCTCCCGCTGATCCGATTACTAGCCGAAGACGTAA AATTG
GCGCTTGATTCAATTTATGCCCTTCCCGGAATAGTTGACCAAAGGGCAAAAAATTAG
TCGGAGATTCCCTATTGGGCGGAATTTAGTAGATCTCTTTCCGTGCATAACGCCCTGCCCG
TTAGTCGTTATTTTACGTTAACATTTTCTTGGCCACTGCGCTATATAAATAAATACATAT
ATATATGTCAAGCACATAAAGAAACTTCCCTTAAATATTGAATAAGTAAATAATAGTTG
AAAAGTGCCCTTTTGTTCGAAGGATTAGAGTGTTCTTAATTTTAGTTTCGTTCAACGGTCTC
AAAAAAGTGTTGAACAAGTAAAGCATAGCACATCCCAAATTACAAGGCACCCTGATTA
AAAATCCAAAAATAAACCATAGTTTATTTTACTAAAAACATTATACGTGAAAGACAAA
CCGCATCAGAAGTTTCGAGGATGAATATTGCAGAAGAACCATCAGATGAAGTAATATCTA
GTGGCCCCGAGGATACAGATATCTGCAGCCAGCAGACATCAGCGAGCGCAGAAGCTGGAG
ACCAATCAATAAAAAATTGAAAGGAAAACCTCCACTGGTCTTCAACTGGAACAATTGGCCA
ACACAAATTTATTAACCATAAGAAATAAAATGGCAGTTACAAGAAGAAGAAGATGATCACT
GCAACTCTAGAATAACCGATCAAATAATGGACACAATACAGCACTACAAAGGTATCTCCG
TTAACAACTCTGATACAGAAACATATGAATTTCTTCCGGATACAAGGAGGTTACAGGTTCT
TCGAACAAAATAAAGACATCTATCTTTACGAGCATGGAAGTCAAGAGTATGAGAAATCTT
ACAAAGATAACGAAGAGGAAGATGATTGGAGATACGATACCGTTTTTGCAAGCACAAATCA
AGTACCCCAAGTCATTAGAAAATGCATGTACAGATATCTCGGAATTACTCAAGAGCGAAC
CTATTGGTCAGCATATTGATAAATGGTCTATCGGTGTGAACAAGCATGCACCTAACCTATC
CTGGAAATATTTTTGTGCGGGGGAATAGCAAAGAGCCCTTTCTATTGGTGAACCTAAGTTTCT
TATTTTCAAAATATGGACCAATTTTATCAATGAAATTGATATATGATAAAACGAAAGGCG
AACCTAACGGATACGGGTTTCATCTCCTACCCCTTGGGTTCTCAAGCTTCACCTTGCATCA
AGGAACCTAATGGAAGGACGGTAAATGGCTCCACACTATTTATCAACTATCACGTTGAGC
GAAAGGAGAGAGAAAGAATCCATTGGGACCATGTCAAAGAAAACAACAATGATGATAATT
TCAGGTGTCTCTTTATAGGCAACTTGCCCTTATCACAATCCTGAAAAAGTAGAGACTTTGA
TTACACCTAAAGAAGTCATAGAAGTAATCAAGAAGGAGTTATCAAAAAAGTTTCCGGACT
TTGATATCATTTTCATATTACTTTCCGAAGAGAAGTAATACAAGAAGCAGTAGTTTCAGTAA
GTTTCAATGAGGAGGGGTCAGTAGAATCAAACAAATCTTCCAATAATACCTAATGGAAATG
CCCAAGATGAAGATATGTTGAAGGGTTATGGTTTCATCAAGCTTATCAACCATGAACAAG
CACTAGCAGCCATCGAGACCTTCAATGGGTTTCATGTGGCATGGAAACAGGCTCGTTGTTA

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ATAAGGCGGTTCAACATAAAGTTTACAACAACCACAATAGCCATGACAGGCACCCTTCCA
TCAGTAACCACAATGATATGGAGGTTTTGGAATTTGCAAATAACCCAATGTATGATTACA
ATAATTATACATATGATAGATATTACTTCAACAATAATAAAAACGGGAACAGCAACGATA
CCTCCAATGTACGGTATTTTGATTCTGTAAGATCAACCCCTGTGGCAGAGAAAATGGATC
TGTTCTATCCTCAAAGGGAATCTTTCAGTGAAGGTCGTGGTCAACGTGTGCCTAGATTCA
TGGGCAACAAGTTTGACATGTACCAGTACCCATCAACTTCTTACAGCTTACCTATACCAA
TGAGTAATCAGCAAGAATCAAACCTATATGTCAAGCACATCCCTCTTCTTGGACAGATG
AAGATTTATATGATTTCTACAAATCTTTCGGTGAAATAATCAGCGTTAAGGTCATTACTG
TTGGGGGTAGTAAGAACAAGTATCGTCAACAATCGAATGATAGCTCATCAGATAATGATC
TGCCAGTGGGATCATCAAGAGGTTATGGTTTTGTTTTCTTTTGAAGCCCATTAGATGCTG
CTAAGGCAATTTTGAATACAGACGGGTATCAAGTGAGCAAAGATCAAGTGTTATCTGTTT
CTTTCGCTCAGAAACGTGGTAATTTATCTTCAAGTGATGATGATGATCAATCCCAAATG
ATAACTCATCAAAGTTCCAAAATTTTCAGCCACATAATGATTATCATAAGGCTTATCCAA
CAAAGTATAATAAGAAATTTATCAATGCCTTGATGACTCAGAACCAATCGCAACAGCAAG
TCTCGAGGGAAAATTATTTTCATACCACTGCAGTACCCTAATACCAACACAAAGCCCGTGA
ACAGTTACAACCTTAATAAGTGCAAACCAAAATAACGCTAACTGGATGATGCCAATGTTCC
CATCATTTGGGTTTTATTCCACAGGTGCCGCCAGTGCCCTATATAATACCTCCGCAGAATC
CTGCAGCAAATCATATTCTTATAATGGCAAACGGTAGTAATGAAGAGGAAGAATTTTCTA
GTGGTGATTATTCTATGGACTACTAG

>YGR250C, 781 aa (SEQ ID NO 192)

MNIAEEPSDEVISSGPEDTDICSQQTSASAEAGDQSIKIERKTSTGLQLEQLANTNLLTI
RIKWQLQEEEDDHCNSRITDQIMDTIQHYKGISVNNSDTETYEFLLPDTRRLQVLEQNKDI
YLYEHGSQEYEKSYKDNEEEDDWRYDTVLQAQFKYPKSLENACTDISELLKSEPIGQHID
KWSIGVNKHALTYPGNIFVGGIAKSLSIGELSFLFSKYGPILSMKLIYDKTKGEPNGYGF
ISYPLGSQASLCIKELNGRTVNGSTLFINYHVERKERERIHWDHVKENNNDDNFRCLFIG
NLPYHNPEKVETLITPKEVIEVIKKELSKKFPDFDIISYFFPKRSNTRSSSVSFNEEGS
VESNKSSNNTNGNAQDEDMLKGYGFIKLINHEQALAAIETFNFGFMWHGNRLVVNKAVQHK
VYNNHNSHDRHPSISNHNDMEVLEFANNPMYDYNNTYDRYFFNNKNKGNNSNDTSNVRYF
DSVRSTPVAEKMDLFYPQRESFSEGRGQVRPRFMGNKFDMYQYPSTSYSLPIPMSNQQES
NLYVKHIPLSWTDEDLYDFYKSFGEIISVKVITVGGSKNKYRQQSNDSSDNDLPVGSRR
GYGFVSFESPLDAAKAILNTDGYQVSKDQVLSVSFAQKRGNLSSDDDDQSQTDNSSKFQ
NFQPHNDYHKAYPTKYNNKFINALMTQNQSQQQVSRENYFIPLQYPNTNTKPVNSYNLIS
ANQNNANWMMPMFPSFGFIPQVPPVPYIIPPQNPAANHIPIMANGSNEEEEFSSGDYSMD
Y

>YHR001W-A, 797 bp, exon1: 501-506, intron1: 507-569, exon2:
570-797 (SEQ ID NO 195)

TTCTATTCCGGCTTATAAAAAGCATGGAATCCAAAAGAATTAGGCTTCTCATTCTATTTT
AATTATACTAGTACGATTTCTCACTCTGTAATTTAATATCAGTGTAATATGCACCTAGTT
ATGGGTAGTTTTTGCTAACGTTACGAGCCGCGAAACTGTCCTCAATCTTCACTACTACCT
CTAATGACTGAAGAATGCTATGCGATATAACGCTGTGCGACTTTGAATATATACTTATAT
TTACATAGTTTTCAAGTGCGTATTACTATTGCAAAGTAGTATTTTGTACAGTGATTTTGA
TCCAATTAATACTAAATATGGTTCAACCCGTTGTTTCCGCATCAAAAAACCATAACATTT
ATCAAGGGGACGGGATATATCACATAACAGTTTGAATGCATAATTTGTTATAGATATCTT
CTGGAATAATCTTCACAGCAAAAGCGCAAGTCGAATAATATATCGATAAATAACAATCCAT
AAGACTTAAATACTAACCTCAATGGCGGTAAGTATCCTATCATATTATGTGAGCTAGAACC
GAATTAGTATACTAACATTTATAATACAGTACACTTCTCATCTGTCTTCAAAAACTGGTC
TACATTTCCGTAGACTTTCTTTAAGAAGTTTAAACAGCTTATGCTCCGAATTTAATGTTAT
GGGGTGGTGCTAGCATGCTTGGGCTATTTGTATTACAGAAGGATGGCCTAAGTTTCAAG
ATACGCTATACAAAAGATTCCGTTGTTAGGACCTACATTGGAAGATCATACTCCACCAG
AAGATAAACCTAATTGA

>YHR001W-A, 77 aa (SEQ ID NO 196)

MAYTSHLSSKTGLHFGRLSLRSLTAYAPNMLMLWGGASMLGLFVFTEGWPKFQDTLYKKIP
LLGPTLEDHTPPEDKPN

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>YJL142C, 893 bp, CDS: 501-893 (SEQ ID NO 225)

TGCTGAATTATTTTTGGGTATACCGATCTTCCCAGGCGCTTCTGAATATAACCAATTAAC
AAGAATAATAGACACGCTTGGATATCCTCCATCGTGGATGATAGATATGGGTAAAACTC
TGGAAAATTTATGAAGAAATTGGCACCAGAAGAAAGTTCTTCTTCTACACAAAAGCATCG
TATGAAAACATATTGAAGAGTTTTGCAGAGAATACAATATAGTGGAAAAGCCCAGTAAACA
ATATTTTAAGTGGAGAAAGTTACCAGATATTATTAGAACTACAGGTATCCTAAAAGCAT
ACAGAACTCCCAAGAACTTATCGACCAAGAAATGCAGAATAGGGAGTGTGATCCACTT
TTTAGGCGGTGTGCTAAATTTGAACCCGTTAGAAAGATGGACACCACAACAAGCTATGCT
ACACCCCTTCATAACAAAGCAGGAGTTTACAGGTGAGTGGTTTCTCCAGGATCGTCTTT
ACCGGGTCCTTCAGAAAAACATGACGATGCAAAAGGCCAGCAAAGTGAATATGGAAGTGC
GAACGACTCTAGTAACAATGCAGGCCACAACATATGTCTATAATCCTAGCTCTGCCACTGG
TGGTGTCTGATAGCGTCGACATTGGTGTCTATCAGTAAAAGGAAGGAGAATACATCTGGCGA
CATCTCCAATAATTTTGTCTGTACTCATTCTGTTCAAGAAGGGCCACAAGCGCGTTCAA
TAAACTTCACATTGTCTGAAGAATAAATCGTTATTTTGTCTGACTTTTCTTAACATACCCAT
TTCATTTTATTACGGCTTGGTGCCATAATGATATACTAAATAAATATGAATTTTGCCTTT
TCTTAATTTTCTTATACGTATAGTCATTACAATTAATAAAGTAACATTATAA

>YJL142C, 130 aa (SEQ ID NO 226)

MTMQKASKVNMEVRTTLVTMQATTMSIILALPLVVLIASTLVLSVKGRRIHLATSPIILL
LLILFKKGQARSINFTLSKNKSLFCLTFLNYPHFITAWCHNDILNKYEFCLFLIFLIR
IVITINKVTL

>YJL144W, 815 bp, CDS: 501-815 (SEQ ID NO 227)

AGAAAGAAGTTTCGTGGTATTAAACCGACGGCAGCAAGTTGGGTCAATACTTGAAGGATTGC
CCATATGAAGGGTATGGCGGGAAAGATAAGAAGAACAATCTGACCAAGCAAAATGTCACA
AATGTCCATCCAACAGAATACGGCCTTTACATTTTACAAAAACAAATCATCGAGGACGTT
GAGTGATTTGTTGGCATGATCTAATAATAGTCTCTTATATAAACCCCTATAATAATTTCTT
ATTTTTGCCTTATATTACAGGTAAATCACCATCTAACTGTATTATCTCTCACGTATCTTCA
CTTATATGGCTCAGAAAACACCGTACGAAACGAAGGGGCTGCGAAAATGTTTCTAGAAGG
TAATGGCAATAATAGGGATACAGATCGATCAGATCCGCCTATATAAAAGACAACGCACCG
AAGGTGAACAAGATCGCAGATAAAGGTATTTACAAGGGAAAAAAGTCAGCAAAAAACAGA
GATAAGATAACAAGAAGAAGATGTTAAGGAGGGAACTTCAACAATATACAGGACACACA
AAAAAAGCAACAGTAGTATACTCAGGAGCCAGCGGGACCAGACTAGAGTGGATTCTTGG
TAGAGGAGTCTCCCATGGGCGATTTCTGGGATCAATAACCAGCCTACACAGCCTGGCGTGA
TATACTACTTTGTAGAGCTGACTAATTTAGGCATACAGGAAAACACAAGCAGTAATAATA
ACAACAACAATAATCATGGTGACGATGAAAACGGCAGTCGATACGGCCACGGCAGCAGTC
TGGGTGGAGACGTTCACTCTCGCCGTTGTTCATGA

>YJL144W, 104 aa (SEQ ID NO 228)

MLRRETSTIYRTHKKSNSILRSQRDQTRVDSLVEESPMGDFGINNQPTQPGVIYYFVEL
TNLGIQENTSSNNNNNNNHGDDENGSRYGHSSLGDDVHSRRCS

>YJL166W, 785 bp, CDS: 501-785 (SEQ ID NO 231)

TGAACAGCTATACCACGAATATGAAGAGTCTATTGCCAAGGATTTGAAGGCCAAAATTTTC
TCAGGTGATGAGTCTCGTGGCTTCAAAGCTGATGTCTTAACTGCGTTCTTGAACAAAGT
TTACAAGAGAAGCAAAATAGAACTAACGCTAATCGATAAAACATTAGATTTCAAACCTAGAT
AAGGACCATGTATAAGAATACTATCTCAATATAATATAGTATAAGCTTTAAGATAGT
ATCTCTCGATCTACCGTTCCACGTGACTAGTCCAAGGATTTTTTTTAAAGCCAATGAAAAT
GAAGAAATGCGTGATCGGAAATTACGGGTAGTACGAGAAGGAACTTGAGCCACCCCCCA
AATTTTATTTCATATAATAATAGGAAAAGCAACGACCTCATCTCTCGAACATTGTTTACTT
GAGCAAGTCCGATTAAGAGTAAGTTGTCTGACGTTAAATACAAATAATCAACAAAACACT
ACACAAAACCTTCTACGATAATGGGTCTCCAAGCGGTAAAACCTTACATGGGATGGTGGG
GTCACATGGGTGGTCCAAAGCAAAAAGGTATAACCTCATATGCTGTGTCTCCATATGCTC
AAAAGCCATTACAAGGTATTTTCCATAACGCTGTATTCAATAGTTTTAGAAGATTTAAGT
CTCAATTTCTATATGTATTAATACCTGCGGGAATTTATTGGTACTGGTGAAGAACGGTA
ACGAGTATAATGAATTTCTGTACAGCAAAGCTGGTAGAGAAGAGCTGGAAGAGTTAATG

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TTTAA

>YJL166W, 94 aa (SEQ ID NO 232)

MGPPSGKTYMGWWGHMGGPKQKGITSYAVSPYAQKPLQGIFHNAVFNFRFKSQFLYVL
IPAGIYWYWWKNGNEYNEFLYSKAGREELERNV

>YKL117W, 1151 bp, CDS: 501-1151 (SEQ ID NO 247)

TTATAGAACTGTTTTATTGTTTAAAAGAGCTTGTTATAGTAATCTAAGTGGAAATACACT
AACAGTAAATAGGGCGTGTGGCGTAGTCGGTAGCGCGCTCCCTTAGCATGGGAGAGGTCT
CCGGTTCGATTCCGGACTCGTCCAATCTTTTATACTTATTAATAATTTTTTTCCTGCCG
TTACTTGCTTTTAAAATAACTGCCTTTTATGAATACAGAGTATAATTTTTGATATACAAA
GAGGTGACTGTGATAATCAATACTTAATTTGTGGTTATTGGTACACATATACCTACAAA
AGTTACCAACAACTGTTTCGACTTTTAATGCTACCCGCCTTCCGAGTGTTTTTGAAGGGG
CGGAGAGGAGCGGCAAGAATTAGCATGGAAAAAGCATAAAAAGACGAAATGGGTGGCAA
TGTATTAACTTGTTTCGAGAAACCTAGTGGACTCAATTCATTACAACAACAAGTTCCCAAG
ATCATCGATTTCATAATAGTCATGTCCGATAAAGTTATTAACCCCTCAAGTTCATGGGCTC
AAAGGTCTAGTACTACTGATCCAGAAAGAAATTATGTCTTAATAACTGTGTCAATTGCAG
ACTGTGATGCCCCCTGAGTTAACCATTAAAGCCATCATACATCGAATTAAAGGCTCAATCAA
AGCCTCATGTTGGCGATGAAAATGTCCATCATTATCAATTACACATTGATCTATACAAGG
AAATTATACCTGAAAAACAATGCATAAGGTTGCTAATGGCCAGCACTACTTTTTGAAAT
TGTATAAAAAGGATTTAGAATCTGAATACTGGCCACGTTTGACAAAGGAAAAGGTGAAGT
ACCCCTTACATCAAACTGATTTTCGATAAATGGGTTGATGAAGATGAACAAGACGAAGTTG
AAGCTGAAGGTAATGATGCCGCTCAAGGAATGGATTTTCAGCCAAATGATGGGAGGTGCTG
GAGGTGCTGGAGGTGCTGGAGGCATGGACTTCAGCCAAATGATGGGAGGTGCTGGTGGCG
CTGGTTCTCCAGATATGGCTCAATTGCAGCAATTATTGGCTCAAAGCGGTGGTAATTTGG
ACATGGGAGATTTCAAAGAAAACGATGAAGAAGATGAAGAAGAGGAAATAGAGCCGGAAG
TGAAAGCTTAA

>YKL117W, 216 aa (SEQ ID NO 248)

MSDKVINPQVAWAQRSSTTDPERNYVLITVSIADCDAPELTIKPSYIELKAQSKPHVGD
NVHHYQLHIDLYKEIIPEKTMHKVANGQHYFLKLYKKDLESEYWPRLTKEKVYPYIKTD
FDKWVDEDEQDEVEAEGNDAAQGMDFSQMMGGAGGAGGAGGMDFSQMMGGAGGAGSPDMA
QLQQLLAQSGGNLDMGDFKENDEDEEEIEPEVKA

>YKR075C, 1424 bp, CDS: 501-1424 (SEQ ID NO 257)

TTCAACAGAAATGCCGTAGCCGGAACCAAGCGGGGACAGTGAAGCGTGAGAGGG
GCCGACAGGGGGAACCTGAATGGGGTATTTTGCTTTTGCTGCATTTTTTCCGCTGGTAC
CTCTATCTTTAGGCGACCGGAAAAATTCATTTTCTCATCTTTTTTTTTTTTCGTTCCG
ACTCGATACTCTTTACAAAGAAACCCCGCGGGGAAATGTTAGATTTGAGCTTTTCCGC
CAGGAAAAGAAAAAACCTGGGGACATTAATCTTGTTTTTCTTTCTTTTGTCTTCCC
TTGGATGACTGCAGAAAAAGTACAGTTACCGGGTCTTAGCAAAAAACAAACATATATATAT
ATATATATGAAAGCGTATGGTCAACACGGTTTTATAGGTTTTACTTTTTGCATTTCAGTTC
AACTTTGGCCCTTTCTCTTATCGCATTTCAGATACTACACACAAGTGTTCATACACACACA
AATAGATACATATACAGAAAATGACTAGTTTGGACGATACAATAATTCGTACCAGAATA
TAATGTTACTGGATAACATGACCAACTACAACAAGCCTGCGATTGACTATTTCCATCATG
AATTTAATGATGCAAGCTTGGAAATATCGGCTTCATGGACACTACTATTGAAGATGCGCA
AACATAAACTACTTCGATTACCAAGTTGCTCTTCAGAGGACGTGCTAGATTACAACATGT
ACCTCGTTAGGCTACATCATTGCCTCTGGAGGCGTTGGTCCATAAATCACTATGGTTTAC
AGAACTCCAAATCCAATCCACTGTCCATCAACTGGAACAAAGAAACCGATGTAACGGTGT
TGTACGGTCCAGATTTGACTAACATAGATAGTAATGAAAACGAAATATCGCCGGTCCAGA
ACCAAATTGACCAGAAACAAACAAAAATCTAAAATCTGCTTTAAAGAAAAATACGGAAT
GCTGGGTAAACCGAGGAGGTGGATGAGATTAACGCTTCTATAGAGAGCAATGACAACGCTT
TGGTGAAATTAGAAGACATTTTCATGCCATCGTCTGTTGATTCTCACACGTCTTCCATTT
TCGACCAGCATTCTACATGCACTAAAATTTCTCCATAGATGAAGATTCTGAAGACCTTA
TGAACGAAAAGAAGGAACAATTTCCCGAGGAAGTTGAAGTTTAACCAAGCCGTGATGAAGA
GGGAGATCGACTCAAAGGGGACTATCCGCGAATCCCTCATCAACATAAACGATATCCAAC

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ATTCCCGCCACCATCGCCGTCACCATCGTCGCCATCATCACCATCACCATCAAATAGTT
CTCATTCTGATGAAACAATAAAAGAAGCTCATTATGAGTTCAGCAACTATACATTTGGCA
CTATGGAAGAAGACATTTTTTTATAGGAACCAGGTTGTTTTTTAA

>YKR075C, 307 aa (SEQ ID NO 258)

MTSLDDTIISYQNIMLLDNMTNYNKPAIDYFHFENDASLEISASWTLKKMRKHKLRL
PSCSSEDVLDYNMYLVRLHHCLWRRWSINHYGLQNSKSNPLSINWNKETDVTVLGPDLT
NIDSNENEISPVQNQIDQKQTKNLKSALKKNTECVWTEEVDEINASIESNDNALVKLEDI
SCPSSVDSHTSSIFDQHSTCTKISSIDEDSEDLMNEKKEQFPRKLKFNQAVMKREIDSKG
TIRESLININDIQHSRHHRRHHRRHHHHHHHQNSSHSDETIKEAHYEF SNYTFGTMEEDIF
YRNQVVF

>YLR216C, 1616 bp, CDS: 501-1616 (SEQ ID NO 279)

GAAGAATACAAAGAGGTCCAAGAAGACGAAGACCCGGATGTGTGGGACACGAGAATATCC
AAGACCGGATGCTACGTAGAGAACCTCGCATTACAGCTGTGCCATGCCGAAACAGGTGAC
TGGAGGCAGTGCTTCAACGAGATGGCGTTATTTAGGAAGTGTGGGAAAAGAATGGTAAT
AGAGAGCGCGTAAGCACAGTGGACGTGGATGGGACGACCAGTAAGGATTCGGAAAAGAAG
AAATGAAAATCTAAATGTCGTGATGTATAACTTGTATATAATAGACAGCTGCAGTGATCG
AAACACATTGTTTCCCTTTATAGAACATAACTGTTACGCTTTTGAACGGCATTCTATGA
GCTTCTAGAATATTTTTCCGCCCTAGCTGGAGAAAGTTCAGACAGAAAATTATTTAAATA
AGTCGAATATCAGAGGTGCTGATGCGCTCACATCAGTAACTGGTAAGACAATATT
CAGGCGATCAAGGAGTAAAATGACTAGACCTAAACTTTTTTTGATATTTCTATTGGAG
GTAAACCCCAAGGCCGTATAGTTTTTGAAGTTGTACAATGACATAGTGCCTAAACCGGCTG
AAAATTTTTTGAAGTTGTGTGAAGGAAATGCTGGTATGGCAAAGACTAAACCTGATGTAC
CATTGTGCTACAAAGGTTCCATTTTCCACAGAGTGATCAAAGACTTCATGTGTCAATTTG
GTGATTTTACCAATTTTAATGGTACTGGCGGTGAGAGCATATACGATGAAAAATTCGAGG
ATGAAAATTTCACTGTTAAACATGATAAACCATTCTTCTATCCATGGCCAACGCCGGTC
CAAATACCAATGGATCTCAAGCTTTCATAACCTGTGTTCTACACCTCATTGGACGGGA
AGCAGCTGTGTTTGGTGAAGTGATTCAAGGTAAAAGAATTGTTGTTGATTGAAAACC
ACAATGTGACCAAGAAAACAACAAGCCATTGCGTGATGTAAAGATTGATGACTGTGGCG
TGTTACCTGACGATTATCAAGTGCCAGAGAATGCCGAAGCTACACCAACAGATGAGTACG
GCGATAATTATGAAGATGTTTTAAACAAGACGAAAAAGTTGACTTGAAGAATTTTCGACA
CCGTCTTGAAAGCTATCGAAACGGTAAAGAACATTGGTACTGAACAGTTCAAGAAACAGA
ACTATTCCGTGGCTTTAGAAAAATATGTCAAATGTGATAAATTCTTGAAAGAGTATTTCC
CAGAAGATTTGGAGAAGGAACAAATTGAAAAAATCAATCAATTGAAAGTGTCTATTCCAT
TGAATATTGCCATCTGTGCTCTTAAATTAAAAGATTACAAGCAAGTATTAGTAGCCTCAT
CGGAGGTGTTATATGCCGAAGCGGCTGACGAAAAAGCCAAGGCCAAAGCTTTGTACCGTC
GTGGCCTGGCCTATTACCATGTTAATGACACAGATATGGCTCTCAATGACCTAGAAATGG
CCACTACTTTCCAGCCAAATGACGCTGCCATTTTGAAAGCTATTCATAATACTAAATTAA
AAAGAAAGCAACAAACGAAAAAGCTAAAAAGTCTCTTTTCAAGATGTTCTCCTGA

>YLR216C, 371 aa (SEQ ID NO 280)

MTRPKTFFDISIGGKPQGRIVFELYNDIVPKTAENFLKLCEGNAGMAKTKPDVPLSYKGS
IFHRVIKDFMCQFGDFTNFNGTGGESIYDEKFEDENFTVKHDKPFLLSMANAGPNTNGSQ
AFITCVPTPHLDGKHVVFGEVIQKRIVRLIENQQCDQENNKPLRDVKIDDCGVLPDDYQ
VPENAEATPTDEYGDNYEDVLKQDEKVDLKNFDTVLKAIETVKNIGTEQFKKQNSVALE
KYVKCDKFLKEYFPEDLEKEQIEKINQLKVSIPLNIAICALKLKDYQVLAASSEVLYAE
AADEKAKAKALYRRGLAYYHVNDTDMALNDLEMATTFQPNDAAILKAIHNTKLKRKQONE
KAKKSLSKMFS

>YLR346C, 806 bp, CDS: 501-806 (SEQ ID NO 289)

CTTATCTCAGGGTACCCATAATTTCAACCATCCTTAGCTTCCATTAAAAACACAATGAGT
TGGCTTACTAGCGAAGCGGCTTATCTGTTAATTCTTGCTTGCAAACATCTTAGCTGAAAG
TGAAAAGGCACAGCGCACCTGCTGAATGCTCAACGTTTGTAAATAATCCGCCTATTTCCGC
GGAATCAATAGGGCTCCTAGCAGGCCGCCATCAATTTTCAGCGTGCCGCATTAAATAT
ATTACCAAGATTTCCATTTCCGCGGCTGATTCTTATCAATATTAAGTAATCAATCTTTTC

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CTCGTGATTCTTTGTGATGCTCATTACAGAGGACTAATTAAGACATGTAGCACAAATATA
TTCATATAAAAAGTTGGTGCAGTTAATGATTAATTGCATTGTTTTCTTGTCTTTCTGT
TATACCTGTGCAATTAACATAAAGTGTATATGAATTTAAGGGGCACAAATAACAAAGG
ATTATTTATCACCTTTAATAATGCAATCGATCAGTAATTGTCCCATCGGGTAGTTTCAA
AAAACACAATCAATTCAGCTTCCACTATTGCAGAGTGGGTAGCATGTCCATGGAAATATA
TCAACGTTGTTGGTTCAGGCAGATATGTGAGCAATAAACCTGATAAAATTACCAGATATG
ATTTACTCAAGGCTGCCCAGGAAGCGGAAATGCAGGAGTTGCTTACAAGAAATGATATGA
AAGGTAGACATAAACGTAATAAGAAAAGTAAGATAGCATTTGGAGACTATAGCGGAAGAAA
ACTCTTCAACTGAAAGCCTTTTTTAA

>YLR346C, 101 aa (SEQ ID NO 290)

MQSI SNCP IGLVSKNTINSASTIAEWVACPWKYINVVGSGRYVSNKPKITRYDLLKAAQ
EAE MQEL LTRND MKGRHKRNKKS KIALETIAEENSSTESLF

>YML129C, 713 bp, CDS: 501-713 (SEQ ID NO 297)

TAATCAACTTGGCCAAGCAGAATACGCAATGGTTGTTTCGGCACTGTTAAGGAGCCTGCTT
ACAAGAGGTACCTACATAACGTTAAAACTGGTCGAAAAGCATATTAGGGTTCAACTAAT
GATTGGGGTGTCAACGTAATGTACTTTTTCTCCCAATTTTTCTTTTCATCCGTATATTTT
ACCGTAAAAATGGACAAGCTAATAGCAAAACGAAAAACACGTTGTCACTTCTATATAACT
TTGCTTAAGTAAGTATTTTGTCTTTATAATGTTACATACTGTGAAATACACTCTTTAGAA
AACACTATTTCTCACTCTCGGAAGCAGATTTTCAAGTTCTTCTTACTTCTGAGCTTTG
CTTCTCCTTCTTGGCATTAAATGTTACCCGGTATACGAAATCGGAGAGGATCAGAATAAA
TGCATTGAAAGGAGCATAAATCTATACAGCGGTTTGGCAATGGTGAGAGGAAGAGAACAA
AAAATAGAACGCAGATAGTCATGTCCAAATACGCTTGGTATACCAGAGTTACAGATACAT
TACATCGTCTAACGGTACTGACGTTGGTTGGTGGTACGTTATACATGTCCGGTGGCTTAG
CTTACACTTTTATACATGAACGGTAAGAAGTACGAACAACAAGTGACCCAACAAAAGGCAC
TTGAAGAAGACAATCAACAACCTGCAAAAGTCCTACTGCACCTCCTACCGAGTAA

>YML129C, 70 aa (SEQ ID NO 298)

MSKYAWYTRVTDTLHRLTVLTLVGGTLYMSGGLAYTLYMNGKKYEQQVTQOKALEEDNQ
LQSPTAPPTE

>YML132W, 1640 bp, CDS: 501-1640 (SEQ ID NO 299)

GTAACCTTGGTTCTATGAATCTTCATGTCAGATACGTAGGACAGACTCTTTCTGTGTAAA
TATTTGTGACAGCTACGTCTATTTTCTACTAGATGTTTACACAGTTTTGTACAGGAAAT
CTACGCTTAAAAATATGTATTTTCAATCAAGCGGTAACCGCTGTACGAGCAGTGACATTGCT
GGTCGCACCCATAATGTGAACCAACGTTACGGCACACCGTGATGTACCCGCATTAAAGTT
TTGTAAATTTCGTTATTACGATTATCGAGTTGGCTAGATAGAAAACCGGAAATGTAATGGA
TGCCCTTTTTCGAATAGCTGAGTTTCTTTGCCTAAAATAGCCCAATATTGTTGCCCTTTT
CTATCACGAGGTTACTGAGCCATTGCATGAACGCGCGCGCTCGGCGGCTTTTTTTTTCT
GCTGTGCTGTATAAAAGCGAAAAGCCAGAAGTTACTATCTCGAATAAAAAACCCCTCGAA
CTGCCATCTCACTACCGAAAATGAAAGAGAATGAACTTAAAAATGAGAAGAGTGTAGATG
TATTATCCTTCAAAACAGCTCGAATCCCAAAAGATTGTTCTACCTCAAGATCTTTTCAGAA
GCAGCTTTACCTGGTTTTGTTATGAAATTTACAAGTCCTTAGCGTTTCGCATCTGGATGC
TATTATGGCTACCACTTAGCGTCTGGTGGAACTTTCCAACAATTGTATTTACCCACTTA
TAGTTTCACTTCTGGTCTTGTCTGGGACCAATATTTGTCTTGTATTTGTGGACTTT
CTCGTAAGCGTTCTTATCGAAACAACCTCATTCAGTTTTGCAAAGAGATTACTGAAAACA
CACCAAGTTCTGATCCTCATGATTGGGAAGTTGTTGCAGCAAATCTAAATTCGTACTTAT
ATGAAATAACGTTTGGAACTACTAAGTACTTTTTTTCAATGCCATGGTCTGTCAAGAAG
CGTTCAGAACAACCCCTTCTCGAACCATTCTTTTGAAAAAAGATAAAGCTGCCAAGGTTA
AGTCATTTAAGGATTCCGTCCCTTACATTGAAGAAGCATTGGGAGTTTATTTTACAGAAG
TTGAAAAACAATGGAAATTTGTTTAATACTGAAAAATCATGGAGCCCTGTTGGCCTGGAAG
ATGCTAAACTTCCCAAGGAAGCTTACCGATTTAAGCTTACTTGGTTTTTAAAGAGGATTT
CCAATATTTTTATGTTGATACCATTCCCTTAATTTTTTGTGCTGCATATATGTGTCACGGG
GAATGTGCCTTCTATTACGCACCTTGTATCTCGGGTGGATTCTTTTCATGTTGGTACAAG
GTTTCCAAAATATAAGGGTTTTGATTATGAGCATGGAACACAAGATGCAGTCTTGTCTGA

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CTATTATAAATGAGCAAGAAAGTGGTGCGAATGGATGGGACGAAATTGCAAGGAAAATGA
ATAGGTACTTGTGAGAAAAAGCCTGGAAGAATGAAGAGTTTTCTTCGACGGGATTG
ACTGTGAATGGTTTTTAACCACCTCTTCTACCGCGTCTATCTGCGAAGAAATCTATGT
GGCCTTTACCATTGAATGTGGAACATATGGCCATACATTAAAGAAGCGCAATTATCCCGCA
GTGAGGTGCTCTTAGTGTAG

>YML132W, 379 aa (SEQ ID NO 300)

MKENELKNEKSVDVLSFKQLESQKIVLPQDLFRSSFTWFCYEIYKSLAFRIWMLLWLPLS
VWVKLSNNCIYPLIVSLLVFLGPIFVLVICGLSRKRSLSKQLIQFCKEITENTPSSDPH
DWEVVAANLNSYLYENNWNKYFFFNAMVCQEAFTTLLEPFSKKDKAAKVKSFKDSV
PYIEEALGVYFTEVEKQWKLFNTEKSWSPVGLEDAPLKEAYRFKLTWFLKRISNIFMLI
PFLNFLCCIYVSRGMCLLLRTLGLWILFMLVQGFQNIIRVLIMSMHEKMQFLSTIINEQE
SGANGWDEIARKMNRYLEKKAWKNEEFFFDGIDCEWFFNHFFYRVLSAKKSMMWPLPLNV
ELWPYIKEAQLSRSEVLLV

>YMR009W, 1040 bp, CDS: 501-1040 (SEQ ID NO 301)

ACCGGTATTTTCATCTCTTCTAGATCAAGACTAACTGCTCGTTCAGTACAAGTATTTTAC
GATAGTCCATATTACTCTTCAATTAATATTTTTTTTTTATATCTGGCCCGTTTTTGACA
CAATTTTTTCTCTCTTTTTCTCCCTATAAACTATGCAGAAGTAGCGATAATCACGATC
TTGTTAATGATTCACATGTGCGCAAGTCGTATTGTCTGTCTAGATAGTGAGATGCCCTTCT
AAATAACAGGAGAGAGGCAAGATAGCATAACGGCGCAATGAAGGTAATTTCTGCCAGTTT
TCTTTGCATTGACGACTGAAAGGGCCCTTGTAAGAGCCGCTCGACAGGGCGACGCCACAG
TAGAGTCGCTAACACCGAAATATGCATATTGAAAAACATCAAAGTATAAAAGAACAAAGA
GGGTGGCATCTGCAGATCAAAAAACAATAACCACCAAACAAGACACTAAAAAAGGTCTG
TAAAAAGGTCAAAAGTTAGAATGGTTAAGGTATATATTCATGACAACAAGTTGACTCCG
ATTATCGCGCACCCCACAATTCTGGAACAGAACTTTCCCTGGATGAATTAGCCAAGTTAG
GAGTGATTTATAAATACTGTGCAAATGAGGAAGAAGTGAATGAAATTGCTAGGCAAAGAG
AATATAAAATAGAGATGTGGTCAACATCTGCGAAGGTTCTTTCAAAAGTGAAGCAGAGT
TTAATGAAAACTAGCAACATTTTACCAAGAGCATTTACATGAAGACGAAGAAATAAGAT
ACTGTCCTCGAGGGTGTCTGGATACTTTGACGTCAGGGATGCTTCCACACCAGAGAATGGA
TTAGAGTGTGTTGGTAGAGTCAGGTGATTTACTGATTCTTCCACCAGGCATCTATCATCGT
TCACCTTCGCAACTAGCAACCACATCAAGGCCTTGAGACTGTTTAAGGACGAGCCCAAT
GGCAAGCTATCAACAGGTCAAATCAGGCTGATTCAATGCCTGTACGCAAGGACTACATTG
CCCTGATCAATCAGTACTAA

>YMR009W, 179 aa (SEQ ID NO 302)

MVKVYIHDNKVSDYRAPHNSGTELSLDELAKLGVYIKYCANEEVNEIARQREYKNRDV
VNICEGSFKSEAEFNEKLATFYQEHLEDEEIRYCLEGAGYFDVRDASTPENWIRCLVES
GDLLILPPGIYHRFTLTTSNHIKALRLFKDEPKWQAINRSNQADSLPVRKDYIALINQY

>YMR011W, 2126 bp, CDS: 501-2126 (SEQ ID NO 303)

GCAGCTTCACTTTTAAAGTTTCTTTTTCTCCTCACGGCGCAACCGCTAACTTAAGCTAATC
CTTATGAATCCGGAGAAAAGCGGGTCTTTTAACTCAATAAAATTTTCCGAAATCCTTTT
TCCTACGCGTTTTCTTCGGGAAGTAGATAGGTGGCTCTTCCACCTGTTTTTCCATCATTT
TAGTTTTTTCGAAGCCATGCGTGCCTTTTCGTTTTTTCGATGGCGAAGCAGGGCTGGAAA
AATTAACGGTACGCCGCCTAACGATAGTAATAGGCCACGCAACTGGCGTGGACGACAACA
ATAAGTCGCCCATTTTTTATGTTTTCAAACCTAGCAACCCCCACCAAACCTGTCTATCGT
TCCCGGATTCACAAATGATATAAAAAGCGATTACAATTCTACATTCTAACCAAGATTGAG
ATTTCTCTTTCTCAATCTCTTATATTAGATTATAAGAACAACAAATTAAATTACAAA
AAGACTTATAAAGCAACATAATGTCTGAATTCGCTACTAGCCGCGTTGAAAGTGGCTCTC
AACAACTTCTATCCACTCTACTCCGATAGTGAGAAATAGAGACGGATGAATCTCCTA
TTCAAACCAAATCTGAATACACTAACGCTGAATCCCAGCAAAGCCAATCGCCGCATATT
GGACTGTTATCTGTTTATGTCTAATGATTGCATTTGGTGGGTTTGTCTTTGGTTGGGATA
CTGGTACCATCTCTGGTTTTGTTAATCAAACCGATTTCAAAGAAGATTTGGTCAAATGA
AATCTGATGGTACCTATTATCTTTCGGACGTCGGACTGGTTTGATCGTTGGTATCTTCA
ATATTGGTTGTGCCTTTGGTGGGTTAACCTTAGGACGCTCTGGGTGATATGTATGGACGTA

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GAATTGGTTTGATGTGCGTCGTTCTGGTATACATCGTTGGTATTGTGATTCAAATTGCTT
CTAGTGACAAATGGTACCAATATTTTCATTGGTAGAATTATCTCTGGTATGGGTGTCGGTG
GTATTGCTGTCTATCTCCAACCTTTGATTTCCGAAACAGCACCAAACACATTAGAGGTA
CCTGTGTTTCTTTCTATCAGTTAATGATCACTCTAGGTATTTTCTTAGGTTACTGTACCA
ACTATGGTACTAAAGACTACTCCAATTCAGTTCAATGGAGAGTGCCTTTGGGTTTGAAC
TTGCCTTCGCTATTTTCATGATCGCTGGTATGCTAATGGTTCCAGAATCTCCAAGATTCT
TAGTCGAAAAAGGCAGATACGAAGACGCTAAACGTTCTTTGGCAAAATCTAACAAAGTCA
CCATTGAAGATCCAAGTATTGTTGCTGAAATGGATACAATTATGGCCAACGTTGAAACTG
AAAGATTAGCCGGTAACGCTTCTTGGGGTGAGTTATTCTCCAACAAAGGTGCTATTTTAC
CTCGTGTGATTATGGGTATTATGATTCAATCCTTACAACAATTAAGTGGTAACAATTACT
TCTTCTATTATGGTACTACTATTTTCAACGCCGTCGGTATGAAAGATTCTTTCCAACTT
CCATCGTTTTAGGTATAGTCAACTTCGCATCCACTTTCGTGGCCTTATACACTGTTGATA
AATTTGGTCGTGTAAGTGTCTATTGGGTGGTTCTGCTTCCATGGCCATTTGTTTTGTTA
TCTTCTCTACTGTGCGTGTCAAGCTTATATCCAAATGGTAAAGATCAACCATTCTCCA
AGGCTGCCGGTAACGTCATGATTGCTTTTACCTGTTTATTCAATTTCTTCTTCGCTATTA
GTTGGGCCCCAATTGCCTACGTTATTGTTGCCGAATCCTATCCTTTGCGTGTCAAAAATC
GTGCTATGGCTATTGCTGTTGGTGCCAACTGGATTGTTGGGGTTTCTTGATTGGTTTCTTCA
CTCCCTTCATTACAAGTGCAATTGGATTTTCATACGGGTATGTCTTCATGGGCTGTTTGG
TATTTTCAATCTTCTACGTGTTTTTCTTTGTCTGTGAAACCAAGGGCTTAACATTAGAGG
AAGTTAATGAAATGTATGTTGAAGGTGTCAAACCATGGAAATCTGGTAGCTGGATCTCAA
AAGAAAAAAGAGTTTCCGAGGAATAA

>YMR011W, 541 aa (SEQ ID NO 304)

MSEFATSRVESGSQQTSTHSTPIVQKLETDESPIQTKSEYTNELPAKPIAAYWTVICLC
LMIAFGGFVFGWDTGTISGFVNQTDKRRFGQMKSDGTYLSDVRTGLIVGIFNIGCAFG
GLTLGRLGDMYGRRIGLMVCVVLVYIVGIVIQIASSDKWYQYFIGRIISGMVGGIAVLSP
TLISETAPKHIRGTCVSFYQLMITLGIPLGYCTNYGTDYSNSVQWRVPLGLNFAFAIFM
IAGMLMPESPRLVEKGRYEDAKRSLAKSNKVTIEDPSIVAEMDTIMANVETERLAGNA
SWGELFSNKGAILPRVIMGIMIQSLQQLTGNNYFFYYGTTIFNAVGMKDSFQTSIVLGIV
NVFTCLFIFFFAISWAPIAYVIVAESYPLRVKNRAMAIAVGANWIWGLIGFFTFFITSA
IGFSYGYVFMGCLVFSFFYVFFVCETKGLTLEEVNEMYVEGVKPKWSGWSISKEKRVSE
E

>YMR099C, 1394 bp, CDS: 501-1394 (SEQ ID NO 307)

AACAGTTCACCTCGATCTACATATATTTCAATGCGAGAATGATTAATTCTTGCCATTGAC
AAACAACCCTTTTACTGCCAGCGCCTTTTATAACCATGTAGTTTTATATGCCTAATTATA
ATAAAGCATGACATATAATGCCAACCCCATATTTATATAGTTAACTTGAAACCGAGATTC
ATCTATTGCACCAGGAAAAGTGCCTTCTTCTTAAACATAAGTTACGTCCCGACCATTC
TCTAAACGGCATCAATCATTGCAGCAGAAGAAATAGTGTGTAGATGTCCTCGTTTCGCTAG
ACGCAGTCAATGATAACAAGGTCTTTCTTCAAGCTGTCTTTCCATAAAAAGGTATCGCAA
ATGGGGTACCAATGCGCCTTTTATTTTTTACGCCGAAAGAAAACCTTAGTAGGTCCCTAG
AAATGAATAAAGAGGTGATTCTGAGGTTTATTATAAGCCTTTGGTAAAACCTTGAACCAAG
AAAGATTAAAACACAAAGCCATGCCTATCAAAGAACTGATAAAGAAGTTGTTTTGACTC
ATCCAGCTGATGAGACCACGAGCTTCATATTCTAAAGTACGGTGCTACAGTTTATTCTT
GGAAATTGAAATCTGAAGAACAGTTGTGGTTGTCTACTGCTGCTAAATTGGATGGTAGCA
AACCTGTGAGAGGTGGTATACCTTTGGTCTTTTCTGTATTTCGGGAAAAATAGCACCGGATG
AACATTTGAGTAAATTACCTCAACATGGTCTTGCAAGAAATCTACTTGGGAGTTTTTGG
GTCAAACCTAAGGAAAACCCACCGACCGTACAATTTGGCTTGAAACCAGAAATTGCTAAC
CAGAATTGACCAAAATTGTGGCCAATGGATTATCTTTTGATTTTACTGTTGAATTAGGCT
CCGATTATTTGAAAACCTGCCATAGAAGTAGAAAACACATCTAGTTCCAAGGAATTAAAGT
TCAACTGGTTGTTCCATACATACTTCCGTATCGAAGATATTGAAGGAACAATGGTCTCTA
ATTTAGCTGGCATGAACTTTATGACCAACTGTTGAAGGAATCCTACGTCGACAAGCACC
CAGTCGTTACCTTCAATCAAGAAACCGATGTAATTTATCAGAATGTCAGCGCCGAACGGG
CCATTCAAATAGTTGACAAGGGCGTTCAAATTCACACTCTAAAAAGATACAACCTGCCCCG
ACACTGTTGTTTGAATCCATGGATTGAGAAGTCTCAAGGGATGGCCGATTTTGAACCAA

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AAACTGGTTACCAACAAATGATATGTATTGAACCTGGTCATGTTTCATGATTTTATTTTCCT
TGGCTCCTGGTAAAAAATGGAATGCTTATCAATTACTTTGCAAAGAAGAATTGAAATATC
AAGCTATTCAATAA

>YMR099C, 297 aa (SEQ ID NO 308)

MPIKETDKEVVLTHPADETTSVHILKYGATVYSWKLKSEQLWLSTA AKLDGSKPVRGGI
PLVFPVFGKNSTDEHLSKLPQHGLARNSTWEFLGQTKENPPTVQFGLKPEIANPELTKLW
PMDYLLILTVELGSDYLKTAIEVENTSSSKELKFNWLFHTYFRIEDIEGTMVSNLAGMKL
YDQLLKESYVDKHPVVTFNQETDVIYQNVSAERA IQIVDKGVQIHTLKRYNLPD TVVWNF
WIEKSQGMADFEPKTYQQMICIEPGHVHDFISLAPGKKWNAYQLLCKEELKYQAIQ

>YMR110C, 2099 bp, CDS: 501-2099 (SEQ ID NO 311)

AAGAGAGAGAAGCTAGATTATCATTACAGCAGCCACATAGTATACCAAATTCCAGTACAG
GCACACCAGAACATGATCAAGACACTTAGAGGAAATGGAACAACGAATTTCCAGCCAAAA
ATTCCGAGTAGTTTCATGATGAAAGATTTTACATGCATTTTATATATAAATATATACCGT
CCTATATGGATTTTCATGCCAACAGGGTATATAATAGACAATTACCGGTGTACTGATATAT
CAACTATCGACTCCAAGCCTTTTATCTATCAGTCAATTTTACATCAAGATCCCACTTTTA
GATAGGTTTCGAAAATTCAATCTAATATTAGTGATTTAATTAGATGGTGGATTGCTTACCC
TTTTTTTTTGTCGTTTTAGGAGGAGATTCTTCGGATTTTAGGGATAAACGGATACTCCATA
TATAAAAAACAAAACCTTCAGGCATATTGATTATCTAAAAGGAATATTCTAAAACCATAGC
CATAGTAATTTTATCACCACATGTCAAACGACGGCTCAAAAATATTGAATTATACCCCAG
TGTCTAAAATAGATGAAATAGTTGAAATCTCAAGAAATTTCTTCTTTGAGAAACAATTGA
AATTGTCCACGAAAATAACCCAAGGAAAAAGATCTAGAATTTCAGGCAGTTGCAGTTGA
AAAAACTCTATTATGCCGTCAAAGATCATGAGGAAGAAGCTGATCGATGCTATGTACAAGG
ACTTTCATCGGAACAAAATTGAATCGGTTCTGAATGAAACGACCAAACCTTATGAACGATA
TACTTCACCTAATTGAGATTTTACCAAATTTGATCAAACCTCGGAGAGTATCTGATTCTT
CTCCTCCATTTATGTTTGGTAAAACAATCGTGGAGAAAATATCAAGGGGCAGTGTCTTGA
TTATTGCTCCTTTCAATTTTCCCCTACTTTTAGCATTTGCCCATTTGGCAGCAGCTCTTG
CTGCAGGTAACACCATTGTTCTGAAGCCAAGTGAACCTAACACCACACACTGCTGTAGTTA
TGGAAAATTTGTTAACCACAGCTGGTTTCCCTGATGGATTGATTCAAGTAGTTTCAGGGAG
CTATAGATGAAACTACAAGACTACTAGATTGTGAGAAAATTTGACCTAATATTCTACACAG
GTTCTCCCCGTGTGCGATCAATAGTTGCTGAGAAAGCAGCAAAAAGTCTAACACCTTGTG
TACTTGAACCTGGTGGTAAATCACCTACCTTTATTACAGAAAATTTCAAAGCAAGTAACA
TAAAAATTGCTTTGAAAAGGATTTTTTTTTTGGTGCTTTTCGGAAATTTCTGGCCAGATTGTG
TTTACCAGATTATTTGTTAGTACATAAATCTATCTATCCAAAAGTCATTAAAGAGTGTG
AATCAGTACTAAATGAATTTTATCCAAGCTTTGATGAACAAACAGATTTCACTCGTATGA
TTCATGAGCCTGCTTACAAAAGGCCGTTGCAAGTATAAACTCAACTAACGGCTCCAAGA
TTGTGCCTTCAAAAATTTCTATCAATTTCAGATACTGAGGATCTATGCCTTGTACCACCAA
CCATAGTTTATAACATTGGTTGGGATGATCCTTTGATGAAACAGGAAAACCTTTGCTCCTG
TATTGCCCATCATTTGAGTACGAGGATCTTGATGAGACCATTAAACAAGATAATAGAAGAAC
ATGACACTCCATTGGTGCAATACATATTCTCTGATAGCCAAACTGAAATAAATCGTATCT
TGACGCGCTTAAGATCTGGTGACTGTGTTGTGCGGTGATACAGTGATTCATGTAGGAATTA
CCGACGCTCCATTTGGAGGGATCGGTACTTCAGGTTATGGTAACTATGGTGGATATTATG
GATTC AATACCTTTAGTCATGAAAGAACAATTTTTAAACAACCATATTGGAATGATTTTA
CCCTTTTTATGAGATACCCTCCAAATAGCGCACAAAAGGAAAAGCTCGTCCGTTTTGCGA
TGGAAAGAAAACCTTGGTTTGACAGAAATGGCAATAACAAGTGGGGGTACGCCAATATT
TTTCATTATCTGCCGCCGTTATTTTAATTAGTACCATTTACGCTCATTGTTCTTCTCTGA

>YMR110C, 532 aa (SEQ ID NO 312)

MSNDGSKILNYTPVSKIDEIVEISRNF FFEKQLKLSHENNPRKKDLEFRQLQLKKLYYAV
KDHEELIDAMYKDFHRNKIESVLNETTKLMNDILHLIEILPKLIKPRRVS DSSPPFMFG
KTIVEKISRGSVLIIPFNFP LLLAFAPLAAALAAGNTIVLKPSELTPHTAVVMENLLTT

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AGFPDGLIQVVQGAIDETTRLLDCGKFDLIFYTGS PRVGSIVA EKAASLT PCVLELGGK
SPTFITENFKASNIKIALKRIFFGAFNGSQICVSPDYLLVHKSIYPKVIKESV LNEF
YPSFDEQTDFTMRIHEPAYKKAVASINSTNGSKIVPSKISINSDTEDLCLVPPTIVYNIG
WDDPLMKQENFAPVLP IIEYEDLDETINK IIEHDTPLVQYIFSDSQTEINRILTRLRSG
DCVVGDTV I HVGITDAPFGGIGTSGYGNYG GYG FNTFSHER TIFKQPYW NDFTLFM RYP
PNSAQKEKLVR FAMERK PWFDRNGNNKWGLRQYFSLSAVILIST IYAHCSS

>YMR173W-A, 1685 bp, CDS: 501-1685 (SEQ ID NO 691)

AAAAAACCACTCCGAAGGTTCTGAGGATGACAAATCGCCCCCTTAGCTGTGGCCATACAAGC
TTGGCACCCGACGAAAAAGGGAAAAAGGAAAAAGAATGTCGTACAAGAACTCTTACAACCAC
GTTGAGATTTTCATTTAACAACGCCCCCTTTCCATTATATAAGAAGGCATTAATTTTTAT
GTAATAAAAAAGAATTTCTCGAAAATGTCTTACAATTAATTTTTCTTTTGTAGAGTAG
GGCTTTAATAGACTGATATATACGGTATTATAAGTGAACGAAAAAACAGCAATGGGTTT
ATTTGATAAAGTGAAGCAATTTGCTAACAGCAATAATAACAACAATGATTCTGGCAATAA
CAATCAAGGCGATTATGTTACCAAAGCTGAGAATATGATCGGCGAAGATAGAGTCAATCA
ATTCAAAAGCAAAATCGGAGAGGACAGATTTGATAAGATGGAGTCCAAGGTTTCGTCAACA
ATTTTCTAATACCTCTATAAATGACAACGACTCCAACAACAACGACTCATATGGTCTTAA
TAACAACGATTTCATATGGTCTTAACAACAATGATTTCATATGGCTCTAACAACAATGATT
ATATGGCTCCAACAACAATGATTTCATATGGCTCTAACAACGATGATTCTACGGTCTTTC
CAACAAGAAGAAGAGCTCTTATGGTCTTAACAATGACGATTTCGTACGGCTCCAGCAACAA
CAATGACTCTTACGGTTCACAACAATGACTCTTACGGTTCACAACAATGACTCTTA
CGGTTCCAACAATGACGACTCTTACGGTTCGTCAAACAAGAATAAGAGCTCTTACGGTTC
CAACAATGACGATTCTTATGGCTCTAACAATGATGATTTCATATGGTCTTCCAACAAGAA
GAAGAGTTCTTATGGTTCAGCAACAACGATTCGTATGGTCTTAACAACGATGATTTCATA
TGGTCTTAACAACAATGATTTCATATGGCTCTAACAACGATGATTCTACGGTCTTCCA
CAAGAAGAAGAGCTCTTATGGTCTTAACAATGACGATTTCGTACGGCTCCAGCAACAACAA
TGACTCTTACGGTTCACAACAATGACGACTCTTACGGTTCGTCAAACAAGAATAAGAGCTC
TTACGGTCTTCTTAGCAACGATGATTCTTACGGATCTTCCAATAACGACGACTCTTACGG
TTCTTCCAACAAGAAGAAGAGTTCTTATGGTTCACAACAATGACGATTCTTATGGCTCTAA
CAATGATGATTTCATATGGTCTTCCAACAAGAAGAAGAGTTCTTATGGTTCAGCAACAA
CGATTCTGATGGTCTTAACAACGATGATTCTACGGTCTTCTTAACAAAAGAAGAGTTC
TTATGGTTCACAACAACGATGATTTCATACGGCTCCAGCAACAACAATGACTCTTACGGTTC
CAACAATGACGACTCTTACGGTTCCTCTAATAGAAACAAGAAGCTCTATGGGCTCTTCCA
CTACGGTTCATCCAACAATGATGACTCTTATGGTTCATCTAATAGAGGCGGTTCGTAATCA
ATACGGTGGTGACGACGATTACTAAGTTTTTGGATGTCTTCGATAAAAAAATATATTAT
TGTGTTTAGACTTAAGTATGAAAATTTTATGTATGAGCTGTGGCTATGTATCCGCTGGCA
AATAG

>YMR173W-A, 394 aa (SEQ ID NO 692)

MTTTPTTTTTHMVLITTIHMLVLTMIHMLTMIHMAPTTMIHMLTMIPTVLPTRRRAL
MVLMTIRTAPATTMTLTVPTMTLTVPTMTLTVPTMTLTVRQTRIRALTVPMTILM
ALTMIMHMLVPTRRRVLMVPATTIRMVLTMIHMLVLTMIHMLTMIPTVLPTRRRALM
VLTMTIRTAPATTMTLTVPTMTLTVRQTRIRALTVLLATMILTDLPITTTTLTVLPTRRR
VLMVPTMTILMALTMIMHMLVPTRRRVLMVPATTIRMVLTMIPTVLLTKRRVLMVPTTM
IHTAPATTMTLTVPTMTLTVPLIETRTPMGLPTTVHPTMTMLMVHLIEAVVINTVVTTI
TKFLDVFDDKKNILLCLDLSMKILCMSCGYVSAGK

>YNL031C, 911 bp, CDS: 501-911 (SEQ ID NO 325)

CAACAGCCCGAGCGAGTGAACAACATATTAAATTAAACGCCTTCTTGTCAGTTGTTTT
GTTCTGGTCTGGTCTGCATTTTCGCGCCCGAAAAAGCTTGAGACGCGAAGCTCCCAGAACG
TCCTGCCATACAAATGCGAAACTCTCGGTCTAGTACCACTTTCCCGGTGCCAAACGACCA
CAGTTGTCCGTTCCGAGCACTTCGCATTAAGCGCGTGAAACTATTGGCAGGCCCTAAGGG
GCTCCTACGGATGGGAGTTGGTCATTTAGCGTTCATTATCGCCCAATGTGACGCACAATC
ACGGCTATGGCTCGGTGTCAAACATAGTTTGCCTGATAACAGCGTGTGTGCTCTCTCG
CGTTGCTTCTTGTGACCGCAGTTGTATATAAATAATCTTTTCTTGTCTTTTATATAGG
ACCACTGTTTTGTGACTTCCACTTTGGCCCTTCCAACGTCTTCCCCTTTTACTAAAGG

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ATCCAAGCAAACACTCCACAATGGCCAGAACTAAACAAACAGCTAGAAAATCCACTGGTG
GTAAAGCCCCAAGAAAACAATTAGCCTCCAAGGCTGCCAGAAAATCCGCCCCATCTACCG
GTGGTGTTAAGAAGCCTCACAGATATAAGCCAGGTACTGTTGCCTTGAGAGAAATTAGAA
GATTCCAAAAATCTACTGAACTGTTGATCAGAAAGTTACCTTTCCAAAGATTGGTCAGAG
AAATCGCTCAAGATTTCAAGACCGACTTGAGATTTCAATCTTCTGCTATCGGTGCTTTGC
AAGAATCCGTCGAAGCATACTTAGTCTCTTTGTTTGAAGACACTAATCTGGCTGCTATTC
ACGCTAAGCGTGTTACTATCCAAAAGAAGGATATCAAATTGGCCAGAAGACTAAGAGGTG
AAAGATCATGA

>YNL031C, 136 aa (SEQ ID NO 326)

MARTKQTARKSTGGKAPRKQLASKAARKSAPSTGGVKKPHRYKPGTVALREIRRFQKSTE
LLIRKLPFQRLVREIAQDFKTDLRFQSSAIGALQESVEAYLVSLFEDTNLAAIHAKRVTI
QKKDIKLARRLRGERS

>YNL134C, 1631 bp, CDS: 501-1631 (SEQ ID NO 331)

AAACTCGGAAACTCTTTTTCTATTTCATCTTCCCTTCTCGTACGTGCCCCACGGAAGCAATA
AAAAGAACCGAAATAACCAACACCCGTAACGTCAAAGCATTTCATGCTTAGAATGGAAACC
ATTTCTGTGAATGAAATGGCAAATTGATCAGATTGATTGCTCGTTCCACTACCTGTGTCC
GCAATTTTTTAATGGTCATCACAGCCCCTGCTGACTAAAGTTCCTCGGATCCGCTTACGG
TTGTGCGCGGTTCCGCCCCCTGCGTACTCTTAGTACCTAGCATATGGGCTCCCTCCGTTG
GATTGGCATCGATTAGTAAGGACAGATGTTAAGGATTTAAGACCGTTTTTAAGGTATTTTC
GGCAATGCTTCGATTTAAAGGAGAGAGTTTTTTTTTTGCCGTTTTCTTCTCTCACTTC
TTGATTAGTACTGTAATTCAGTTGAAAAAAATCGTTAACTATACACAGCAAAAAGCAA
TATCATACTGCATATCAAGCATGTCCGCCTCGATTCCAGAAACCATGAAAGCCGTTGTCA
TTGAAAATGGCAAGGCTGTAGTCAAACAGGACATTCCAATTCCCTGAATTAGAAGAAGGAT
TTGTTCTAATTAAGACTGTCGCCGTTGCCGTAACCCCTACCGATTGGAAACATATTGATT
TCAAGATTGGTCCCTCAAGGTGCCCTCTTAGGCTGTGATGCAGCCGGCCAAATCGTAAAGT
TGGGCCCCAATGTTGATGCTGCACGCTTTGCCATTGGTGATTACATTTATGGGGTTATTC
ACGGTGCTTCAGTGAGGTTCCCTCAAACCGGTGCCTTTGCTGAGTACTCTGCCATTTTCAT
CCGAGACTGCTTATAAACCAGCCAGAGAGTTTAGATTGTGCGGTAAAGACAAGCTACCAG
AAGGCCCGTAAATCTTTAGAAGGGGCAGTATCCCTCCCAGTCTCATTGACCACGGCTG
GTATGATCCTTACACATAGTTTTGGCTTGGACATGACATGGAAGCCCTCCAAAGCGCAA
GAGATCAACCCATCTTATTTTGGGGTGGTGCCACTGCTGTTGGCCAGATGCTTATTCAAT
TGGCAAAAAAACTAAACGGTTTCAGCAAGATCATCGTCGTTGCTTCTCGTAAACATGAAA
AATTGTTGAAAGAGTACGGTGCAGATGAACTTTTTGAATACCACGATGCTGACGTTATCG
AACAGATAAAAAAGAAGTACAACAACATTCTTACTTGGTGGACTGTGTCTCCAACACAG
AACTATTCAACAGGTGTACAAATGTGCCGCTGATGACTTAGACGCTACGGTCGTTCAAT
TGACCGTTTTTAACCGAAAAAGATATCAAGGAGGAAGACAGGAGGCAAAACGTCAATTTG
AAGGAACCCCTTCTATATTTGATAGGAGGTAACGACGTCCCATTTGGCACGTTTACTTTGC
CAGCAGACCCTGAATACAAGGAAGCCGCCATAAAATTTATTAAGTTCATCAATCCAAAA
TCAATGATGGTGAAATCCACCACATCCCAGTGAAAGTTTACAAGAACGGGTTAGATGATA
TCCCACAGTTACTTGATGATATTAAGCACGGGAGGAATTCTGGCGAAAAGTTGGTTGCCG
TCTTGAAATAA

>YNL134C, 376 aa (SEQ ID NO 332)

MSASIPETMKAVVIENGKAVVKQDIPIPELEEGFVLIKTAVAGNPTDWKHIDFKIGPQG
ALLGCDAAAGQIVKLGPVDAARFAIGDYIYGVHIGASVRFPSNGAFAEYSAISSETAYKP
AREFRLCGKDKLPEGPVKSLEGAVSLPVSLTTAGMILTHSFGLDMTWKPSKAQRDQPILF
WGGATAVGQMLIQLAKKLNGFSKIIVVASRKHEKLLKEYGADELFDYHDADVIEQIKKKY
NNIPYLVDCVSNTEIQQVYKCAADDLDATVVQLTVLTEKDIKEEDRRQNVSIEGTLLYL
IGGNDVPFGTFTLPADPEYKEAAIKFIKFINPKINDGEIHHPVKVYKNGLDDIPQLLDD
IKHGRNSGEKLVAVLK

>YNR002C, 1349 bp, CDS: 501-1349 (SEQ ID NO 339)

ATGGACAATTTGAAGTTCTTGACTACCCCTATCTCACACTAGTACGTAATTCAATGTATC
ATTCGTATTGTAAGTAGATAGAGACGCAATACAGGAAAGCTGACCTTCCTTCCAATCACC

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ACGGCTGAAATGCTTTGTTGACCAATTACGGACGCTTAAGAGCGGACGCGGCTGGAACGG
CTCCATCCTAAATCGGCGGAGGGAGAAGTCCGATACCAGCCGACATGGCAATAATAGTGA
CAGTAGATGCTACCAGCCCCGCAATAATTTACAGTAGATCATCAACAGTCTCCTCATTTT
CTGGAAATGATCAGCAACTTCGACGGATTTAACTCTCAAGCAGTTACGCACCTCCGAGAAC
AGCCGTGATCATCTTTGAACAAGCAAAATATATAAAGCAGGAGAACTGTCTTACCTAGAG
CTAGAATAGCCATAACTAACTATGTAACATTCTACAGATCAATCAAAAACAATCTTCAAT
CACAGAAAAAATAAAAAGGCATGTCTGACAGAGAACAAAGCAGCGGCAACACCGCTTTTG
AGAACCCTAAGGCACTCGATTCTTCCGAGGGTGAGTTCATCTCTGAAAACAACGATCAGA
GCCGCCACTCGCAAGAGTCCATATGCAAAATATATACTGCGGGCAAAAACAACGAGTATA
TTTACATCGGCCGTCAAAAATTTTTAAGGGATGATTTGTTCGAGGCATTCCGGTGGTACTC
TGAATCCCGGTTTAGCCCCCGGCCAGTCCATAAATTCGCAAATCCTGCTCCACTAGGAC
TTTCCGGTTTTGCCCCTCACTACGTTTGTCTTATCCATGTTCAATGCAAGAGCCCAAGGCA
TCACTATCCCTAATGTTGTTGTTGGGTGTGCCATGTTTTACGGTGGCCTCGTTCAACTCA
TTGTGTTGTTGGGAAATCGCTTTAGAGAACACTTTCCGGTGGTACAGCCCTGTGTTCCT
TCGGCGGTTTTTGGTTAAGCTTCGGTGCTATATACATCCCTTGGTTTGGAAATCTGATG
CCTATAAGGACAAGGAATCCGACCTTGGAAATGCGCTAGGGTTTTACCTCCTAGGATGGG
CACTCTTCACCTTCGGTCTTTCCGTCTGCACCATGAAATCAACTATAATGTTTTTTCCT
TATTCTTCTCTTAGCAGTGACCTTCTTACTTCTATCCATTGCAAACTTCACAGGCGAAG
TTGGCGTCACTAGAGCTGGTGGGGTCTTGGTGTGATAGTAGCCTTCATTGCCTGGTACA
ACGCTTACGCAGGTATTGCCACAAGACAAAACCTCGTACATTATGGTCCATCCATTTCGCAT
TACCTAGCAATGATAAGGTGTTCTTCTAA

>YNR002C, 282 aa (SEQ ID NO 340)

MSDREQSSGNTAFENPKALDSSEGEFISENNDQSRHSQESICKIYTAGKNNEYIYIGRQK
FLRDDLFEEFGGTLNPLAPAPVHKFANPAPLGLSGFALTTFVLMSFNARAQGITIPNVV
VGCAMFYGGVLVQLIAGIWEIALENTFGGTALCSFGGFWLSFGAIYIPWFGILDAYKDKE
DLGNALGFYLLGWALFTFGLSVCTMKSTIMFFALFFLLAVTFLLLSIANFTGEVGVTRAG
GVLGVIVAFIAWYNAYAGIATRQNSYIMVHPFALPSNDKVFF

>YOL139C, 1142 bp, CDS: 501-1142 (SEQ ID NO 347)

ACAAGTTTGGATACTGGTATTGTGACTCTTGTAAGAAGAAGAATACATCTTGTGTTCTAT
GTGAAAGACCATTAAAGAAAGTACCATGGTCATCCTCCCCTGTGGACACGAAGGTCAC
TCCAGTGCATACAAGAATGGTTTTCTCGATGAGAATGAACAAGAATGTCCCGGCGGTTGCC
CCGGTGTTCATTCTAGGTTCTCCACATAATGTATAGTTTAAACATATCATCACCATT
GTTTAGTTAAATCGTTTAGAGTAATATTACCCGTCAAAAAGGTCCGGTAAAATTTTATTA
CCCTCTCCGAAAAGAAAATTTTTTTCGTCTGTCATAGAGTTTAAATGCAATACCTGATAAA
GAGAGTTTTACATTGCAAGAGGTAGTGTAAATCTGGATTTATATTGTACATATGTGTTT
GTGTTAGTGCTTGAGTACTTCTAGGAGTTTTACGAAAATAAAAGCATTTTTGTCTGAA
AACTAGTGAAAGGAAGAAAATGTCCGTTGAAGAAGTTAGCAAGAAGTTTGAAGAAAACG
TTTCAGTCGATGATACCACAGCTACTCAAAGACTGTTTTAAGTGACAGTGCTCACTTCG
ATGTCAAGCACCCATTGAACACCAAATGGACTTTATGGTACACAAAGCCAGCCGTCGATA
AATCTGAGTCGTGGTCTGATCTATTACGTCCCGTCACTTCATTCCAAACTGTTGAAGAAT
TTTGGGCTATCATTCAAAATATTCTTGAGCCACACGAAGTACCATTGAAATCAGATTACC
ACGTCTTCCGTAATGACGTTAGACCTGAATGGGAAGATGAAGCCAATGCTAAAGGTGGTA
AATGGTCTTTCCAACCTAGAGGAAAAGGTGCTGATATTGATGAATTATGGCTAAGAACTT
TACTAGCAGTTATTGGTGAAACAATTGATGAAGACGACTCCCAAATTAACGGTGTCTGTTT
TAAGCATTAGAAAAGGTGGTAACAAGTTTGCCTTATGGACTAAATCTGAAGACAAAGAAC
CACTATTGAGAATTGGTGGTAAATTCAAGCAAGTTTTAAATTAACCGATGACGGGCATT
TGGAATCTTTCCACATTCCAGTGCCAATGGTAGACACCCTCAACCATCAATCACCTTGT
AA

>YOL139C, 213 aa (SEQ ID NO 348)

MSVEEVSKKFEENVSVDDTTATPKTVLSDSAHFDVKHPLNTKWTLWYTKPAVDKSESWS
LLRPVTSFQTVEEFWAIIQNIPEPHELPLKSDYHVFVRNDVRPEWEDEANAKGGKWSFQ
LKGADIDELWLRTLLAVIGETIDEDDSQINGVVL SIRKGGNKFALWTKSEDKEPLLRIGG
KFKQVLKLTDDGHLEFFPHSSANGRHPQPSITL

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>YOR120W, 1439 bp, CDS: 501-1439 (SEQ ID NO 353)

TGTCTTACATATTGCAATGGATATGCTTGGGTGATCATACTTCCTGGCTTTAGATATTTG
AAACTTAACTCTTGTCAACAACTTCCTATGGAGTGTATAAGAATTGTAAGTTATAACAC
CGGCGAACAATCGGGGCAGACTATTCCGGGGAAGAACAAGGAAGGGCGGTCTTTTCTCCC
TCATTGTTCATAGCAAGGTCATTTTCGCCTTCTCAGAAAGGGGTAGAATCAATCTAGCACGC
AGATTGCAAACACGGCTTAATAATATGCCTATCAGGCATTCACCCGTGTGACGAATCGCA
CACCGCTGCTCTCCTTAATTCCCTAGAGTAGAAACCGAGCTTTCAGGAAAAGACTACGGC
AGTAAAGAATTGCTTTACTGGGCGTATAAAACCGGGAGAATCAAGACATTCTAATGACTT
GATTTCAGGATGAGAGCTTAATAGGTGCATCTTAGCAAGCTAAAATTTGGACAGCTCTCAT
TACTAAATTAAGATAGAAAAATGCCTGCTACTTTACATGATTTCTACGAAAATCCTTTCTC
TAAATACTGGAGCCCAAATCCCTCAAATAGGTTTAGGTACGTGGCAGTCGAAAGAGAACG
ATGCTTATAAGGCTGTTTTAACCGCTTTGAAAGATGGCTACCGACACATTGATACTGCTG
CTATTTACCGTAATGAAGACCAAGTCGGTCAAGCCATCAAGGATTCAGGTGTTCTCGGG
AAGAAATCTTTGTTACTACAAAGTTATGGTGTACACAACACCACGAACCTGAAGTAGCGC
TGGATCAATCAGCTAAAGAGGTTAGGATTGGACTACGTAGACTTATATTTGATGCATTTGGC
CTGCCAGATTAGATCCAGCCTACATCAAAAATGAAGACATCTTGAGTGTGCCAACAAAGA
AGGATGGTTCTCGTGCAGTGGATATCACCAATTGGAATTTTCATCAAAACCTGGGAATTAA
TGCAGGAACCTACCAAGACTGGTAAACTAAGGCCGTTGGAGTCTCCAACCTTTTCTATAA
ATAACCTGAAAGATCTATTAGCATCTCAAGGTAATAAGCTTACGCCAGCTGCTAACCAAG
TCGAAATACATCCATTACTACCTCAAGACGAATTGATTAATTTTTGTAAAAGTAAAGGCA
TTGTGGTTGAAGCTTATTCTCCGTTAGGTAGTACCGATGCTCCACTATTGAAGGAACCGG
TTATCCTTGAAATTGCGAAGAAAAATAACGTTCAACCCGGACACGTTGTTATTAGCTGGC
ACGTCCAAAGAGGTTATGTTGTCTTGCCAAAATCTGTGAATCCCGATCGAATCAAAACGA
ACAGGAAAATATTTACTTTGTCTACTGAGGACTTTGAAGCTATCAATAACATATCGAAGG
AAAAGGGCGAAAAAAGGGTTGTACATCCAAATTGGTCTCCTTTTCAAGTATTCAAGTAA

>YOR120W, 312 aa (SEQ ID NO 354)

MPATLHDSTKILSLNTGAQIPQIGLGTWQSKENDAYKAVLTALKDGYRHIDTAAIYRNE
QVQQAIKDSGVPREEIFVTTKLWCTQHHEPEVALDQSLKRLGLDYVDLYLMHWPARLDP
YIKNEDILSVPTKKDGSRAVDITNWNFIKTWELMQELPKTGKTKAVGVSNFSINNLDLL
ASQGNKLTAPANQVEIHPLLPQDELINFCKSKGIVVEAYSPLGSTDAPLLKEPVILEIAK
KNNVQPGHVVISWHVQRGYVVLPKSVNPDRIKTNRKIFTLSTEDFEAINNISKEGKEKRV
VHPNWSPFVFK

>YOR122C, 1090 bp, exon1 : 501-513, intron1: 514-722, exon2:
723-1090 (SEQ ID NO 357)

AGGAAGAGGAGGCTGCGTTTGACGACGAAGAGGATGATAATGAGGAAGAAGAAGAAG
AGGACGCGGATGAAGAGAACGCCTCTCGTCTAAGAAATTTAAAAAGAGAAGGAGCAGCAA
TGTACAGAGAAGAGGAAGAAGAAGAAAAAGATAGGAGCGAGACAAAAGAAGAAGGGTTG
CGGTCATCGAGGACGACGAAGACGAGGATTAGAGGAGACGTTACTTTGTTTATATATATT
AGTATGTACAATCGCAAAGAAATGGAGTGATGACATGTTGTAGTATTTAGTATGAGGTTA
CTGTGTGGGAGGTTTTACCATGATTTTTTGGCGAGAACACGCCATGAAATGTCTTTGTACG
AAACTCATTACCCGCATTAATATTTTTTTCTTTTTTAAAGCTCAGTTGACCCTTTCTCAT
TCCCTTCTTAAACAACCTGTGTGATCCTTGAGAAAAGATAAATTACATACACAACATAAA
CCCAACTACGATCGCAAATTATGTCTTGGAAGGTATGTGAACGAGACAATTATCAATTG
ATTAAGAAAGAAATGAGTCGGAGGTTAGCTTGTGTGACAATGTTTGGCAATGCCCGATTT
TTGTTGATCGCGTAATTTCAAGATTAAACCACTCAGAGTAAATTACTAACTGGAATATC
AAAAACATATGAAATTTCAACATGAATTTCTTTCCGTTTTTTTCTCCTACTTTTAAAC
AGCATACACTGATAACTTAATAGGAACCGGTAAAGTCGACAAAGCTGTCATCTACTCGAG
AGCAGGTGACGCTGTTTGGGCTACTTCTGGTGGCCTATCTTTGCAACCAAACGAAATTGG
TGAAATTGTTCAAGGCTTCGACAATCCAGCTGGTTTGCAAAGCAATGGTTTGCATATTCA
AGGCCAAAAGTTCATGTTGTTGAGAGCTGACGATAGAAGTATCTACGGTAGACATGATGC
TGAGGGTGTGTTTGTGTAAGAACTAAGCAAACCGTTATTATTGCTCATTATCCACCAAC
CGTACAAGCCGGTGAGGCCACCAAGATTGTGCGAGCAATTGGCTGACTACTTGATTGGTGT
TCAATACTAA

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>YOR122C, 126 aa (SEQ ID NO 358)

MSWQAYTDNLIGTGKVDKAVIYSRAGDAVWATSGGLSLQPNEIGEIVQGFDPAGLQSNGLHIQGGQKFMLLRADDRSIYGRHDAEGVVCVVRTKQTVIIAHYPPTVQAGEATKIVEQLADYLIGVQY

>YOR261C, 1517 bp, CDS: 501-1517 (SEQ ID NO 361)

GTAAGGTAAGGCATCATTAGCAGGATCCATATTCACCTACCTGGGAATGTCTTCCGATGGCATTGAAGAACTGTGAGCAGCCGTTGCAATAGGTTGACTTCCCTGAACCTGGTGGACCAATAACAATCTGAGCGAAGGGCATTATTGTACTCTCTAGTAGAAAATCAAACTATTGACACAACAACAATCAAATGAAAACAAACCATTCTATTACGGTAAGTAGTGAAGACTCACAAATGCAATCTTTCAATGAGCATCACTTACTTTAAGTAGCAATATTCCTAATCACTTATTACGAAATTTGATTTTACTAAAGTTCGGGGATACCTCAGTGGCAAATCGTTACTCAAGTTGCACGTAACTGAGAATCTACAATGAAATAATTGTGAAGCCAACAGCTAAGCAATCTATAGTGTAAACGTGGCTTTCTGTACAACCTGCTACTGATTGAGGGCATTTCGAAATTTAAAAAGAAAGAAAGAAAGGAAAATCAAATTACAATGTCTCTACAACACGAGAAAGTTACCATTGCACCACCTAGTTTGTCTATCTGCTTTGGATCATTATGAGCGTACGCAGACAAAAGAAAACAAAAGATGCGTTGGTGTCTATCTTAGGTGATGCTAACAGTTCCACTATCAGAGTCACTAATTCCTTTGCCTTACCGTTTGAAGAAGATGAGAAAACTCTGACGTGTGGTTTGTAGACCATAATTATATTGAAAACATGAATGAAATGTGTAAAAAGATTAAATGCCAAGGAAAACTCATTTGGATGGTATCATAGTGGTCTCTAAATTAAGGGCTTCTGACCTCAAGATTAATGAGCTGTTTAAAAATATATCTCAGAATAATCCGCTATTATTAATTGTTGATGTCAAACAACAAGGTGTTGGTTTACCAACAGATGCATATGTGCGGATTGAGCAAGTTAAGGATGATGGTACGCTACAGAAAAGACGTTCTTCATTTGCCTTGTACTATTGAGGCCGAAGAAGCTGAAGAAATTGGTGTAGAACACTTATTGAGAGACGTACGTGATCAAGCAGCAGGTGGCTTATCTATCCGGTTGACCAACCAATTAAATCTTTGAAAGGATTACAAAGCAAATAAAAGACGTTGTGCGAGTACTTAGACAAAAGTCATTAATAAGGAATTACCGATAAACACACTATATTGGGCAAGCTACAAGATGTTTTCACACCTTTTACCAAATCTGGGAACACCTGATGATGACGAAATAGATGTGGAGAATCATGACAGAATTAATATTTCAAATAACTTACAAAAGGCTTTAACTGTGAAAATAATGATGAATTAAATGGTTATATATAAGCAATTTGGTTAGGTCAATTATCGCGTTTGTATGATTGATTGAAAACAAAATTCAAATAAAAAAATTAAGAACAAAGAGTAAAGGACAAACAATCAAAAGTCTCTGATGACAGTGAGAGTGAGAGTGGTGACAAAGAAGCAACTGCGCCATTGATCCAACGAAAGAACAAGAAAAATTAA

>YOR261C, 338 aa (SEQ ID NO 362)

MSLQHEKVTTIAPLVLLSALDHYERTQTKENKRCVGVILGDANSSTIRVTNSFALPFEEDEKNSDVWFLDHNYYIENMNEMCKKINAKEKLIGWYHSGPKLRASDLKINELFKKYTQNNPLLIVDVKKQGGVGLPTDAYVAIEQVKDDGTSTEXTFLHLPCTIEAEAEIEIGVEHLLRDVRDQAAGGLSIRLTNQLKSLKGLQSKLKDVVEYLDKVINKEPINTILGLQDVFNLLPNLGTPTDDDEIDVENHDRINISNNLQKALTVKTNDELMVIYISNLVRSIIAFDDLIENKIQNKKIQEQRVKDKQSKVSDDSESESGDKEATAPLIQRKNKK

>YPL271W, 689 bp, CDS: 501-689 (SEQ ID NO 391)

CAGCAGCGACAAGTCAGAGTGCTTACAAAAAAGAGTTGATCCGGCTAAAGAAAGTCGATTTACGTATTTATCCAGGTTCAAACGGATTGCCAAAAATAGTCGATAACCTCGGAGTAAGCAAAGCAACAATATATTTGTTCTTCGAAAAGGTAACTTCTTAATCTTATAGAAAGATTGTACTAGTTCTCTCGAAGAAAAAAGCTAAGAAAGCTATAGCTGTATCTTACCAAGCCATGAACCTTGAGGAATTGGTAATCCTTATTAGGAAATACGCTAACTAGGTAATAGCAGATGATTTACTAGCTTACTATCTCACACTAAGTCTGGCAACGCGCTTATTTTTTAATACTTTTATACGAACCAATGAAATTTGATCCTCCCTTTTTTCGTCTAGTTAAATGAAGAGATACAAGTAGGCCCTTTCTATTGAGTACTTAGCAAGATATGTATTCTAAGAAACATCAACAGTTTCAGCCACAACCGATTCAAAAATGTCTGCCTGGAGGAAAGCTGGTATATCATATGCTGCATATTTGAATGTGGCCGCTCAGGCTATCCGTTCTTCATTGAAAAGTGAATTACAAACCGCTAGTGTCTTAAACAGATCGCAAACAGATGCTTTTTATACCAATATAAAAATGGCACTGCAGCTTCTGAACCCACTCCAATAACAAAATAG

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>YPL271W, 62 aa (SEQ ID NO 392)

MSAWRKAGISYAAYLNVAQAIRSSLKTELQTASVLNRSQTDAFYTQYKNGTAASEPTPI
TK

>YPR035W, 1613 bp, CDS: 501-1613 (SEQ ID NO 395)

TAGTGCCATTTGTGGTCATTATTATTCCTCCCAATATGCGAAAATAGTACACTATTTTTGG
CAGGAGAGTAGGCTGATATGCCGCATTGATGTCTGTGTAGCGAAACACAAACAAAAA
GAAAAAGTAGGATGAAAAAAGAAAAGTAATATGAAAAAGAGTGAAAAATTAATTCATT
TGTTAGTGTAAAGCGTCAGGTGTAAGTAGTAGGCTTGATAATGAATTAAAGATGACTCCG
ACGCATATTGTTTGCCATGTTTTATTTTTAGTTTGTAGATTTCCTTTTTTTGTAATATATA
AGGGAGTGATTCTATATATCGAATTCTCAGGCTTGGTTGGTTCGTAGGTTGTTCTGTCTT
TGTTTTTCGTTAGGTAAGAACATCACACAAAGATAACTATAGAATCACATACATATTTGTG
AGAAATTAACCTTCATTTTCAATTTATAGAAGAAGTTCAACCGAAAACAAAAATTAAACATAAT
ATAATATAATATAATCAAAAATGGCTGAAGCAAGCATCGAAAAGACTCAAATTTTACAAA
AATATCTAGAACTGGACCAAAGAGGTAGAATAATTGCCGAATACGTTTGGATCGATGGTA
CTGGTAACCTTACGTTCCAAAGGTAGAACTTTGAAGAAGAGAATCACATCCATTGACCAAT
TGCCAGAATGGAACCTTCGACGGTTCTTCTACCAACCAAGCGCCAGGCCACGACTCTGACA
TCTATTTGAAACCCGTTGCTTACTACCCAGATCCCTTCAGGAGAGGTGACAACATTTGTTG
TCTTGGCCGCATGTTACAACAATGACGGTACTCCAAACAAGTTCAACCACAGACACGAAG
CTGCCAAGCTATTTGCTGCTCATAAGGATGAAGAAATCTGGTTTGGTCTAGAACAAGAAT
ACACTCTATTTGACATGTATGACGATGTTTACGGATGGCCAAAGGGTGGGTACCCAGCTC
CACAAGGTCCTTACTACTGTGGTGTTGGTGCCGGTAAGGTTTATGCCAGAGACATGATCG
AAGCTCACTACAGAGCTTGTTTGTATGCCGGATTAGAAATTTCTGGTATTAACGCTGAAG
TCATGCCATCTCAATGGGAATTCCAAGTCGGTCCATGTACCGGTATTGACATGGGTGACC
AATTATGGATGGCCAGATACTTTTTGACAGAGTGGCAGAAGAGTTTGGTATCAAGATCT
CATTCATCCAAAGCCATTGAAGGGTGACTGGAACGGTGCCGGTTGTACAGCTAACGTTT
CCACCAAGGAAATGAGACAACCAGGTGGTACGAAATACATCGAACAAGCCATCGAGAAGT
TATCCAAGAGACACGCTGAACACATTAAGTTGTACGGTAGCGATAACGACATGAGATTAA
CTGGTAGACATGAAACCGCTTCCATGACTGCCTTTTCTTCTGGTGTCGCCAACAGAGGTA
GCTCAATTAGAAATCCCAAGATCCGTGCCAAAGGAAGGTTACGGTTACTTTGAAGACCGTA
GACCAGCTTCCAACATCGACCCATACTTGGTTACAGGTATCATGTGTGAAACTGTTGCG
GTGCTATTGACAATGCTGACATGACGAAGGAATTTGAAAGAGAATCTTCATAA

>YPR035W, 370 aa (SEQ ID NO 396)

MAEASIEKTQILQKYLELDQRGRIIAEYVWIDGTGNLRSKGRITLKKRITSIDQLPEWNFD
GSSTNQAPGHDSDIYLPVAYYPDPFRRGDNIVVLAACYNNDGTPNKFNRHEAAKLF
HKDEEIIWFGLEQEYTLFDYDDVYGPWPKGGYPAPQGPYYCGVGAGKVYARDMIEAHYRAC
LYAGLEISGINAEVMPSQWEFQVGPCTGIDMGDQLWMARYFLHRVAEEFGIKISFHPKPL
KGDWNGAGCHANVSTKEMRQPGGTYIEQAIKLSKRHAHIKLYGSDNDMRLTGRHETA
SMTAFSSGVANRGSSIRIPRSVAKEGYGYFEDRRPASNIDPYLVTGIMCETVCGAIDNAD
MTKEFERESS

YBR133C, 2984 bp, CDS: 501-2984 (SEQ ID NO 53)

AACCTACGACAGAGTTGTAATGAATGCTACTGATGTCTGCTCTACTGCCA
TCCGCTGTCTTTTCATGCATAAAAGCTCCATTCTTTATTTATCTCATACC
ACGAGAAAAAAAATCACCTGACATATTTTTATAACCCGCCTTTTAGACC
CTAAAACAGATCTCAGGGCTCGAGTACTGTTTTATCTGAAAATTCTTCGA
GCCCTCGTTTTGCACTGAGCTAAACCAAAAAGAAAAATAACAATCACAAA
TGGAACCCGAAACAGCACGCTGCGCAGTGTTTTATATTTTTTTGAAACA
AATGGCTTTATACAATGTGTATGTGTGATAGAAAAATGGTATATTTTGA
GTGACTTGTGATCTTATCCCAAGCCCTATAGGAGCTATTTCAAATTGCG
TGTGTGAAAGCGTGTGTGTGTGTGTGTGTGGAATTGTGCGGACGTTCC
TCTTCTTTTATACATATAATTTTTATATATACAAAGGGTTCAGTTTGCAT
ATGCATAGCAACGTATTTGTTGGTGTCAAACAGGCTTTAATCATAAACA
GCACAGCAAAAAGTCACGTTTCTAGAAAATGTCTCTAGTCATTCACCAG

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AACTGCCTAGTAACTATGATTACGTTTTGCTTCCTATAACAACGCCAAGA
TATAAGGAAATAGTTGGGCAAGTTTTCAAAGATTTCCAAAGACAATCCAT
ACAGAACTGGAAACCGCTTCAAATTCCTGAACCGCAGTTGCAGGATATCT
GTATACCCCCGTTCAACGTCAAGAAGCTAGACAATGACGATACGCCGTCT
TACATAGGGCTGTTATCCTCTTGGCTGGAGCTGGAGAGTCGCGATCCAAA
TGTAAGAGATCTTGGCTTAAAGGTCCTTCTAAACGAATGTAAGTACGCGA
GGTTTGTGGAATCAATAAGCTAATATTGGCGCCTCCACGGGACCTGTCC
AACCTGCAATTGTATGGACAGATGATTTACAGGCTCCTGCAAAATCGCAT
CGTCTTTGCTGCGCCTGCGTTAACCATATCCATTTCTCTGCCACTTTACG
AAGACAGCGATCCATTGGCCACTTGGGAACTGTGGAATACCGTGCGGAAA
CAATGCGAATATCATCCCTCTTTGACTATCTCTTTGGCTTTGCCAAGAAC
CAGGACTCCTTCGTATGTGCTGAATAGATGGTTAGCCGAACCCGTCTCGT
GTCTTTTGGTATCTTCATCCATCTTTGCCAGTAATCAGTACGATTATCCC
GTTTTACACAAGTTTAACCAGAATTTGATTTTAAAGTTCCAAAAGGTTAA
TGGAGATTACAAAATTTTGGGTAATGAATTATGCGTGATATTGCATGGGA
TGGAGAAATATGCCAATAATGTTAAGGGCGGAGAATCTGCCTATTTGGAA
TATATAAACTACTTATTGAAAAAGGGCGACAAAGTATTAAATTCCAATAG
TAATCACCATTTTGTCTCCAAGAGGACTCTCGGATAATGCCGCCTCTGA
AACCTCATTACAGATAATTTATTAAATTCCACATATTTGACTTTTGAAAA
GATTTGGTGAAGTACGATCTTTACGAATCTGCCATATTAGAGGCGCTTCA
AGATCTTGCTCCTCGAGCGAGTGCCAAGAGACCGTTGGTGATCCTAGTAG
CCGGTGCGGGAAGAGGACCTTTAGTGGATCGAACTTTTAAGATAATATCA
ATGTTGTTTATGGATAGTAAGGTTTCTATAATTGCCATTGAAAAAATCC
ACAGGCATATCTGTACTTGCAAAAAAGAAATTTGACTGTTGGGATAATA
GAGTGAAATTAATCAAGGAGGATATGACCAAATGGCAAATCAACGAGCCG
TCGGAAAAGCGTATTACAGATAGATCTGTGCATAAGTGAAGTGTGGGTTT
GTTCCGGTTGCAATGAATTATCACCAGAATGTCTCTGGTCTATTGAAAAAT
ATCATTCCCACAATGACACAATTTTCATACCGAGGTCATACTCTTCATAC
ATAGCACCCATTTGTCACCATTTATTCTACCAAAAACCTCTCACAACAAA
TCGCTCTTTGGAGGCGCCCTGGATAGTCCATAGAGTGCCATACTGTATAT
TATCCTCAAGGGTAAATGAAGTGTGGCGGTTTCGAGCATCCCATGGCCAA
AAAGATACTGTCCAAGACGAAGATGATTTTACAGTTGAATTTTCTCAAAG
TTCATTAAATGAGTTCAAGATAAAGCACCGCGCGAAATCCATGGCTTTA
TCGGATTCTTCTCGGCAAACTTATATAACAATATATTCTTGTCAACTTTG
CCCAATGACAGCACAGTCCGTTTAAAATTTAGCGAAGAAACGTTGATGAA
TACCAGACGAGAAGAAAATCTAATCAAGAAATGTGACCATAACCAAATA
TGACCTCGTGGTCTCCAATTATCTTTCCTTTGAAGCAACCAATATCCTTT
ATAGATGACTCCGAACCTTCTGTGCTGATGTCTCGGATACACTCCGATAC
AGAACAAAAAGTTTTGGTATGAATGGTCTTTGGAGAGTTTCATATACCTTA
TGTTGTCAAATTACACTTCGGCGGTAAGTGTGCAAGCATGACTATTCCG
AGGTCTATAGTTACAGATGACACTAAAACCTTTAGCCCATAATCGACATTA
TTCAGCGACTACCAATCAAAGCTAGATAATCAAATTGATCTTGACCAAG
ACATTGAAAACGAAGAAGAACAGGGATTCTATCCAATCTAGAAACTGGT
TGGCAAAGCGTACAAGATATTACGGACTCAGCGAAACCGCCAAACCGGA
CCATTTAGATTCTATCAATAAGCCTATGTTTGATCTCAAATCTACTAAAG
CGCTTGAACCCTCTAACGAATTGCCAAGGCACGAAGACCTCGAGGAAGAT
GTTCCAGAAGTTCATGTACAGAGTCAAGACTAGTGTTCACGCTACATAA
TGTCTGTGGCAGAGCCTTTTCCCTGCCTCTGTGA

YBR133C, 827 aa (SEQ ID NO 54)

MHSNVFVGKPGFNHKKSRFLENVSSHPELPSNYDYVLLPITTPR
YKEIVGQVFKDFQRQSIQNWKPLQIPEQLQDICIPIPFNVKKLDNDTPS
YIGLLSSWLELESRDPNVRDLGLKVLLNECKYARFVGINKLILAPPRDLS
NLQLYGMIMYRLQNRIVFAAPALTISISLPLYEDSDPLATWELWNTVRK
QCEYHPSLTISLALPRTRTPSYVLNRWLAEPVSCLLVSSSIFASNQYDYP
VLHKFNQNLILKFQKVNGDSQILGNELCVILHGMEKYANNVKGGESAYLE

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YINYLLKKGDKVLNSNSNHQFLQEDSRIMPPLKPHSDNLLNSTYLTFEK
DLVKYDLYESAILEALQDLAPRASAKRPLVILVAGAGRGPLVDRTFKIIS
MLFMDSKVSIIEKPNQAYLYLQKRNFDCWDNRVLIKEDMTKWQINEP
SEKRIQIDLCISELLGSFGCNELSPECIWSIEKYHSHNDTIFIPRSYSSY
IAPISSPLFYQKLSQTNRSLEAPWIVHRVPYCILSSRVNEVWRFEPMAQ
KDTVQDEDDFTVEFSQSSLNEFKIKHRGEIHGFIGFFSANLYNNIFLSTL
PNDSTVRLKFSEETLMNTRREENLIKCDHTPNMTSWSPPIIFPLKQPISE
IDDSLSVLMSRIHSDTEQKVWYEWSELSFIYMLSNYTSAVTAASMTIP
RSIVTDDTKTLAHRHYSATTNQLDNQIDLDQDIENEEQGFSLNLETG
WQSVQDIHGLSETAKPDHLDKSTKALEPSNELPRHEDLEED
VPEVHVRVKTSTLHNVCGRFSLPL

YBL085W, 3443 bp, CDS: 501-3443 (SEQ ID NO 31)

AAAGGGAAGTATGGCATGCCTAGAAATCTTTCTGGAAAACCTGAAGCAT
ATCATATAATTGTATGAACCTTGTCCTTCAAAGATGTTACCAAATATTCA
AGAGTATGTGAGCTTTCTATTCTATTGACGCGTAAGAAAGGCTATCACGT
GTGGGGGGGAGAGCTCAGCCACATTGCACTACTTTGAAACCGCGTAGTC
GGAAACGACATTCCCCGTACCAAAACAAACGAAAGGACGTGAAAGGTAA
ATGAATAACATGGCACTAAAAATTTGGCAGAAAACGAAAAAAAAGGAA
AAAGAACTGAAACTATACGCTTCCCTTAGGATACTTTCTGATTTACAT
CCGAAGAATTGGGTGCGTCAATTAAAGGCAATTCTTCGCTCTATCAAGCA
GTTTTACTGCGTCTGTCTAAAGAAACAATTGTTTTACTGAATTTCAACAA
AGTTCTAACTCGAGGTGACCGGAGGCCACTGTAATAATAAAAAATAGAAG
ATGAGTCTCGAAGGAAATACCTTAGGCAAAGGGGCCAAATCTTTTCTCT
GTATATTGCGGTAAATCAGTACTCTAAACGAATGGAGGACGAGCTCAATA
TGAAACCAGGTGATAAAATTAAAGTCATTACTGATGATGGGGAGTACAAT
GACGGCTGGTATTATGGGCGCAATTTGAGAACCAAAGAGGAAGGTTTATA
CCCAGCGGTATTTACCAAAAGAATAGCAATAGAAAAACCAGAGAACCTGC
ACAAATCACCAACCCAAGAGAGTGGAATTTCTGGTGTTAAATATGGAAT
TTAAATGATTCTGCGAGTAACATAGGTAAAGTCTCCTCGCATCAACAGGA
GAACAGATATACATCATTGAAAAGTACAATGAGCGATATAGACAAAGCCT
TGGAAGAGCTAAGAAGTGGTTCAGTTGAACAAGAGGTATCAAATCGCCC
ACACGCGTGCCCGAAGTTAGCACTCCACAGTTGCAAGATGAACAGACTTT
GATTCAGAAAAAACAGAAATGAGGAAAACACGACACATGACTCGTTAT
TTTCTAGCACAGCGGATTTAACTTAAGTTCTGAATCTTTGAAGAATATA
AGTAAGTCAAATATATCAACAAAATCCCTAGAACCGAGTTCGGAATCAGT
TCGTCAATTAGATTTGAAAATGGCTAAAAGTTGGAGCCCAGAAGAGGTTA
CTGATTACTTTAGCTTGGTTGGATTTGATCAATCCACTTGCAATAAATTC
AAAGAGCATCAAGTCTCCGGAATAATACTACTGGAATTAGAACTGGAACA
CCTAAAAGAATTGGAATAAATTTCTTTTGGTATAAGATTTTCAGATATTCA
AAGAAATAAGGAACATCAAGTCTGCAATTGATTGCTCGTCAAATAAACTG
GACGCCGACTACTCTACCTTTGCTTTTGAACCAAGCTGCCCACTAAT
GCCTGCAGCCACTGTAAATAGAGACGAAATCCAACAACAAATTTCTCCA
AGTGTAAACAAGTTGTCAAGTGAAAGCTCTGATAGAAAATCATCTTCGGTC
ACCACAGAATTGCAAAGACCAAGCTCGGTTGTTGTTAATCCAATTTTAA
ACTTCACGACCCAGCTGAGCAGATCCTAGATATGACAGAAGTTCCTAATT
TGTTTGCTGATAAAGATATTTTCAATCACCGGGAAGGGCTCCAAAACCA
CCATCATATCCAAGTCCAGTTCAACCTCCACAATCGCCCTCTTTTAATAA
CAGGTACACAAATAATAACGCAAGGTTTCTCCTCAAACAACATATCCAC
CTAAAAACAAGAACCAACCGTTTATTCAAATGGGCTAATTCCAAATTCT
TCGACATCTTCCGATAATTCAACGGGCAAGTTCAAATTCCTGCCATGAA
TGGTCATGACTCGAACTCTAGGAAAACAACACTGACATCTGCTACTATAC
CTTCTATTAAACACGGTTAACACAGATGAATCTCTACCCGCAATTTCAAAT
ATATCTTCAAATGCTACATCTCATCATCCGAACAGAAATTCGGTTGTTTA
CAATAACCATAAGAGGACGGAATCCGGAAGCTCATTTGTTGATTTGTTCA
ACAGGATTTCAATGCTATCGCCAGTCAAGTCAAGTTTCGACGAAGAAGAA

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ACGAAACAACCTTCAAAAGCTAGCAGAGCAGTTTTTGGACTCAGCACGCAG
AAAGTCGTCTTACGGACATTCAAGAGATGCCTCACTTTCTGAAATGAAAA
AGCATAGGAGAACTCTTCTATATTATCTTTTTTTTCTTCAAAAAGTCAG
TCTAATCCAACGTCACCAACCAACAACTTTCACTATCGATCCCGCAA
GATGACTTCCCATTTCTCGTTCTCAGTCGAATTCCTATTCGCATGCAAGAT
CACAATCTTACTCCCATAGTAGAAAACACTCGTTAGTTACCAGCCCCCTTG
AAAACCTCTTTAAGCCCTATAAATTCCAAATCCAATATTGCTTTAGCGCA
TAGCGAAACTCCTACTAGTAGTAATAATAAGGAGGCAGTATCACAACCAA
GTGAAGGGAAGCACAAGCACAAGCACAAGCACAAGCACAAGCACAACAC
AAGAACAGTAGCTCCAAAGATGGCTCTTCCGAAGAAAAAAGCAAAAAGAA
ATTATTTAGTAGCACCAAAGAATCATTTGTAGGAAGCAAGGAATTCAAAA
GATCTCCCAGTGAACCTACCCAAAAATCTACCAAATCGATACTTCCCAGG
TCGAATGCTAAAAAGCAACAAACATCTGCTTTTACCGAAGGTATACGCTC
TATCACAGCAAAGGAATCTATGCAAACCTGCGGACTGTTTACGGCTGGATGA
GCAAAAAGGTACCGGTGCTATGGGGACTTGGAACAACGGTTTTTCACA
CTTCATGGAACAAGGCTTTCTTATTTTACGAATACCAATGATGAGAAGGA
GCGTGGCCTGATAGATATAACGGCACATAGGGTCTTACCTGCCAGTGATG
ATGATAGGCTCATTTTCCTTATACGCTGCGAGCTTAGGAAAAGGAAAATAC
TGTTTTCAAATTGGTCCCTCCGCAACCGGGGTCCAAAAAGGGGCTAACCTT
TACAGAACCTCGCGTTCACTATTTTGCAGTTGAGAATAAATCTGAAATGA
AGGCATGGCTGTGAGCCATAATAAAGGCCACTATTGATATTGATACAAGC
GTCCCTGTCTATTAGTTCATATGCCACACCAACGATACCTCTAAGCAAGGC
ACAGACGCTATTGGAAGAAGCTAGGTTACAAACCCAGTTAAGAGATGCTG
AAGAGGAAGAGGGAAGAGATCAATTTGGATGGGATGACACCCAAAATAAA
AGAAATTCTAATTATCCAATCGAACAAGATCAATTTGAGACCAGCGATTA
CCTGGAAAGTTTACGATTTGAATACCCTGGTGGCAGACTTTGA

YBL085W, 980 aa (SEQ ID NO 32)

MSLEGNTLGKGAKSFPLYIAVNQYSKRMEDELNMKPGDKIKVITDDGEYN
DGWYYGRNLRKTKEGLYPVFTKRIAIEKPENLHKSPTQESGNSGVKYGN
LNDSASNIGKVSSHQENRYTSLKSTMSDIDKALEELRSGSVEQEVSKSP
TRVPEVSTPQLQDEQTLIQEKTRNEENTTHDSLFSSTADLNLSSSLKNI
SKSNISTKSLEPSSSVRQLDLKMAKSWSPVEVTDYFSLVGFQDQSTCNKF
KEHQVSGKILLELELEHLKELEINSFGIRFQIFKEIRNIKSAIDSSSNKL
DAHYSTFAFENQAAQLMPAATVNRDEIQQQISSKNKLSSESSDRKSSSV
TTELQRPSSVVVNPNFKLHDPAEQILDMTEVPNLFADKDFESPGRAPKP
PSYPSPVQPPQSPSFMNRYTMNARFPPTTYPKKNKPTVYSNGLIPNS
STSSDNSTGKFKFPAMNGHDSNSRKTTLTSATIPSINTVNTDESLPAISN
ISSNATSHHPNRNSVVYNNHKRTESGSSFVDLFNRISMLSPVKSSFDEEE
TKQPSKASRAVFDASARRKSSYGHSRDASLSEMKKHRRNSSILSFFSSKSQ
SNPTSPKQTFITIDPAKMTSHSRQSNSYSHARSQSYSHSRKHS�VTSPL
KTSLSPIINSKSNIALAHSETPTSSNNKEAVSQPSEGGKHKHKHKHKSKHKH
KNSSSKDGSSEKSKKKLFSSTKESFVGSKEFKRSPSELTQKSTKSILPR
SNAKKQQTSAFTEGIRSITAKESMQTADCSGWSKKGKGAMGTWKQRFPT
LHGTRLSTYFTNTNDEKERGLIDITAHRLVLPASDDRLISLYAASLGKGY
CFKLVPQPGSKKGLTFTEPRVHYFAVENKSEMKAWLSAIKATIDIDTS
VPVISSYATPTIPLSKAQTLLLEEARLQTLRDAEEEEGRDQFGWDDTQNK
RNSNYPIEQDQFETSDYLESSAFEYPPGRL

YDR545W, 5891 bp, CDS: 501-5891 (SEQ ID NO 137)

TTCTATTATATTGGTCTTTTCGAGAGCGGAAGAAGTTGTAGGCTAAGCGC
AGGCTAAGCGTAGGTCCATATTTAAAGTATCCAAGAGAATATCCACGAAG
CGGCTGAGCAACGAACAGAATCCTGGTTCTCCTCGACTAAGCAGATAGTT
AAGATACTGTGCACCATGGAAAATTGAAAACGAAAGTACGTACCGACTACT
TTATTTTTGCAGGCCGGAATCAAGCGATGAATGAGACATCCTTCTGTTT
TCTATGTTGGGACAGACAGTCGCTTATCTTAGTGAGATTTCTTATTAAT

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GAATTTTCTTTGCTGCTGCTGGAGATTTGCACCTGCATAGCGCAGATTCT
GCTTCTTCTCAATAGAGTAGCTTAATTATTACATTCTTAGATGATGATAA
GACGGAACTGGACAATCTTTTGTATTATTTGATGGATTTCTTGTCAAAA
AGCATAACAATCAACATACTATTGTTAATTTCGAACTTACAAAAATAAA
ATGAAAGTTTCCGATAGGCGTAAGTTTGAAAAAGCAAACCTTGACGAGTT
TGAGTCGGCTCTAAATAACAAAAACGACTTGGTACATTGTCCCTCAATAA
CTTTATTTGAATCGATCCCCACGGAAGTGCGGTCATTCTACGAAGACGAA
AAGTCTGGCCTAATCAAAGTGGTAAAATTCAGAACTGGTGCAATGGATAG
GAAAAGGTCTTTTGAAAAAATTGTCATTTCCGTCATGGTCGGGAAAAATG
TACAAAAGTTCTTGACATTTGTTGAAGACGAACCAGATTTCCAGGGCGGA
CCAATCCCTTCAAAGTATCTTATTCCCAAGAAAATCAACTTGATGGTCTA
CACGTTGTTTCAAAGTCATACTTTGAAATTCAATAGAAAGGATTACGATA
CCCTTTCTCTTTTTTACCTCAACAGAGGATACTATAATGAGTTGAGTTTC
CGTGTCTTGAACGTTGTCACGAAATAGCGAGTGCCAGGCCGAACGACAG
CTCTACGATGCGTACTTTCACTGACTTTGTTTCTGGCGCACCTATTGTAA
GGAGTCTTCAGAAAAGCACCATAAGGAAATATGGGTACAATTTGGCACCC
TACATGTTCTTGTACTACACGTAGATGAGCTATCGATTTTTTCTGCATA
CCAAGCAAGTTTACCTGGCGAAAAGAAAGTCGACACAGAGCGGCTGAAGC
GTGATCTATGCCCACGTAAACCCATTGAGATAAAGTACTTTTCACAGATA
TGTAACGATATGATGAACAAAAAGACCGATTGGGTGATATTTTGCATAT
TATCTTGCGAGCATGTGCGCTCAATTTCGGGGCGGGTCCCCGTGGTGGCG
CTGGTGACGAAGAGGATCGATCTATTACGAATGAAGAACCATTATTCCC
TCTGTGGACGAGCATGGCTTGAAAGTATGTAAGTTGCGTAGTCCCTAACAC
TCCACGAAGACTCAGAAAAACACTAGATGCCGTGAAAGCTTTATTGGTGT
CGTCTTGTGCTTGTACTGCAAGGGATTTAGATATATTGATGACACCAAC
GGCGTTGCAATGTGGAATGGATCAAAATTCTGTACCACGAAGTAGCGCA
GGAAACCAAGCTGAAGGACTCTTATAGAATAACTTTGGTACCTTCTTCTG
ATGGTATATCAGTATGTGGAACCTTTTAAATCGCGAGTATGTCCGCGGC
TTTTACTTTGTCATGCAAGGCTCAGTTCGATAACCTTTGGGGAGAGTTGAA
CAACTGCTTTTATATGCCTACAGTGGTTGATATTGCCAGCCTCATTTTGC
GTAATCGAGAAGTTTGTTCAGAGAGCCAAAGCGAGGAATTGACGAGTAT
CTGGAAAACGATTCTTTTCTTCAAATGATACCTGTTAAATATCGTGAAAT
TGTGCTGCCCAAGTTGAGAAGAGATACTAACAAAATGACCGCGGCTCTTA
AAAATAAAGTCACTGTTGCAATTGACGAGCTTACGGTGCCACTTATGTGG
ATGGTCCATTTTGGCGTAGGATACCTTACCGTTATCCAGAGCTTCAGCT
ACTCGCTTTTGGCGGCTCCTCAGCGCAACGTATACGTCGATGATACAACAA
GACGCATCCAACGTACACTGATTACAACAAGAACGGTTTCATCGGAGCCT
CGACTTAAGACGCTTGACGGACTCACTTCAGATTACGTGTTTTATTTTGT
CACTGTGCTAAGGCAAATGCAAATATGTGCGCTTGGTAACAGTTATGACG
CTTTTAAATCATGATCCTTGGATGGATGTGGTGGGATTTGAGGATCCAGAT
CAAGTAACAAATCGAGACATTTTCGAGGATAGTTTTGTATTCTTACATGTT
TCTGAATACCGCGAAGGGCTGTCTGGTTGAATACGCAACTTTTCGGCAGT
ACATAGAGGAACCTCCGAAGAATGCACCTCAGAAGCTGAATTTTCGGGAG
ATGCGTCAGGGGTTGATTGCCCTAGGACGGCACTGCGTAGGTAGCAGATT
TGAAACAGATTTGTACGAGTCGGCGACGAGTGAACCTCATGGCCAATCATT
CCGTTCAAACAGGGCGAAATATTTACGGTGTGGATTCTTTTTCGTTAACT
AGTGTCACTGGGACGACCGCCACTTTATTGCAGGAACGAGCTTCCGAGCG
CTGGATTCAATGGTTAGGCCTTGAAAGCGACTACCATTGTTTCTCTA
GTACTCGGAATGCGGAAGACGTAGTGGCAGGTGAGGCGGCGAGTTCAGAT
CATGATCAAAAAATTTCAAGAGTAACGCGAAAAAGCCCCGAGAGCCCAA
GAGTACAAACGATATCCTCGTCGACGGCCAGAACTCTTTGGCAGCTCCT
TTGAATTCAGGGACTTGCATCAGTTGCGCTTATGTCATGAAATATACATG
GCAGACACACCCTCTGTGGCAGTACAGGCCCCACCGGGCTATGGTAAGAC
GGAGTTATTTTCATCTCCCCTTGATAGCACTGGCGTCTAAGGGCGACGTGA
AATATGTGTCGTTTCTGTTTGTACCGTACACAGTGTGCTTGCTAATTGC
ATGATCAGGTTGAGCCGATGCGGTTGCTTGAATGTGGCCCCCTGTAAGAAA

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CTTTATTGAAGAAGGTTGCGATGGCGTTACTGATTTATACGTGGGGATCT
ACGATGATCTTGCTAGCACTAATTTACAGACAGGATAGCTGCGTGGGAG
AATATTGTTGAGTGCACCTTTAGGACCAACAACGTAAAATTGGGTTACCT
CATTGTAGATGAGTTTCACACTTTGAAACGGAGGTCTACCGGCAGTCGC
AATTTGGGGGCATAACTAACCTTGATTTTGACGCTTTTGAGAAAGCAATC
TTTTTGAGCGGCACAGCACCTGAGGCTGTAGCTGATGCTGCGTTGCAGCG
TATTGGGCTTACGGGACTGGCCAAGAAGTCGATGGACATCAACGAGCTCA
AACGGTCGGAAGATCTCAGCAGAGGTCTATCCAGCTATCCAACACGGATG
TTTAATCTAATCAAGGAGAAATCCGAGGTGCCTTTAGGGCATGTTCTATA
AATTTGGAAGAAAGTGGAATCACAGCCCGAAGAAGCACTGAAGCTTCTTT
TAGCCCTCTTTGAAATTGAACCAGAGTCGAAGGCCATTGTAGTTGCAAGC
ACAACCAACGAAGTGGAAGAATTGGCCTGCTCTTGAGAAAAGTATTTTAG
GGTGGTATGGATACACGGGAAGCTGGGTGCTGCAGAAAAGGTGCTCTCGCA
CAAAGGAGTTTGTCACTGACGGTAGCATGCGAGTTCTCATCGGAACGAAA
TTAGTGACTGAAGGAATTGACATTAAGCAATTGATGATGGTGATCATGCT
TGATAATAGACTTAATATTATTGAGCTCATTCAAGGCGTAGGGAGACTAA
GAGATGGGGGCTCTGTTATCTATTATCTAGAAAAAACAGTTGGGCGGCA
AGGAATCGTAAGGGTGAATTACCACCGATTAAAGGAAGGCTGTATAACCGA
ACAGGTACGCGAGTTCTATGGACTTGAATCAAAGAAAGGAAAAAGGGCC
AGCATGTTGGATGCTGTGGCTCCAGGACAGACCTGTCTGCTGACACAGTG
GAACTGATAGAAAGAATGGACAGATTGGCTGAAAAACAGGCGACAGCTTC
CATGTGCGATCATTGCGTTACCGTCTAGCTTCCAGGAGAGCAATAGCAGTG
ACAGGTGCAGAAAGTATTGCAGCAGTGATGAGGACAGCGACACGTGCATT
CATGGTAGTGCTAATGCCAGTACCAATGCGACTACCAACTCCAGCACTAA
TGCTACTACCACTGCCAGCACCAACGTGAGGACTAGTGCTACTACCACTG
CCAGCATCAACGTGAGGACTAGTGCGATTACCACTGAAAGTACCAACTCC
AGCACTAATGCTACTACCACTGCCAGCACCAACGTGAGGACTAGTGCTAC
TACCACTGCCAGCATCAACGTGAGGACTAGTGCGACTACCACTGAAAGTA
CCAATCCAAACACTAGTGCTACTACCACCGAAAGTACCGACTCCAACACT
AGTGCTACTACCACCGAAAGTACCGACTCCAACACTAGTGCTACTACCAC
TGCTAGCACCAACTCCAGCACTAATGCCACTACCACTGCTAGCACCAACT
CCAGCACTAATGCCACTACCACTGAAAGTACCAACGCTAGTGCCAAGGAG
GACGCCAATAAAGATGGCAATGCTGAGGATAATAGATTCCATCCAGTCAC
CGACATTAACAAAGAGTCGTATAAGCGGAAAGGGAGTCAAATGGTTTTGC
TAGAGAGAAAGAACTGAAAGCACAATTTCCCAATACTTCCGAGAATATG
AATGTCTTACAGTTTCTTGGATTTCGGTCTGACGAAATTAAACATCTTTT
CCTCTATGGTATTGACGTATACTTCTGCCAGAGGGAGTATTCACACAAT
ACGGATTATGCAAGGGCTGTCAAAGATGTTGAGCTCTGTGTCTGTTGG
GCTGGCCAGAAAGTATCGTATCGGAGGATGGCTTGGGAAGCACTAGCTGT
GGAGAGAATGCTGCGAAATGACGAGGAATACAAAGAATACTTGGAAGACA
TCGAGCCATATCATGGGGACCTGTAGGATATTTGAAATATTTTAGCGTA
AAAAGGGGAGAGATCTACTCTCAGATACAGAGAAATTATGCTTGGTACCT
GGCCATTACTAGAAGAAGAGAAACAATTAGTGTATTGGATTGACAAAGAG
GCAAGCAAGGGAGCCAAGTTTCCGCATGTCTGGAAGGCAGATCAAAGAG
TTGTATTATAAAGTATGGAGCAACTTGCCTGAATCGAAGACAGAGGTGCT
GCAGTACTTTTTGAACTGGGACGAGAAAAAGTGCCGGGAAGAATGGGAGG
CAAAAGACGATACGGTCTTTGTGGAAGCGCTCGAGAAAGTTGGAGTTTTT
CAGCGTTTTGCGTTCCATGACGAGCGCTGGACTGCAGGGTCCGCAGTACGT
CAAGCTGCAGTTTAGCAGGCATCATCGACAGTTGAGGAGCAGATATGAAT
TAAGTCTAGGAATGCACCTTGCAGATCAGCTTGCCTGGGAGTTACCCCA
TCTAAAGTGCCGCATTGGACGGCATTCTGTGCGATGCTGATAGGGCTGTT
CTACAATAAAACATTTCCGCAGAACTGGAATATCTTTTGGAGCAGATTT
CGGAGGTGTGGTTGTTACCACATTGGCTTGATTTGGCAAACGTTGAAGTT
CTCGCTGCAGATAACACGAGGGTACCGCTGTACATGCTGATGGTAGCGGT
TCACAAAGAGCTGGATAGCGATGATGTTCCAGACGGTAGATTTGATATAA
TATTACTATGTAGAGATTTCGAGCAGAGAAGTTGGAGAGTGA

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YDR545W, 1796 aa (SEQ ID NO 138)
MKVSDRRKFEEKANFDEFESALNNKNDLVHCPSITLFESIPTEVRSFYEDE
KSGLIKVVKFRTGAMDRKRSFEKIVISVMVGKNVQKFLTFVEDEPDFQGG
PIPSKYLI PKKINLMVYTLFQVHTLKFNRKDYDTLSLFYLNRGYYNELSF
RVLERCHEIASARPNDSSMTMRTFTDFVSGAPIVRSLQKSTIRKYGYNLAP
YMFLLLHVDELSIFSAYQASLPGEKKVDTERLKRDLCPRKPIEIKYFSQI
CNDMMNKDRLGDILHIILRACALNFGAGPRGGAGDEEDRSITNEEPIIP
SVDEHGLKVCKLRSPNTPRRLRKTLDVAKALLVSSCACTARDLDIFDDTN
GVAMWKWIKILYHEVAQETTLKDSYRITLVPSSDGI SVCGKLFNREYVRG
FYFACKAQFDNLWGELNNCFYMP TVVDIASLILRNREVLFREPKRGIDEY
LEND SFLQMI PVKYREIVLPKLRRDTNKM TAALKNKVTV AIDELTVPLMW
MVHFAVGYPYRYPELQLLAFAGPQRNVYVDDTTRRIQLYTDYNKGSSEP
RLKTL DGLTSDYVFYFVTVLRQM QICALGNSYDAFNHDPWMDVVG FEDPD
QVTNRDISRIVLYSYMFLNTAKGCLVEYATFRQYMRLEPKNAPQKLNFRE
MRQGLIALGRHCVGSRFETDLYESATSELMANHSVQTGRNIYGVDSFSLT
SVSGT TATLLQERASERW IQWLGLES DYHCSFSSTRNAEDVVAGEAASSD
HDQKISRVT RKRPREPKSTNDILVAGQK LFGSSFEFRDLHQLRLCHEIYM
ADTPSAVAVQAPPGYGKTELFHLPLIALASKGDVKYVSFLFVPYTVLLANC
MIRLSRCGCLNVAPVRNFIEEGCDGVTDLYVGIYDDLASTNFTDRIAWE
NIVECTFR TNNVKLG YLIVDEFHNFETEYRQSQFGGITNLDFDAFEKAI
FLSGTAPEAVADAALQRIGLTGLAKKSM D INELKRSEDL SRGLSSYPTRM
FNLIKEKSEVPLGHVHKIWKVESQPEEALKLLLALFEIEPESKAIVVAS
TTNEVEELACSWRKYFRVWVIHGKLGAAEKVSRTKEFVTGDSMRVLIGTK
LVTEGIDIKQLMMVIMLDNRLNIIELIQGVGRLRDGGLCYLLSRKNSWAA
RNRKGELPPIKEGCITEQVREFYGLSEKKGKQHVGCCGSRDLSADTV
ELIERMDRLAEKQATASMSIIALPSSFQESNSSDRCKYCSSDESDTCTI
HGSANASTNATNSSTNATTTASTNVRTSATTASINVRTSAITTESTNS
STNATTTASTNVRTSATTASINVRTSATTTESTNSNTSATTTESTDSNT
SATTTESTDSNTSATTASTNSSTNATTTASTNSSTNATTTTESTNASAKE
DANKDGN AEDNRFHPVTDINKESYKRKGSQMVLLERKKLKAQFPNTSEN
NVLQFLGFRSDEIKHLFLYGIDVYFCPEGVFTQYGLCKGCQKMFELCVCW
AGQKVSYRRMAWEAL AVERMLRNDEEYKEYLEDIEPYHGD PVGYLKYFSV
KRGEIYSQIQRNYAWYLAITRRRETISVLDSTRGKQGSQVFRMSGRIKE
LYYKVWSNLRESKTEVLQYFLNWDEKKCREWEAKDDTVFVEALEKGVF
QRLRSMTSAGLQGPQYVKLQFSRHRQLRSRYELSLGMHLRDQLALGVTP
SKVPHWTAFLSMLIGLFYNKTFRQKLEYLLEQISEVWLLPHWLDLANVEV
LAADNTRVPLYMLMVAVHKELDSDDVPDGRFDIILLCRDSSREVGE

YCR005C, 1883 bp, CDS: 501-1883 (SEQ ID NO 71)
AGAGTTGTTGCCACAACATAAGCCGCTTTGGAGTGTGAACAAATCCGTC
CTTGGGTCATTC AATCAATGGCTTGGCGGTATCTCAAAGAGCGCAAAC
AATAGCGCGCACATTCGACGCATTTATCCGGTGGTCATCGACTAGGGGCG
AAGAGGTCACGACCTATTTTTTCTTGCAGAAAAAAGTGTGACCTTTTCC
GTAGCTAGACGCTATCAGGGCGTCAGCAATGGGAGGCACAGCGGAAAA
CAATAACAATGGTAAGCGCAATTACCTTTTGAGCGTTACATTCGTATGAA
ATTGGTGACGTTAATCTAAAGATAGTCATGCTCTCAAAGGGCCCATTAT
TCTCGACGTTGAGCGTATATAAGACTATTAAAACTTGGTTCTTTAGATAT
GGTGTTCGTTCCCTCATTATTAAGTTTCAGGGAACAATATCAACACATATC
ATAACAGGTTCTCAAACCTTTTTGTTTAAATAACTAGTAACAAGAAAA
ATGACAGTTCCCTTATCTAAATCAAACAGAAATGTTGCATCATATTTACA
ATCAAATCAAGCCAAGAAAAGACTCTAAAAGAGAGATTTAGCGAAATCT
ACCCCATCCATGCTCAAGATGTAAGGCAATTCGTTAAAGAGCATGGCAAA
ACTAAAAATTAGCGATGTTCTATTAGAACAGGTATATGGTGGTATGAGAGG
TATTCCAGGGAGCGTATGGGAAGGTTCCGTTTTGGACCCAGAAGACGGTA
TTCGTTTTAGAGGTCGTACGATCGCCGACATTCAAAAGGACCTGCCCAAG
GCAAAAAGGAAGCTCACACCCTACCAGAAGCTCTCTTTTGGTTATTGCT

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AACTGGCGAGGTTCCAACCTCAAGCGCAAGTTGAAAACCTTATCAGCTGATC
TAATGTCAAGATCGGAACTACCTAGTCATGTCGTTCAACTTTTGGATAAT
TTACCAAAGGACTTACACCCAATGGCTCAATTCTCTATTGCTGTAACGTC
CTTGGAAAGCGAGTCAAAGTTTGTCTAAGGCTTATGCTCAAGGAATTTCCA
AGCAAGATTATTGGAGTTATACTTTTGAAGATTCAGTAGACTTGCCTGGGT
AAATTGCCAGTTATTGCAGCTAAAATTTATCGTAATGTATTCAAAGATGG
CAAAATGGGTGAAGTGGACCCAAATGCCGATTATGCTAAAAATCTGGTCA
ACTTGATTGGTTCTAAGGATGAAGATTTTCGTGGACTTGATGAGACTTTAT
TTAACCATTCATTCCGATCACGAAGGTGGTAATGTATCTGCACATACATC
CCATCTTGTGGGCTCAGCACTATCATCACCTTATCTGTCCCTTGCATCAG
GTTTGAACGGGTGGCTGGCCCACTTCATGGGCGTGCTAATCAAGAAGTA
CTAGAATGGTTATTTGCACTTAAAGAAGAGGTAAATGATGACTACTCTAA
AGATACGATCGAAAAATATTTATGGGATACTCTAACTCAGGAAGAGTCA
TTCCCGGTTATGGTCATGCTGTGCTAAGGAAACTGATCCTCGTTATATG
GCTCAGCGTAAGTTTGCCATGGACCATTTTCCAGATTATGAATTATTCAA
GTTAGTTTCATCAATATACGAGGTAGCACCTGGCGTATTGACTGAACATG
GTAAACTAAAAATCCATGGCCAAATGTAGATGCTCACTCTGGTGTCTTA
TTACAATATTATGGACTAAAAGAATCTTCTTTCTATACCGTTTTATTGG
CGTTTCAAGGGCATTTGGTATTCTTGCTCAATTGATCACTGATAGGGCCA
TCGGTGCTTCCATTGAAAGGCCAAAGTCCTATTCTACTGAGAAATACAAG
GAATTGGTCAAAAACATTGAAAGCAAACATATAG

YCR005C, 460 aa (SEQ ID NO 72)

MTVPYLNSNRNVASYLQSNSSQEKTLKERFSEIYPIHAQDVRQFVKEHGK
TKISDVLLLEQVYGGMRGIPGSVWEGSVLDPEDGIRFRGRTIADIQKDLPK
AKGSSQPLPEALFWLLLTGEVPTQAQVENLSADLMSRSELPSHVQLLDN
LPKDLHPMAQFSIAVTALESESKFAKAYAQGISKQDYWSYTFEDSLDLLG
KLPVIAAKIYRNVFKDGKMGVDPNADYAKNLVNLIGSKDEDFVDLMRLY
LTIHSDHEGGNVSAHTSHLVGSALSSPYLSLASGLNGLAGPLHGRANQEV
LEWLFALKEEVNDYSDKTIEKYLWDTLNSGRVIPGYGHAVLRKTDPRYM
AQRKFAMDHFPDYELFKLVSSIIYEVAPGVLTEHGKTKNPWPVNDAHSGVL
LQYYGLKESSFYTVLFGVSRAFGILAQLITDRAIGASIERPKSYSTEKYK
ELVKNIESKL

YOL126C, 1772 bp, CDS: 501-1772 (SEQ ID NO 345)

ATCCCCCTCACTTTTCCGTTTGTATCTCCTACTTTCTTACTTCCTTTTT
TTCTTCTTTATTTGCTTGGTTTACCATTGAAGTCCATTTTTACTACAGAC
AATAGCTAGTCATTGCTATCTTCCGTTTGTCACTTTTTTTCAAATTTCT
CATCTATATAGCGAAGTACGGAAAAGATGTCACTTGCCGGCATCTCGGCC
TTCCCCGGCCAAATGGACTCATCATCTACGATACGGCCCCCTTTAATCCGC
AATTACTTTGCCCCATTGCGCCGTAGCCGTTCTAAAGCCGCCGTGCCTTGC
CCCCAATACTCCCCTAATGATCCGGGAAGTTCCGGTTTTTTTCTTTGTT
TAGTGGCATTTTGTGTTGCCCAAGGTTGGGAAGGTCCGATTTGACTTTAA
GGAACACGGAAGGTATCTAAGGTTTCTAAAAACAATATACACGCGCGTG
CGTAGATATATAAAGATAAAGATTTATCGATATGAGATAAAGATTGCTGC
ATGATTCTCCTTCTGATTCTTTTTTCCCTGTATATATTTTCTCCCCTTCTG
TATAAATCGTACAGTCAGAAGTAGTCCAGAATATAGTGCTGCAGACTATT
ACAAAAGTTCAATACAATATCATAAAAGTTATAGTAACATGCCCTCACTCA
GTTACACCATCCATAGAACAAGATTGTTAAAAATTGCCATTTTAGGTGC
TGCCGGTGGTATCGGGCAGTCGTTATCGCTGCTTTTGAAAGCTCAGTTGC
AATACCAGTTAAAGGAGAGCAACCGGAGCGTTACCCACATTCATCTGGCT
CTTTACGATGTCAACCAAGAAGCCATCAACGGTGTACCGCCGACTTGTCT
TCATATAGACACCCCCATTTCCGTGTCGAGCCACTCTCCTGCAGGTGGCA
TTGAGAACTGTTTGCATAACGCTTCTATTGTTGTCATTCTGCAGGTGTT
CCAAGAAAACCTGGCATGACTCGTGATGACTTATTTAACGTGAATGCTGG
TATCATTAGCCAGCTCGGTGATTCTATTGCAGAATGTTGTGATCTTTCCA

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AGGTC TTCGTTCTTGTCAATTTCCAACCCTGTAAATTCCTTAGTCCCAGTG
ATGGTTTCTAACATTCTTAAGAACCATCCTCAGTCTAGAAATTCGGGCAT
TGAAAGAAGGATCATGGGTGTCACCAAGCTCGACATTGTCAGAGCGTCCA
CTTTTCTACGTGAGATAAACATTGAGTCAGGGCTAACTCCTCGTGTTAAC
TCCATGCCTGACGTCCCTGTAATTGGCGGGCATTCCTGGCGAGACTATTAT
TCCGTTGTTTTACAGTCAAAC TTCCATCGAGATTAATGAGGATCAAT
TGAAATATTTAATACATAGAGTCCAATACGGTGGTGATGAAGTGGTCAAG
GCCAAGAACGGTAAAGGTAGTGTACCTTATCGATGGCCCATGCCGGTTA
TAAGTGTGTTGTCCAATTTGTTTCTTTGTTATTTGGGTAACATTGAGCAGA
TCCATGGAACCTACTATGTGCCATTAAAAGATGCGAACAACTTCCCCATT
GCTCCTGGGGCAGATCAATTATTGCCCTCTGGTGGACGGTGCAGACTACTT
TGCCATACCATTAACTATTACTACAAAGGGTGTTCCTATGTGGATTATG
ACATCGTTAATAGGATGAACGACATGGAACGCAACCAATGTTGCCAATT
TGCGTCTCCAGTTAAAGAAAAATATCGATAAGGGCTTGGAATTCGTTGC
ATCGAGATCTGCATCATCTTAA

YOL126C, 423 aa (SEQ ID NO 346)

MILLILFLPCIFYFLPCINRTVRSSPEYSAADYYKSSIQYHKSYSNMPHS
VTPSIEQDSLKIAILGAAGGIGQSLSLLLKAQLQYQLKESNRSVTHIHLA
LYDVNQEAINGVADLSHIDTPISVSSHSPAGGIENCLHNASIVVIPAGV
PRKPGMTRDDLNFVNAGIISQLGDSIAECCDLSKVFVLVISNPVNSLVPV
MVSNILKNHPQSRNSGIERRIMGVTKLDIVRASTFLREINIESGLTPRVN
SMPDVPVIGGHSGETIIPLFSSQSNFLSRLNEDQLKYLIHRVQYGGDEVVK
AKNGKGSATLSMAHAGYKCVVQFVSLLLGNIEQIHGTYVPLKDANNFPI
APGADQLPLVDGADYFAIPLTITTKGVSYVDYDIVNRMNDMERNQMLPI
CVSQLKKNIDKGLEFVASRSASS

YBR019C, 2600 bp, CDS: 501-2600 (SEQ ID NO 39)

ATCGCTTCGCTGATTAAATTACCCAGAAATAAGGCTAAAAAATAATCGC
ATTATCATCCTATGGTTGTTAAATTTGATTTCGTTAAATTTGAAGGTTTGTGG
GGCCAGGTTACTGCCAATTTTTCCTCTTCATAACCATAAAAGCTAGTATT
GTAGAATCTTTATTGTTCCGGAGCAGTGC GGCGCGAGGCACATCTGCGTTT
CAGGAACCGGACCGGTGAAGACGAGGACGCACGGAGGAGAGTCTTCCGTC
GGAGGGCTGTGCCCCGCTCGGCGGCTTCTAATCCGTACTTCAATATAGCA
ATGAGCAGTTAAGCGTATTACTGAAAGTTCCAAAGAGAAGGTTTTTTTAG
GCTAAGATAATGGGGCTCTTTACATTTCCACAACATATAAGTAAGATTAG
ATATGGATATGTATATGGTGGTAATGCCATGTAATATGATTATTAACTT
CTTTGCGTCCATCCAAAAAAAAGTAAGAATTTTTGAAAAATTCATATATA
ATGACAGCTCAGTTACAAAAGTGAAGTACTTCTAAAAATGTTTTGTTTAC
AGGTGGTGTCTGGATACATTGGTTCACACACTGTGGTAGAGCTAATTGAGA
ATGGATATGACTGTGTTGTGCTGATAACCTGTGCAATTCAACTTATGAT
TCTGTAGCCAGGTTAGAGGTCTTGACCAAGCATCACATTCCCTTCTATGA
GGTTGATTTGTGTGACCGAAAAGGTCTGGAAAAGGTTTTCAAAGAATATA
AAATTGATTTCGTAATTCATTGCTGGTTTAAAGGCTGTAGGTGAATCT
ACACAAATCCCGCTGAGATACTATCACAATAACATTTTGGGAAGTGTCTGT
TTTATTAGAGTTAATGCAACAAATACAACGTTTCCAAATTTGTTTTTTCAT
CTTCTGCTACTGTCTATGGTGATGCTACGAGATTCCCAATATGATTCCCT
ATCCCAGAAGAATGTCCCTTAGGGCCTACTAATCCGTATGGTCATACGAA
ATACGCCATTGAGAATATCTTGAATGATCTTTACAATAGCGACAAAAAA
GTTGGAAGTTTGTCTATCTTGCCTTATTTTAACCAATTGGCGCACATCCC
TCTGGATTAATCGGAGAAGATCCGCTAGGTATACCAAACAATTTGTTGCC
ATATATGGCTCAAGTAGCTGTGGTAGGCGCGAGAAGCTTTACATCTTCG
GAGACGATTATGATTCCAGAGATGGTACCCCGATCAGGGATTATATCCAC
GTAGTTGATCTAGCAAAAGGTCATATTGCAGCCCTGCAATACCTAGAGGC
CTACAATGAAAATGAAGGTTTGTGTGCTGAGTGGAACTTGGGTTCCGGTA
AAGGTTCTACAGTTTTTGAAGTTTATCATGCATTCGCAAGCTTCTGGT

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ATTGATCTTCCATACAAAGTTACGGGCAGAAGAGCAGGTGATGTTTTGAA
CTTGACGGCTAAACCAGATAGGGCCAAACGCGAACTGAAATGGCAGACCG
AGTTGCAGGTTGAAGACTCCTGCAAGGATTTATGGAAATGGACTACTGAG
AATCCTTTTGGTTACCAGTTAAGGGGTGTCGAGGCCAGATTTTCCGCTGA
AGATATGCGTTATGACGCAAGATTTGTGACTATTGGTGCCGGCACCAGAT
TTCAAGCCACGTTTGCCAATTTGGGCGCCAGCATTGTTGACCTGAAAGTG
AACGGACAATCAGTTGTTCTTGGCTATGAAAATGAGGAAGGGTATTTGAA
TCCTGATAGTGCTTATATAGGCGCCACGATCGGCAGGTATGCTAATCGTA
TTTTCGAAGGGTAAGTTTAGTTTATGCAACAAAGACTATCAGTTAACCGTT
AATAACGGCGTTAATGCGAATCATAGTAGTATCGGTTCTTTCCACAGAAA
AAGATTTTGGGACCCATCATTCAAAATCCTTCAAAGGATGTTTTTACCG
CCGAGTACATGCTGATAGATAATGAGAAGGACACCGAATTTCCAGGTGAT
CTATTGGTAACCATAACGTATACTGTGAACGTTGCCCAAAAAAGTTTGA
AATGGTATATAAAGGTAAATTGACTGCTGGTGAAGCGACGCCAATAAATT
TAACAAATCATAGTTATTTCAATCTGAACAAGCCATATGGAGACACTATT
GAGGGTACGGAGATTATGGTGCGTTCAAAAAAATCTGTTGATGTCGACAA
AAACATGATTCTACGGGTAATATCGTCGATAGAGAAATTGCTACCTTTA
ACTCTACAAAGCCAACGGTCTTAGGCCCAAAAAATCCCCAGTTTGATTGT
TGTTTTGTGGTGGATGAAAATGCTAAGCCAAGTCAAATCAATACTCTAAA
CAATGAATTGACGCTTATTGTCAAGGCTTTTCATCCCGATTCCAATATTA
CATTAGAAGTTTTAAGTACAGAGCCAACCTTATCAATTTTATACCGGTGAT
TTCTTGCTGCTGGTTACGAAGCAAGACAAGGTTTTGCAATTGAGCCTGG
TAGATACATTGATGCTATCAATCAAGAGAAGTGGAAAGATTGTGTAACCT
TGAAAACGGTGAACTTACGGGTCCAAGATTGTCTACAGATTTTCTCTGA

YBR019C, 699 aa (SEQ ID NO 40)

MTAQLQSESTSKIIVLTGGAGYIGSHTVVELIENGYDCVVDNLSNSTYD
SVARLEVLTKHHIPFYEDLCDRKGLEKVFKEYKIDSVIHFAGLKAVGES
TQIPLRYYHNNILGTVVLLLELMQQYNVSKFVSSSATVYGDATRFPMIP
IPEECPLGPTNPYGHTKYAIENILNDLYNSDKKSWKFAILRYFNPIGAHP
SGLIGEDPLGIPNNLLPYMAQVAVGRREKLYIFGDDYDSRDGTPIRDYIH
VVDLAKDGHIAALQYLEAYNENEGLCREWNLGSGKGSTVFEVYHAFCKASG
IDLPHYKVTGRRAGDVLNLTAKPDRAKRELKWQTELQVEDSCKDLWKWTTTE
NPFQYQLRGVEARFSAEDMRYDARFVTIGAGTRFQATFANLGASIVDLKV
NGQSVVLGYENEELNPD SAYIGATIGRYANRISKGFSLCNKDYQLTV
NNGVNNANHSSIGSFHRKRFLGP I IQNPSKDVFTA EYMLIDNEKDTEFP GD
LLVTIQYTVNVAQKSLEMVYKGKLTAGEATPINLTNHSYFNLNKPYGDTI
EGTEIMVRSKKSVDVDKNMIPTGNIVDREIATFNSTKPTVLGPKNPQFDC
CFVVDENAKPSQINTLNNELTLIVKAFHPDSNITLEVELSTEPTYQFYTG
FLSAGYEARQGFAIEPGRYIDAINQENWKDCVTLKNGETYGSKIVYRFS

YDR345C, 2204 bp, CDS: 501-2204 (SEQ ID NO 123)

TCTTAGCTATATTCTTCCAGCTTCGCCTGCTGCCCGGTTCATCGTTCCCTGT
CACGTAGTTTTTCCGGATTTCGTCCGGCTCATATAATACCGCAATAAACAC
GGAATATCTCGTTCCGCGGATTTCGGTTAAACTCTCGGTCGCGGATTATCA
CAGAGAAAGCTTCGTGGAGAATTTTCCAGATTTTCCGCTTTCCCGGATG
TTGGTATTCCGGAGGTCATTATACTGACCGCCATTATAATGACTGTACA
ACGACCTTTCGGAGAAAGAACTCAATAACGATGTGGGACATTGGGG
GCCCACTCAAAAAATCTGGGGACTATATCCCAAGAGAATTTCTCCAGAAG
AGAAGAAAAGTCAAAGTTTTTTTTTCGCTTGGGGGTTGCATATAAATACAG
GCGCTGTTTTATCTTCAGCATGAATATTCCATAATTTTACTTAATAGCTT
TTCATAAATAATAGAATCACAAACAAAATTTACATCTGAGTTAAACAATC
ATGAATTCAACTCCAGATTTAATATCTCCACAAAAGTCAAGTGAGAATTC
GAATGCTGACCTGCCTTCGAATAGCTCTCAGGTAATGAACATGCCTGAAG
AAAAAGGTGTTCAAGATGATTTCCAAGCTGAGGCCGACCAAGTACTTACC
AACCCAAATACAGGTAAAGGTGCATATGTCACTGTGTCTATCTGTTGTGT

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TATGGTTGCCTTCGGTGGTTTCGTTTTCGGTTGGGATACGGTACCATTT
CTGGTTTTCGTCGCCCAAACCTGATTTCTTGAGAAGATTCCGGTATGAAGCAT
AAAGATGGTAGTTATTATTTGTCTAAGGTTAGAACTGGTTTAAATTGTCTC
CATTTTTCAACATTGGTTGTGCCATTGGTGGTATTATTTTGGCTAAATTGG
GTGATATGTACGGTCGTAAAATGGGTTTGATTGTCGTTGTTGTTATCTAC
ATCATCGGTATTATTATTCAAATTGCATCCATCAACAAATGGTACCAATA
TTTCATCGGTAGAAATTATTTCCGGTTTGGGTGTTGGTGGTATTGCCGTTT
TATCTCCTATGTTGATTTCTGAAGTCGCTCCTAAGGAAATGAGAGGTACT
TTAGTCTCCTGTTACCAACTGATGATTACCTTGGGTATTTTCTTGGGTTA
CTGTACCAACTTCGGTACTAAGAACTACTCCAACCTCTGTGCAATGGAGAG
TTCCATTAGGTTTGTGTTTTGCCTGGGCTTTGTTTATGATCGGTGGTATG
ACTTTCGTTCCAGAATCCCCACGTTATTTGGTTGAAGCTGGTCAAATTGA
CGAAGCAAGAGCATCTCTTTCCAAAGTTAACAAGGTTGCCCCAGACCATC
CATTCATTCAACAAGAGTTGGAAGTTATTGAAGCTAGTGTGAAGAAGCT
AGAGCTGCTGGTTTCAGCATCATGGGGTGAGTTGTTCACTGGTAAGCCGGC
CATGTTTAAGCGTACTATGATGGGTATCATGATCCAATCTCTACAACAAT
TGACTGGTGATAACTATTTCTTCTACTATGGTACTACCGTTTTTAACGCT
GTTGGTATGAGTGATTTCTTTCGAACTTCTATTGTTTTCGGTGTCTGTC
CTTCTTCTCTACTTGTGTTCTTTGTACACTGTCGATCGTTTTGGACGTC
GTAAGTGTGTTTATATGGTGCCATTGGTATGGTCTGCTGTTATGTAGTT
TACGCTTCTGTTGGTGTCAACAGACTATGGCCAAATGGTGAAGGTAATGG
TTCATCCAAGGGTGCTGGTAAGTGTATGATTGCTTTGCCCTGTTTCTATA
TTTTCTGTTTTGCTACCACTTGGGCTCCAATTGCTTATGTTGTTATTTCT
GAAACTTTCCCATGAGAGTCAAGTCTAAGGCTATGTCTATTGCTACAGC
TGCTAATTGGTTGTGGGGTTTCTTGATTGGTTTCTTCACTCCATTTATTA
CTGGTGCTATTAACTTCTACTACGGTTACGTTTTTCATGGGCTGTATGGTT
TTCGCCCTACTTCTACGTTTTCTTCTTTGTGCCAGAACTAAGGGTTTGAC
TTTGGAAGAAGTCAATGATATGTACGCTGAAGGTGTTCTACCATGGAAGT
CTGCTTCATGGGTTCCAACATCTCAAAGAGGTGCTAACTACGATGCTGAT
GCATTGATGCATGATGACCAGCCATTCTACAAGAAAATGTTCCGGCAAGAA
ATAA

YDR345C, 567 aa (SEQ ID NO 124)

MNSTPDLI SPQKSSSENSNADLPSNSSQVMNPPEEKGVQDDFQAEADQVLT
NPNTGKGAYVTVSICCVMAFGGFVFGWDTGTISGFVAQTDFLRRFGMKH
KDGSYYLSKVRTGLIVSIFNIGCAIGGIILAKLGDYGRKMGLIVVVVIY
IIGIIIIQIASINKWYQYFIGRIISGLGVGGIAVLSPLMISEVAPKEMRGT
LVSCYQLMITLGI FLGYCTNFGTKNYSNSVQWRVPLGLCFAWALFMIGGM
TFVPESPRYLVEAGQIDEARASLSKVNKVAPDHPFIQQELEVIEASVEEA
RAAGSASWGELFTGKPAMFKRTMMGIMIQLSLQQLTGDNYFFYYGTTVFNA
VGMSDSFETSIVFGVVNFSTCCSLYTVDRFGRNCLLYGAIGMVCCYV
YASVGVT RLWPNGEGNGSSKGAGNCMIVFACFYIFCFAT' TWAPIAYVVIS
ETFPLRVKSKAMSIATAANWLWGFLIGFFT PFITGAINFYGYVFMGCMV
FAYFYVFFVFPETKGLTLEEVNDMYAEGVLPWKSASWVPTSQRGANYDAD
ALMHDDQPFYKKMF GKK

YKR097W, 2150 bp, CDS: 501-2150 (SEQ ID NO 263)

ATAGGAAAAAACCGAGCTTCTTTTCATCCGGCGCGCTGTGTTCTACATA
TCACTGAAGCTCCGGGTATTTTAAGTTATACAAGGGAAAGATGCCGGCTA
GACTAGCAAGTTTTAGGCTGCTTAACATTATGGATAGGCGGATAAAGGGC
CCAAACAGGATTGTAAAGCTTAGACGCTTCTGGTTGGACAATGGTACGTT
TGTGTATTAAGTAAGGCTTGGCTGGGGATAGCAACATTGGGCAGAGTATA
GAAGACCACAAAAAAAAGGTATATAAGGGCAGAGAAGTCTTTGTAATGTG
TGTAAC'TTCTCTTCCATGTGTAATCAGTATTTCTACTTACTTCTTAAATA
TACAGAAGTAAGACAGATAACCAACAGCCTTTCCAGATATACATATATA
TCTTTATTTT CAGCTTAAACAATAATTATATTTGTTTAACTCAAAAATAAA

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AAAAAAAAACCAAACTCACGCAACTAATTATTCCATAATAAAATAACAAC
ATGTCCCCCTTCTAAATGAATGCTACAGTAGGATCTACTTCCGAAGTTGA
ACAAAAATCAGACAAGAAATTGGCTCTTAGTGACGAAGTCACCACCATCA
GACGCAATGCTCCAGCTGCCGTTTTGTATGAAGATGGTCTAAAAGAAAAAT
AAAACGTGCATTTTCATCAAGCGGTGCATTGATCGCTTATTCGGGTGTTAA
AACCAGGAAGATCTCCAAAGGACAAACGTATTGTTGAAGAACCTACCTCGA
AAGACGAAATTTGGTGGGGTCCGGTCAATAAACCATGTTCTGAAAGAACA
TGGTCTATCAACCGTGAAAGAGCTGCAGATTACTTGAGAACAAGAGACCA
CATTTATATTGTTCGATGCATTTGTCAGGATGGGATCCAAAAATACAGAATCA
AAGTCCCGGTTGTTTGTGCCAGGGCTTACCACGCTTTATTCATGACAAAT
ATGCTTATTAGACCTACAGAAGAAGAAATTAGCCCATTTTGGAGAACCTGA
TTTACTGTCTGGAAACGCTGGTCAGTTCCAGCCAAATTTACACACCCAGG
ATATGTCCTTCAAAGAGTACTATAGAAATTAACCTTCAAAGCAATGGAAATG
ATCATTTTATAGGTACCGAATACGCCGGTGAAATGAAAAAAGGTATTTTCAC
AGTTATGTTTTTACTTGATGCCTGTGCACCATAACGTTTTAACTTTGCACT
CTTCCGCCAACCCAGGGTATTCAAAACGGTGACGTTACTTTATTCCTTTGGC
CTAAGTGGTACCGGGAAAACCACTTTATCCGCAGACCCACATAGATTGTT
GATCGGCGATGATGAACATTGTTGGTCCGACCATGGTGTCTTCAATATCG
AAGGTGGTTGTTACGCCAAGTGATTAAATTTATCTGCCGAAAAGGAGCCT
GAAATTTTCGACGCTATCAAGTTTGGTTCTGTATTAGAAAACGTTATCTA
TGACGAGAAGTTCGCATGTAGTCGACTATGACGACTCTTCTATTACTGAAA
ATACTAGATGTGCCTACCCAATTGACTACATTCCAAGTGCCAAGATTCCA
TGTTTTGGCGGACTCTCATCCAAAGAACATTATCCTGCTAACTTGTGATGC
TTCCGGGTGTTTTACCACCAGTATCTAAATTGACTCCTGAACAAGTCATGT
ACCATTTTCATCTCTGGTTACACTTCTAAAATGGCTGGTACTGAGCAAGGT
GTCCTGAACCTGAACCAACATTTTCATCTTGTTCGGACAACCCCTTCCCT
AGCCTTGACCCCTATTAGATACGCAACCATGTTAGCTACAAAGATGTCTC
AACATAAAGCTAATGCGTACTTAATCAACACCGGCTGGACTGGTTCTTCC
TACGTATCTGGTGGTAAACGTTGCCCATTTGAAGTACACAAGGGCCATTCT
GGATTCTATTTCATGATGGTTCGTTAGCCAAATGAAACGTACGAAACTTTAC
CGATTTTCAATCTTCAAGTACCTACCAAGGTTAACGGTGTTCAGCTGAG
CTTTTGAATCCTGCTAAAACTGGTCTCAAGGTGAATCCAAATACAGAGG
TGCAGTTACCAACTTGGCCAACTTGTTTGTTCAAAATTTCAAGATTTATC
AAGACAGAGCCACACCAGATGTATTAGCCGCTGGTCCCTCAATTCGAGTAA

YKR097W, 549 aa (SEQ ID NO 264)

MSPSKMNATVVGSTSEVEQKIRQELALSDEVTTIRRNAPAAVLYEDGLKEN
KTVISSSGALIAYSVKTGRSPKDKRIVEEPTSKDEIWWGPVKNKPCERT
WSINRERAADYLRTRDHIYIVDAFAGWDPKYRIKVRVVCARAYHALFMTN
MLIRPTEEEELAHFGEPDFTVWNAGQFPANLHTQDMSSKSTIEINFKAMEM
IILGTEYAGEMKKGIFTVMFYLMPVHHNVLTLHSSANQGIQNGDVTLLFFG
LSGTGKTTLSADPHRLIGDDEHCWSDHGVFNIEGGCYAKCINLSAEKEP
EIFDAIKFGSVLENNIYDEKSHVVDYDDSSITENTRCAYPIDYIPSAKIP
CLADSHPKNIILLTCDASGVLPPVSKLTPEQVMYHFISGYTSKMAGTEQG
VTEPEPTFSSCFGPFLALHPIRYATMLATKMSQHKANAYLINTGWTGSS
YVSGGKRCPLKYTRAILDSIHDGSLANETYETLPIFNLQVPTKVNGVPAE
LLNPAKNWSQGESKYRGAVTNLANLNFVQNFKIYQDRATPDVLAAGPQFE

YMR173W, 1793 bp, CDS: 501-1793 (SEQ ID NO 313)

AAACAAGTGTAACATAAATACATTCTGTAAATCTACAAAAATCGTTAGTG
CTGTTTTCTTTTTGAGATTGAAAAGTACGAATCATAACATCTCTTATTC
TGAGAAGGGTGCAATATGACGTAAATCAATGCGTACAAAGCGGTTTCCGGT
GCTGGCCTGGCCCAACACAGTTTTGGCGTGGTTGATTTTAAAAACCTTCG
GGAAGGTGAAAAAACCACTCCGAAGGTTGAGGATGACAAATCGCCCCCTT
AGCTGTGGCCATACAAGCTTGGCACCGACGAAAAAGGGAAAAAGGAAAAG
AATGTCGTACAAGAACTCTTACAACCACGTTGAGATTTTCATTTAACAACG

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CCCCCTTTCCATTATATAAGAAGGCATTAATTTTTATGTAATAAAAAAA
GAATTTCTCGAAAATGCTTACAATTAATTTTTCTTTTGTAGAGTAGGG
CTTTAATAGACTGATATATACGGTATTATAAGTGAACGAAAAAACAGCA
ATGGGTTTATTTGATAAAGTGAAGCAATTTGCTAACAGCAATAATAACAA
CAATGATTCTGGCAATAACAATCAAGGCGATTATGTTACCAAAGCTGAGA
ATATGATCGGCGAAGATAGAGTCAATCAATTCAAAAGCAAAATCGGAGAG
GACAGATTTGATAAGATGGAGTCCAAGGTTTCGTCAACAATTTTCTAATAC
CTCTATAAAATGACAACGACTCCAACAACAACGACTCATATGGTTC TAATA
ACAACGATTCATATGGTTC TAACAACAATGATTCATATGGCTCTAACAAC
AATGATTCATATGGCTCCAACAACAATGATTCATATGGCTCTAACAACGA
TGATTCCTACGGTTCCTTCCAACAAGAAGAAGAGCTCTTATGGTTC TAACA
ATGACGATTCGTACGGCTCCAGCAACAACAATGACTCTTACGGTTCCAAC
ACAATGACTCTTACGGTTCCAACAACAATGACTCTTACGGTTCCAACA
TGACGACTCTTACGGTTTCGTCAAAACAAGAATAAGAGCTCTTACGGTTCCA
ACAATGACGATTCCTTATGGCTCTAACAATGATGATTCATATGGTTCCTTCC
AACAAGAAGAAGAGTTCCTTATGGTTC CAGCAACAACGATTCGTATGGTTC
TAACAACGATGATTCATATGGTTC TAACAACAATGATTCATATGGCTCTA
ACAACGATGATTCCTACGGTTCCTTCCAACAAGAAGAAGAGCTCTTATGGT
TCTAACAATGACGATTCGTACGGCTCCAGCAACAACAATGACTCTTACGG
TTCCAACAATGACGACTCTTACGGTTTCGTCAAAACAAGAATAAGAGCTCTT
ACGGTTCCTTACGCAACGATGATTCCTTACGGATCTTCCAATAACGACGAC
TCTTACGGTTCCTTCCAACAAGAAGAAGAGTTCCTTATGGTTC CAACAATGA
CGATTCCTTATGGCTCTAACAATGATGATTCATATGGTTCCTTCCAACAAGA
AGAAGAGTTCCTTATGGTTC CAGCAACAACGATTCGTATGGTTC TAACAAC
GATGATTCCTACGGTTCCTTCAACAAAAAGAAGAGTTCCTTATGGTTC CAA
CAACGATGATTCATACGGCTCCAGCAACAACAATGACTCTTACGGTTCCA
ACAATGACGACTCTTACGGTTCCTCTAATAGAAACAAGAACCTCTATGGG
TCTTCCAACCTACGGTTCATCCAACAATGATGACTCTTATGGTTCATCTAA
TAGAGGCGGTTCGTAATCAATACGGTGGTGACGACGATTACTAA

YMR173W, 430 aa (SEQ ID NO 314)
MGLFDKVKQFANSNNNNDSGNNNQGDYVTKAENMIGEDRVNQFKSKIGE
DRFDKMESKVRQQFSNTSINDNDSNNNDSYGSNNNDSYGSNNNDSYGSNN
NDSYGSNNNDSYGSNNDDSYGSSNKKKSSYGSNNDDSYGSSNNNDSYGSNN
NDSYGSNNNDSYGSNNDDSYGSSNKNKSSYGSNNDDSYGSNNDDSYGSS
NKKKSSYGSNNNDSYGSNNDDSYGSNNNDSYGSNNDDSYGSSNKKKSSYGS
NNDDSYGSSNNNDSYGSNNDDSYGSSNKNKSSYGSSNDDSYGSSNNDD
SYGSSNKKKSSYGSNNDDSYGSNNDDSYGSNNKKKSSYGSNNNDSYGSNN
DDSYGSSNKKKSSYGSNNDDSYGSSNNNDSYGSNNDDSYGSSNRNKNSYG
SSNYGSSNNDDSYGSSNRGGRNQYGGDDDY

YIL057C, 995 bp, CDS: 501-995 (SEQ ID NO 217)
 CCCAACAGATTTCAAGTCTGTGCGCTTAACCACTCGGCCATAGTGCCTAA
 AACAATGTAGGTTATTTAAGCAAGTATTGTAGATACTTTTCGTAATAAAC
 TACAATGCACCCACGACTCGCGGTGTAATGATGGCATGAAATCATTGAAC
 GAAGTTTTGCGGCTATACGGCTGAAGGACGAGACTAAAGGGACAGGAATT
 ATTAATGCGGGGTATAATTTGAATAGTATTAACGGGCACTGCCGTTTAGC
 CATCAAATGCTATTGTTGGGGTATTCTCTCTACTTTTTGTCTTGGCCTTG
 AACCTTTTCGGCGGTTGGCAATCGTCCGTATATAAGCATCGGCTGTCCCA
 ATCCTCTATTGCCCTTTTCCCTTGACCTCCTTCTCAATTCTTCGTATCT
 TTCGCGTAAAGGTAGATCTTGATTACCTATCTGTGAAACACGATTAAG
 TGCAAACGAAACAACGTACAGTATATAACAAAGTATTTTAAATAATAAGA
 ATGACGAAAAAGGATAAGAAAGCAAAAGGGTCTTAAGATGTCCACCATCA
 TACAAAAAGTGGTGAGTCCCTTAAAGGTTTTTTGAGGATTGTCATGATTTG
 AAACATATTTAAAGGGTGAGACGGAAGATCAAGAGTTGCACCATTGCCAT
 TGCCAACTGAAGTACTATCCACCCTTTGTCCTGCATGATGCGCATGATGA

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TCCGGAAAAGATCAAAGAGACTGCCAATTCGCACTCTAAGAAGTTTGTTTC
GCCATTTACACCAGCATGTTGAGAAGCACCTGCTAAAGGACATCAAAACC
GCTATCAACAAGCCAGAATTGAAATTCCACGATAAGAAAAAGCAGGAATC
CTTTGACCGGATTGTTTGGGAATTATGGCGAAGAAACGGAGTTGAACGCCA
AGAAATTCAAGGTGTCTGTCTGAAGTTGTATGTAAACACGATGGCGCAATG
GTAGATGTTGATTACAAGACAGAACCCTTGCAGCCACTCATCTAA

YIL057C, 164 aa (SEQ ID NO 218)

MTKKDKKAKGPKMSTITTKSGESLKVFEHLDFETYLKGETEDQEFDHVH
CQLKYYPFVLHDAHDDPEKIKETANSHSKKFVRHLHQHVEKHLKDIKT
AINKPELKFHDKKKQESFDRIVWNYGEETELNAKKFKVSVEVVKHDGAM
VDVDYKTEPLQLI

YDR544C, 929 bp, CDS: 501-929 (SEQ ID NO 135)

TAAAGTAGTCGGTACGTACTTTCGTTTTCAATTTCCATGGTGCACAGTAT
CTTAACATATCTGCTTAGTCGAGGAGAACCAGGATTCTGTTTCGTTGCTCAG
CCGCTTCGTGGATATTCTCTTGGATACTTTAAATATGGACCTACGCTTAG
CCTGCGCTTAGCCTACAACCTTCTTCCGCTCTCGAAAAGACCAATATAATA
GAAAGTTATAAATTACATTTCCCTTATTAGGTATACGACCTCGCGCTTCGA
AGTAGAGGAGCCCTTTTGGCGTACCTACATATGGCGCGTCAGACAGACA
AACTTCCCCCAAAAATGTATTACCCCGCCGAATAAGAAAACAGACCCATT
CACCCACGACGTATCAAGTTACTTCCCTTGGTGCAATGTCCCACTATAAAA
AAATTCCTTGACGCTAGATCGTTGGACTAAAATCTGCGTCACAATCGCCT
AAACAGGAAATATTGCCTATTTTCGTACAAGGTTACTTCCTAGATGCTAT
ATGTCCCTACGGCCTTGTCTAACACCATCCAGCATGCAATACAGTGACAT
ATATATACACACCACACCACACCCACACACACCACACCACACCCACCACA
CCCACACCACACCACACCCACACCACACCCACACACCCACACACCCACA
CCAGAGAGAAGCCTAAGCCTAAGACTAAGACAAGCCAAGCCTGACCAACC
TGTCTCTCAAATTACCCTCCATTACCCTACCTCCCCACTCGTTACCCTGA
CTCATTAACATATACACCCCAACCACCATCCATCTCCCTGTGTACTACC
ACCAACCGACCGTCCACCATAACCGTTACCCTCCAATTACCCATATCCAA
CTCCACTACCACTTACCCTACCATCTCCCATCTACTACTCACCATACTAT
TGTTCTACCCACCACTATTGAAACGCTAA

YDR544C, 142 aa (SEQ ID NO 136)

MSLRPCLTPSSMQYSDIYIHTTPHPHTPHHHTHTTPTPTPHPHTHTPT
PERSLSRLRLQAKPDQPVSQITLHYPTSPLVTLTHSTIPPQPPSISLCTT
TNRPSTITVTLQLPISNSTTTYPTISHLLLLTILFYPPLLKR

YKR040C, 1004 bp, CDS: 501-1004 (SEQ ID NO 255)

GGGCTTTTCCAGTGCCGCGGCTCGAGATCCAGGCACCAGGAAGTAGGCA
CGCTGTGTATTCTAACACATTGAAGGGCCTAGGCCGCTGACGTGGGGTC
TAGTTCCACTTTTTTCATTACCTTTTCTCGGTCTTTTCTTGCTCCACAGG
CCGTTAATGGCCTGAAACAGTTTGTGACTTTGGACTTATGATAACGATG
TTTGTCCGGGTGCCACCGGATTCTATCGCGGCGAATCAAGTCTAGTCTGT
TTGCATCCATCAAGGCACTGCTCATTGTGTAAAATTGTTCTACGCTTTTG
TCATCAATCATATCTAAACTCACAGCCGCTAGGGTAGGTGTGCCTGGCAG
TGGTAAGGTAGCCGGCTCGTCTTTGGTCATGCGCCAATACTGTGGAACGG
CCCGCGCGTAGCGTTCTTCCGCTTCAACCTTAGAGCTGATACCTTTTGCC
TGGTCAAAGGCGAAAACGTCTACCTCGCTTTCACTGCTGCTTTTCGCTTTC
ATGACTTCGTTTCAAGCGGTCTCTTTCGCTCTCGGTTGTAACACACTTGT
AGCCTGCTATGCTTTCACCGTACTCGAAAAGCGTAGCCTCATGACTAGTT
GTACCAACGCCCTTTCTTTTCTTTTTTCTCTTGACACTTCGGCGTATT
CATCGCCACTGGTACAAGCCGATGGTGCTTTTTTGCTCATTTTCGTTTT
GACGTTGCGATGGTTTCGCGGACCAATCGCATGGGTGGTGGTGGATGTTG
TCTTTGCTAGTTGCAACGTAGTCTTCTCTCTCTCGGCTTTCTGACGAA

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AATTGGCCTTACGTATCTTTTTTCGGCGTCGTTGTCGTCATCGCTGTTCA
TATAATCGTCGTCACATCATATCGGCGCTTTTACTGCATGCTGCTTTTTGA
AGAGAGTTTCATTGAAAAGTAGTGAAGAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAGGAAAAAGCTTACATACGGAAGAGAAAAAAAAAAAAAAAAAGAAATT
TTAA

YKR040C, 167 aa (SEQ ID NO 256)

MTSFQAVSFALGNTLVACYAFTVLEKRLMTSCTNALSFLFFLLTLRRI
HRHWYKPYGAFLLIFVLTLRWFRGPIAWVVVDVVFASCNVFFSPALSDE
NWPYVSFFGVVVVIAVHIIIVVTHIGAFTACLLKRVSLKSSEEKKKKKKK
KKEKSLHTEREKKKKKF

YNL338W, 659 bp, CDS: 501-659 (SEQ ID NO 337)

TAAAGTAGTCGGTACGTACGTTTCGTTTTCAATTTCCATGGTGCACAGTAT
CTTAACATCTGCTTAGTCGAGGAGAACCAGGATTCTGTTTCGTTGCTCAG
CCGCTTCGTGGATATTCTCTTGGATACTTTAAATATGGACCTACGCTTAG
CCTGCGCTTAGCCTACAACCTTCTCCGCTCTCGAAAAGACCAATATAATA
GAAAGTTATAAATTACATTTCCCTATTAGGTATACGACCTCGCGCTTCGA
AGTAGAGGAGCCCTTTTTGGCGTACCTACATATGGCGCGTCAGACAGACA
AATTTCCCCCAAAAATGTATTACCCCGCCGAATAAGAAAACAGACCCATT
CACCCACGACGTATCAAGTTACTTCCCTTGGTGCAATGTCCCACTATAAAA
AAATTCCTTGACGCTAGATCGTTGGACTAAAATCTGCGTCACAATCGCCT
AAACAGGAAATATTGCCATTATTTTCGTACAAGGTTACTTCCTAGATGCTAT
ATGTCCTTACGGCCTTGTCTAACACCATCCAGCATGCAATACAGTGACAT
ATATATACCCACACCCACACCCACACACCACACCCACACACCCACACCCAC
ACCCACACCCACACACCCACACCCACACCCATCACAACCCCTAACCCCTACC
CTATTCTAA

YNL338W, 52 aa (SEQ ID NO 338)

MSLRPCLTPSSMQYSDIYIPTPTPHHTHTPTPHPHPTHHTHTHNPNT
LF

YJR115W, 1010 bp, CDS: 501-1010 (SEQ ID NO 235)

GCCAGTATCCCTTTCTGAAATAAGCTAAACCCCTTGCAACCACCAGGGTG
CCGCCGTCCCTAATTTCCAGCCTGGCAGCGCGTCGAGTCGCCGAATGTTG
CGGGCGCTGCCCCGCCCCGAACACCGCGCCCCGCCCTGCCTCAGCTTAACC
GAAACCACACGGGTCTGCCATCTTCCATATACCCCTGGCTCTTCTTTCACA
ATGCCCGCTCACAACGCCAACTGCAAAAGAAGCCCGCCCTTAGTCGGTTT
TCCCCACTTTGATATAACCCCCCCCCCCCCCCCCCGCATCAACTGGTAA
TTTAACCCAAACACCACGGGGTCATAATTTAAAAGCGAAAAACCTTAAAG
CGTTCTCGAAGAAATCTTCCCTGTAGATGATGTCGTAGCAAACTTATCTTT
TAGAGTGTTTGTGCTTACTGCATTGTCAGATCAAAATTTACGTAGCCGCC
CTTTTCAACCCCTGTCTGAAGAGTAGCATAACAGCAGCGTAGTGAACGTGC
ATGTTCAAAAATACAGTACAATATTAATATACAATAGTAAGGTGATGAA
CACACACACACACACACACACACACACACACACATATATATATATA
CAGGAGATCAAGTTAGTGTGAGGGGACGACTACTGAGTTTGAAGTTCTTT
AAAGTGTTAAAGTTATTTTTCCCTCTCCACCTCGTTGGCAACCTCTCA
CCCACCGCTTAGCAGCATGCTCCGTACATGACCATACTCAGCAATACT
TATACATAAGCAAGATACGTTCCAAGCTGTCTCAGTGCGCCCTTACTCGA
CACCACCACAGAGAACTTGATCTACGAAAAATGGTGGGCCACGCCAATAT
GCTGGACAGGATCCTCGACGAAATAGACGAAATCGACAGCGAGGTAGTAC
TGTGTGACGCTGCCGATGGTTCTTCTACTGCAGAAGCTCATTCCGCTTCC
CCAGCATCCAGCGACTCTTCTCCTCTCACTAATAACATCCGGCCCATTAG
CATTATGTGA

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YJR115W, 169 aa (SEQ ID NO 236)
MFTNTRTILIIYNSKVMNTHTHTHTHTHTHIYITGDQVSVRGRLLSLKFF
KVLKLFPSPTSLATSHPLSSMSPYMTIPQQYLYISKIRSKLSQCALTR
HHHRELDLRKVMGHANMLDRILDEIDEIDSEVVLCDADGSSTAEHSAS
PASSDSSPLTNNIRPISIM

YBL072C, 1103 bp, CDS: 501-1103 (SEQ ID NO 27)
GTCCTACACACGAGCATCGCTGGGAAAGCTTGAGGGCTTTCTCTTACGCAGTGTTTCATGGTGTTACGGG
ATGGAAGTGTTCATATACGTTATTTACAGGCCTATCTTAAAGTTATAGGAAATTACACTTGCCATTTG
CTTTTTGGTACTCACAAGAAGACGTTATAAACACACCAGGACAAAAAGTATGTGCTATGGTCATATGAG
TAATGGAAGTACATATTATTTTGAATGCTACAGGACCTCTCTTTGAATGGAATAGATAGTGGAAAAAGT
AAACTTAACTAAAAGGGATGATATAAATTGTGACAGGAGCAGTGCACTAACTGAATCCTTTGTGTACC
CCAAAAATCAAGCCTCTTATGAAACGCCGAGTTTTTCACAAGAAGAGATGAAAAGAAACCAAAGCATAT
TTCAAGATAAGAAAAAATTCCGCAACTTTTGTACGTTCTTTATTTTACTAACAAGCGTCATTAAATTT
TCTATTACAGTTACAAAATGGGTATTTCTCGTGATTCTCGTCACAAAAGATCCGCTACCGGTGCCAAGC
GTGCTCAATTCAGAAAGAAGAGAAAGTTCGAATTAGGCCGTCAACCAGCCAACACCAAGATCGGTGCTA
AGAGAAATTCACCTGTAGAACTAGAGGTGGTAACAAGAAATACAGAGCTCTAAGAATTGAAACCGGTA
ACTTTTTCTTGGGCTTCTGAAGGTATCTCCAAGAAGACCAGAATTGCTGGTGTGTTTACCATCCATCCA
ACAATGAATTGGTTAGAACTAACACTTTGACCAAGGCTGCCATTGTCCAAATTGATGCTACTCCATTCA
GACAATGGTTCTGAAGCTCACTACGGTCAAACCTTGGGTAAGAAGAAGAACGTCAAGGAAGAAGAACTG
TTGCCAAGAGCAAGAACGCTGAAAGAAAGTGGGCTGCTAGAGCTGCTTCTGCCAAGATCGAATCTTCCG
TTGAATCTCAATTCAGCGCCGGTAGATTATACGCTTGTATCTCTTCCAGACCAGGTCAATCCGGTAGAT
GTGATGGTTACATCTTGGAAGGTGAAGAATTAGCTTTCTACCTAAGAAGATTGACTGCTAAGAAATAG

YBL072C, 200 aa (SEQ ID NO 28)
MGISRDSRHKRSATGAKRAQFRKKRFELGRQPANTKIGAKRIHSVTRGGNKKYRALRIETGNFSWAS
EGISKKTRIAQVYHPSNNELVRTNTLTAAIVQIDATPFRQWFEAHYGQTLGKKKNVKEETVAKSKN
AERKWAARAASAKIESSVESQFSAGRLYACISSRPGQSGRCDGYILEGEELAFYLRRLTAKK

YBL092W, 893 bp, CDS: 501-893 (SEQ ID NO 33)
TACTGGAGAAGAGTGTGTTGATTCCAGCAGAAGGTAATACGCACCTTTCTCATCTATTTGCAGAATCGTT
TTATTAAATACTTTTAAAGAATTTAGATTTTGATAATTAGTTCATTCTCTTTTACAAAGATAATCACC
AAACAGGGACAATACACTGAACGATAAAAGTATGTGACATATAGAATGCTAGAATGAATAGCCTAGACT
GCATTGTTATGAGAGCAACGTTTGATATTTGTGGCGATTGGAACAAACATAGTACATGCCAAAATGAGA
TGAAATGTCCAATTTGAAC TGATTAACATACACGCGCAAGCTCGTATTTGTTTACTGGTACACCTAGAG
TTAGCCGATCAAAGAGACAGTGGCAGATATATGGGAAAATTTTCTCCGGAAGATTGCATGCGAGAGTCT
CATAACCAGTCATTTCCCAAGATACAATTCTCGGAGCTGTTATACTAACAACTTTTAATTTTCATTTT
TTTTTTTTTTTTGATTAGATGGCCTCCTTACCTCACCCAAAGATTGTCAAGAAGCACACCAAGAAGTTCA
AGCGTCATCACTCTGACCGTTACCACAGAGTTGCTGAAAACCTGGAGAAAGCAAAGGGTATTGACTCTG
TTGTTAGAAGAAGATTCAGAGGTAACATCTCTCAACCAAGATCGGTTACGGTTCTAACAAGAAGACCA
AGTTTTTGTCAACCATCTGGTCACAAGACTTTCTTAGTCGCTAACGTTAAGGATTTGGAAACCTTGACCA
TGCACACCAAGACTTACGCCGCTGAAATTGCTCACAACATCTCCGCTAAGAACAGAGTTGTCATTTTGG
CTAGAGCTAAGGCTTTGGGTATCAAGGTCACCAACCCAAAGGGTCGTTTGGCTTTGGAAGCTTAA

YBL092W, 130 aa (SEQ ID NO 34)
MASLPHPKIVKKHTKKFKRHHS DRYHRVAENWRKQKGIDSVVRRRFRGNISQPKIGYGSNKKTKFLSPS
GHKTFVLVANVKDLETLTMHTKTYAAEIAHNISAKNRVVILARAKALGIKVTNPKGRLLALEA

YBR009C, 812 bp, CDS: 501-812 (SEQ ID NO 37)
GAAAAATCGCCCGGGCATTTCTGTTATCTTCCACGCTAAAAGTCAAGGAGAGATATTACGGCCAGGATCG
CAAAGGTGCAGAGCAAGGAAATGTGAGAAATTGTGAGAACGATAATGTATGGGACAATGCGAAAATGTG
AGAACGAGAGCAAAAATCTTTTTTGTATCTCCCCGCCGAATTTGGAAACCGCGTTCTGAAAACCTTCGCA
TCTTCACATAGTAAAACCTGTTCCGAGCGCTTCTCCCCATAATGGTTAGTGGTAAAAACCGAAGTTGTTT

AC'TTTAGCAAATGCCCGCGAAATACGGTGGTAAATTTGCCACCCCCCTTCCCCATTCAATTGGGTAAAGAC
CAATTTGATGGATAAAATTGGTTGTGGAAAAGGTCTAAATCTCTTTTCCCTATAAAATACCGAGATATTTTTTT
CTATATGATGGTTTCCGTCGCATTATTGTACTCTATAGTACTAAAGCAACAAACAAAAACAAGCAACAA
ATATAATATAGTAAAATATGTCCGGTAGAGGTAAAGGTGGTAAAGGTCTAGGTAAAGGTGGTGCCAAGC
GTCACAGAAAGATTCTAAGAGATAACATCCAAGGTATTACTAAGCCAGCTATCAGAAGATTAGCTAGAA
GAGGTGGTGTCAAGCGTATTTCCTGGTTTGATCTACGAAGAAGTCAGAGCTGTCTTGAAATCCTTCTTGG
AATCCGTCATCAGAGACTCTGTTACC'TACACCGAACACGCCAAGAGAAAGAC'TGTTACTTCTTTGGATG
TTGTTTATGCTTTGAAGAGACAAGGTAGAACCTTATACGGTTTCCGGTGGTTAA

MSGRGKGGKGLGKGGAKRHRKILRDNIQGITKPAIRRLARRGGVKRISGLIYEEVRAVLKSFLESVIRD
SVTYTEHAKRKTTVTSLDVWYALKROGRTLYGEGG

TGCGCTTCTTCTTTTGCCCTGTTTTGCCACGCTGGTTGATACGGGCACGTAACGTAAATTCATTCTTGGTCCCTTTCTAGTGATAAATCTCGCAGAGAGGGCATACTGGTTGTAAAAAGTAGTCGCAACAAGTAAGTCGTAA
AAAAGTAGATGTAATGGAAGGCTTTGAAGGAACGGCTAGCCAGCTTTTCTGTATCATTCCTAGCCTAAT
TGACAGCATCTTGACCTTCTAGTATGGAAGCTTTCAATTTTCAGAAAGCGGTGTTCCCCGCTGCGACGAT
TTAATCCGTACATTTACACATCTGTACATTTTTCATATTCGCAAAACAAAGGTTACTTGAAAAAATCAT
AAAGTTGGCGGCTTCAGGTGGACGCGCTTCACTCATGTAGCTTAACATTCATCCCATTAAGCATTTATG
CATAAATTTTCATGAAGTTTACTTTAATAAAAATTGTTTCATTTGCATAGACAAGAAAGAAAGCAACAAGACA
ACTAAGACTAAGCAACAATGCCAAGTACGTATTAGACTATATCGAAGAGGAGGGAAATTCCTTCACTCTG
ACTCGTTGATTTTGAAGAGGTTCCGGTCCCTATAAAATATTTGAGAATATGAAATTCATAATAGTATA
CCTTCATTGAGTAGCACGACAACAGCCTGAATTACTATCCATATTATGAATATCTTTATTTTACACTGAA
CTCCCGACACTTTCAGTTAAACAGGGATACATTTAGAGATCAAGGTGATCTAATAGGGAACATCTCTCTCG
TAACAAATGGGACAGTATTTTATTTTCCAAAGGCGGATACCTAATTTATGCGTTTTTAAATCATATCTCTACA
ATATTTTATGAGCACTTACTTGGGCCCCTTGCAGACTTTTGTTCGGGGAAAACTTTTGACTAACAAGAAATC
CAATTTTACTTTTTTTTTTTTTTAGGAGCTCCAAGAACTTACTCTAAGACTTACTCTACACCAAAGAGACC
TTACGAATCTTCTCGTTTGGACGCAGAAATTGAAGTTGGCCGGTGAATTCGGTTTGAAGAACAAAGAGAGA
AATTTACAGAAATTTCTTTCCAAATTGCTCAAAATTCGTCTGCTGCCAGAGACTTGTAACTAGAGACGA
AAAGGACCCAAAGAGATTGTTTCGAAGGTAATGCCCTGATCAGAAAGATTGGTTAGAGTTGGTGTCTTGTC
CGAAGACAAGAAGAGTTGGATTATGTTTGGCTTTGAAGGTTGAAGATTTCTTGGAAAGAAGATTGCA
AACTCAAGTCTACAAGTTGGGTTTGGCCAAAGTCTGTCCACCACGCCAGAGTTTTAATCACTCAAAGACA
CATTGCTGTTGGTAAGCAAAATCGTCAACATCCCATCTTTTCATGGTCAGATTGGACTCTGAAAAGCACAT
TGACTTCGCTCCAACTTCTCCATTCGGTGGTGCCTAGACCAGGTAGAGTTGCTAGAAGAAACGCTGCCTAG
AAAGGCTGAAGCTTCCGGTGAAGCTGCTGAAGAAGCCGAAGACGAAGAATAA

MPRAPRTYSKTYSTPKRPYESSRLDAELKLAGEFGLKNKREIYRISFQLSKIRRAARDLLTRDEKDPKR
LFEGNALIRRLVRVGVLSDEKKLDYVLALKVEDFLERRLQTQVYKLGAKSVHHARVLITQRHIAVGK
QIVNIPSMVRLDSEKHIDFAPTSPPGGARPGRVARRNAARKAEASGEAAEEAEDEE

AATCCCTTATTTGTCAGAAATTGAAGCCGTTAATATTTAAAGGCTAATTCCTCCATGCCATCTTGCATTAC
TTTGGTATATATCTCTTGACCTCAATATATCTCGATAATATAAATCGCAATATTATACCTTGTTAGTCTG
ACAGTTTTACACCTGTACATCTTCACCATCACCACACCCTTTTTTTACTGGAGGCAAGGATGAGTTTGAA
TATCGCCTTTTTTCCCAGCCGCTAGAACATGCTCAGAACCGAGGAAAAGCACCCGCTGCCAAACCTCCTTT
GATGTGTTGGCCCACCGCTACTAGTGGCCGTGCTGGAAGCCCAGGCAGCGGTGGGGGCCACAATACGAG
AGCTGGAAAGGTAAACGGTCTCTGCGCCTCTGTGAAATTTTATCACC AATGGAGTGTCTATGTCTGGTAA
AGATAATATAGAAAGTAGTGTGCAATTTTCAGGCATTACCGATTGAACTTTGGAAATAAGAGAACCAAGAC
AAAAATAACTAGCAACAATGGGTAAATCGTATGTCATTTAATCCTATGAATCTACAGCAGCAAGCAATC
ATGGTATCTCAAACCGAACAATCTGTCACAGAAATAAAAAGATTTAAAGACGTGTCAGTGTGAATAAAA
GCAAACATATCATTAGAGCAAAAATATTGGGCAGATAAGATGATGCTAACACTGATTTTGAGAAAAATTACG
TGACATGATAGGCTTTTTAACGGGCTGTAAGTCATTAGTTTACAGTCGTTGCTTTGAAAATTAGTTCAAC

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ATTAGAAGTGTAGTAATTACAAGCCCTTTTTCCAAACATTTCGGTTATGTGCTGGGACGCATCTCAGAAA
CTCGCAAAACAATAGAATACTAACATGATTTCTTATAAATCTTAATTTTGATTTATTTCTTATAATAC
AGACACGGTTACAGATCTCGTACTCGTTACATGTTCCAACGTGACTTCAGAAAGCATGGTGCCGTCCAT
CTTTCTACTTACTTGAAGGTCTACAAGGTTGGTGACATTGTCGACATCAAAGCCAATGGTTCTATCCAA
AAGGGTATGCCACACAAGTTTACCAGGTAAGACCGGTGTTGTCTACAACGTTACTAAGTCTTCTGTT
GGTGTATCATCAACAAGATGGTCGGTAACAGATATCTAGAAAAAGATTAAACTTAAGAGTTGAACAC
ATCAAGCACTCCAAGTGTAGACAAGAATTTTTGGAAAGAGTTAAGGCCAATGCTGCTAAGCGTGCTGAA
GCTAAGGCTCAAGGTGTTGCTGTTCAATTGAAGAGACAACCAGCTCAACCAAGAGAATCCCGTATCGTT
TCTACTGAAGGTAACGTTCCCTCAAACTTTGGCCCCAGTCCCATACGAAACTTTTCATCTAA

YBR191W, 160 aa (SEQ ID NO 62)

MGKSHGYRSRTRYMFQRDFRKHGAHLSTYLVYKVGDIVDIKANGSIQKGMPHKFYQGKTGVVYNVTK
SSVGVIINKMVGNNRYLEKRLNLRVEHIKHSKRQEFLEVRKANAAKRAEAKAQGVAVQLKRQPAQPRES
RIVSTEGNVPQTLAPVPYETFI

YCL035C, 833 bp, CDS: 501-833 (SEQ ID NO 65)

CCGAAAGAAACCCCATGTTCTTGTGTTTGCCTGCCATGCTTTATCCTCTCTCACACTGTCACAAT
CGTGTTGTCTTCATCCTTAGAAAGGATACCACATTGATAAACAACATATATAAAGTTTAACTATTACCT
TGATCCTTTACACGTCAAGGTCAAACAGTTTCATAGTTATCACCTTGAAGTATGGCTCCATCATCTA
TAAACATGAACCTCATGCACAAGTGAGCTGTCTACAGATAACGAGCAGCCGCAACGGCGTTTCCAGAT
TGCGATGCTTGTGTTTCTTTATCTACTACTGCCTTACTACCCCCCTTGCGCCTCCTGATTACGATGATG
GGGAATTTTGTCTTGAAAGGAGTAAATATATAAAATAAATGAAAAGTTTATATAATATAAAAAGGGACT
TTAGCATAAAATAAAGAACTTCGTGCAGTACTTATACGAGCATTCGCATAATTATACAAATAGACAAAA
CCTCAGAAGGAAAAAAATGGTATCTCAAGAACTATCAAGCACGTCAAGGACCTTATTGCAGAAAACG
AGATCTTCGTGCGATCCAAAACGTACTGTCCATACTGCCATGCAGCCCTAAACACGCTTTTTGAAAAGT
TAAAGGTTCCAGGTCCAAAGTTCTGGTTTTCGCAATTGAATGACATGAAGGAAGGCGCAGACATTGAGG
CTGCGTTATATGAGATTAAATGGCCAAAGAACCGTGCCAAACATCTATATTAAATGGTAAACATATTGGAG
GCAACGACGACTTGCAGGAATTGAGGGAGACTGGTGAATTGGAGGAATTGTTAGAACCATTCTTGCAA
ATTAA

YCL035C, 110 aa (SEQ ID NO 66)

MVSQETIKHVKDLIAENEIVASKTYCPYCHAALNTLFEKLVPRSKVLVLQLNDMKEGADIQAALYEI
NQRTVPNIYINGKHHGGNDLQELRETGELEELLEPIAN

YDL004w, 983 bp, CDS: 501-983 (SEQ ID NO 81)

ATAAACATAAGATATAATAGTTTTTAAAATGGTCAACGTATGCGATGCACAACATAAAGGTACCAATTC
ATTAAATATATAATATTTACTTCTTACTATTACACGAAAGACAAGTGTGAAATGCCTAGGAGATTGAT
GATTGACAAGCTCTGGCCTTGCAATAAAAATACTTATACACAACCTTCAAATAATATAGAAAAGAAAGAA
GACTATAAGCTAAAAATGTAGACAACCTCATTTAAATATTTATCTTAGGACTTGGTAATAATAGCTAAT
TTGTATATTATTCACCTCGGTCACCGCCTGTAATCACCTTTAACGAAAATAGATGCCAGCCAATCAAA
GCGCATTATGGAGTCGCTTAGGAAGGGGCCGTCCTCATTTGTAAGTTTCATGTTAAATTAGATGGAG
GATAACAATAAAGGTATCGTACACACACTGCTAAAAGAGCCTCAATCAATTTGTGAAGGTATAACTGTA
GCCGTGAGGATAGGAAAATGTTACGTTCAATTATTGGAAAGAGTGCAATCAAGATCATTTGAATTTCTGTCG
CTAAGCGTTTCATATGCAGAAGCTGCTGCCGCATCATCAGGTTTGAAGTTACAATTTGCTCTACCACACG
AACTTTTATATAGTGGCTCCGAAGTTACTCAAGTGAACCTGCCCTGCTAAGTCAGGACGTATTGGTGTAT
TGGCCAACCATGTTCCACCGTTGAACAATTACTACCAGGTGTCGTTGAAGTTATGGAAGGCTCTAACT
CTAAAAAATTTCTTTATATCAGGTGGATTTGCAACAGTTCAACCAGACTCGCAGTTATGTGTAAGTCAA
TTGAAGCTTTTCCATTGGAATCCTTTTACAAGAAAATATAAAAAATTTGTTGGCAGAAGCTAAGAAGA
ACGTTAGTTTCATCTGATGCCAGGGAAGCCGAGAGCTGCAATTCAGTAGAAGTTTGTAGAAAACCTAC
AATCCGTATTGAAATAG

YDL004W, 160 aa (SEQ ID NO 82)

MLRSIIIGKSASRSLNFVAKRSYAEAAAASSGLKLQFALPHETLYSGSEVTQVNLPAKSGRIGVLANHVP
TVEQLLPGVVEVMEGSNSKKFFISGGFATVQPDSQLCVTAIEAFPLESFSQENIKNLLAEAKKNVSSSD
AREAAEAAIQVEVLENLQSVLK

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YDL075W, 1263 bp, exon1: 501-557, intron1: 558-978, exon2: 979-1263
(SEQ ID NO 85)

ACTATATTTTGTTCCTCCCGAACCTCTCCCTTCTGGGCCCTTTTCCATTATTACACAATATTTTCATAC
CTTTACCTCCGTACACCAATCTTTATTTTACCCCATACCTTTGTATTCTGAAATTGAGAAATGATTT
GTGGTGCCTTTTGGACAATCTGCCTTCGTGGACAGTTTGAACGCTAGGCGACAGTTTGGCAA
CGGAAGGAAGTGGGAGAGCCAGAAAGGCTTCTCTCGATGGTGGATCATTCTTGCAGGCGGAGGAT
GGGAAAGCTCCGTTCAAGTTTGCAGGCTTTCTTCTGGCATTTTCGTTCTCCCAACTGCGCAGGCAGAC
ATAGCTTGACTTTACTCATGCTCGCATTAGGCGGGTTGAATCTCATAGCTTGAAAGATAGTATTGAATT
ATATTGAAGATTTTATAACTAGTGATAATTTCAATCAAGTTTTAAAGAAAGAATTAATAAGCAAACAGA
ACTCAATCAAAGGAAAAATGGCCGGTTTGAAGACGTTGTCACTCGTGAATACACCATTAACCTTGCACA
AAAGAGTATGTGAAAGAATAAAATATAATGCCCAAGGGCTTGTCACTGAATGGTTAATTAAGAAGAT
ATTTCTATAGTCAAGGAATACAATATCAAGAATTTGTACCACAGAAACCTATCAACAAAGATCATTTGAT
CAAGATATATTTTATAATACGGAATTTGAAGACCATAATCAATATTATAACATCCAAGAGGGGAAAGAT
ACACTTCGGCTGGACTTAAAGAGCGATGAAGACAGAAATAGTTATCTTAAATAGTGGAAATCCTAGATTT
TAAGTCGACAATTTATCCATATCCCAAGTTTGACTAAATATGAATCAGAACAATTTGGGTCTCCAATATA
CAAAACCATTCATCAAGATTACACTAATATTAAAATGAACAATCGTTACTAACAAAAATTTACCATTT
TATTTTAAATAGTTGCACGGTGTCTCCTTCAAGAAGAGAGCTCCAAGAGCTGTCAAGGAAATTAAGAAG
TTCGCCAAGTTACACATGGGTACTGATGATGTCCGTCTAGCTCCAGAATTGAACCAAGCTATCTGGAAG
AGAGGTGTCAAGGGTGTGAATACAGATTGAATTTGAGAATTTCCAGAAAGAGAAACGAAGAAGAAGAC
GCCAAGAACCCATTTGTTCTCCTACGTTGAACCTGTCTTAGTTGCTTCTGCCAAGGGTCTACAACTGTT
GTTGTCTGAAGAAGATGCTTAA

YDL075W, 113 aa (SEQ ID NO 86)

MAGLKDVVTREYTLNLHKRLHGVSFKKRAPRAVKEIKKFALHMGTDVRLAPELNQAIWKRGVKGVEY
RLRLRISRKRNEEDAKNPLFSYVEPVLVASAKGLQTVVVEEDA

YDR064W, 1495 bp, exon1: 501-521, intron1: 522-1060, exon2: 1061-1495
(SEQ ID NO 89)

TGACGGTCGTTTACAGGAATGGAAGATGCTTTATGCCGGCGCATTAGAAATGATCAGAGAGGAGTGCG
GTACTTTTAAATTGATAGAGGTTTCTTCAGGTTTGGAGGATGACTCAGACGTTGAAGAATTGAGGGAGC
AATTAGAAAAATGTTAGTATAGTCTATCTTAAACATAAACTACCTCCTATAATCATGTAGTGACTTT
AAACATTTTTTTATCTTTCATAGCAATAATAAGCCTTTTACCACCCATAAAACATAAAGTAGACCCAA
ACATTTTTTAAAAAAATTTTACGTTATAATTTTTTCTTTTGTCTGTTTCTTGAGCGCGCAAAGTAGCGGT
GAAATTTTGATACGAATGAGATTTCCACTTCTGTACAGATGGAAATTTATGTTGGCCGACATATATCAC
AGTCGTGATTGAATTAACAATTTCTTTCTCATTAATATTTATTTCTAAACGGTTAACCACATAATCAATC
AACAACAATCAGTCAAAATGGGTGCTATGCACAGTGCCGTATGTTTATTAACACCATAGCGAGATATTA
ATGCAAAAGTTGCATTGAATAGTTTCGCTAAATCAGATGACACTCTAATGTGGAATTCAAAAGTGGATTT
CTAATATAATTTGTCTCTGTCTCGGATCACAATTTCTATTACAAGTTCCGGTGTGTACACAGGTATAGTTTA
TACTGGAGAGTAGTTTCTACTCGCTGTACATTAGCTGGGTGATTCCAATTTCTTTTACAAATATGTTGC
ATTAGTTTAAACAGGTTATACTATCTGCCGTTTCTCAGTATAATTTACGCCGGAATAATTAAGTGGCTA
GCCGCCCTTTATGAATTAGTTTTCACAAAGCTCATAACATAACACGTTAACCCTATCGGAGGAGAACCAAG
ATTGAAGAATCACCCGGAATAGTTATACTTTAATGGAATTTGTATGGTCTGAACGAGGAAATATGTCATG
ATACACTTTTCTTCAAGCCATATGAATCTTCATGTTACTAACATTTCGATAAATTTTTTGGAAATATCCAA
TTCCACTAAATATTACTTTTAAACAGGGTAAAGGTATTTCTTCTCTGCTATTCCATACCTCTAGAAATGC
TCCAGCTTGGTTCAAGTTGTCTCTGAATCTGTCAATGAACAAATGTCAAGTACGCGAGAAAGGGTTT
GACTCCATCTCAAATGGTGTCTTGTGAGAGATGCTCACGGTGTACCCAAAGCTCGTGTATCACTGG
TAACAAGATCATGAGAATCTTGAAGTCCAATGGTTTGGCTCCAGAAATCCCAGAAGATTTGTACTACTT
GATTAAGAAGGCTGTCTCTGTGTTAGAAAGCACTTGGAAAGAAACAGAAAGGACAAAGACGCTAAGTTTCA
ATTGATTTTGATTCGAATCTAGAATTCACAGATTGGCCAGATACTACAGAATGTTGCTGTCTTACCACC
AAACTGGAAGTACGAATCCGCCACTGCCTCCGCTTTGGTCAACTAG

YDR064W, 151 aa (SEQ ID NO 90)

MGRMHSAGKGISSAIPYSRNAPAWFKLSSESIVIEQIVKYARKGLTPSQIGVLLRDAHGVTVQARVITGN
KIMRILKSNGLAPEIPEDLYYLIKKAIVSVRKHLERNRKDKDAKFRLLILIESRIHLARYYRTVAVLPPN
WKYESATASALVN

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YDR099W, 1322 bp, CDS: 501-1322 (SEQ ID NO 93)

TTGTTACGACCAATCCGTAATTCAAGCGTGGGTATTCATATGACCAGAGATAATAATACAGCGAATACT
ATTGAAATCGTCCCTTTTTTGTAGGAAGAACGGACAAATCGGTCGTCTGCTCGAAATGATTAGTAGT
GTGTCACCCGGATCAGCAAAATGACACACAGAAATACGAGGAAAAAGTCGGTCGAAAGGGGCAAATGT
TATTATAAGTCCCTCCAGTAGTCTTTTTTTTTTCAAATATTCATCATCAAAGGTTACGAAATCTTTTGA
GCTATCTTAAACATTCGTTCTTTTTATCAAATTTCAATTACTAACTTATTTTTTCAAAAAAATTGCCCT
CTCCCGGTTTTTAATCATTATTTTTTTCGATTGATTAAGGGGGAAAAGCAAAGAACGAGAAAACCTTGGA
CAGAAGGTAAATACTCTGACAATTTCAAACGAAGTAAAAAGAAAAATTATCAAATCAACAAAAAGTAC
CCGTTACAACAAAAAAATGTCCCAAACCTCGTGAAGATTCTGTTTACCTAGCTAAATTAGCTGAACAAG
CCGAACGTTATGAAGAAATGGTCGAAAACATGAAGGCCGTTGCTTCATCAGGTCAGAGCTTATCTGTCTG
AAGAACCGGAATCTATTTGTCGGTTGCTTACAAGAACGTCATCGGTGCTCGCCGTGCTTCATGGAGAATAG
TTTCTTCGATCGAACAAAAAGAAGATCAAAGGAGAAATCTGAACATCAAGTTGAATTAATCCGTTCTT
ACCGTTCTAAAAATTGAAACTGAATTGACCAAAATCTCTGACGACATTTTATCTGTGTTAGATTCTCATT
TAATCCCTTCTGCTACTACTGGTGAGTCTAAAGTATTTTACTATAAGATGAAGGGTGACTACCACCGTT
ATTTAGCTGAATTTTCCAGCGGAGATGCAAGAGAAAAGGCAACCAACTCCTCTTTGGAGGCTTATAAAA
CCGCTTCCGAAATCGCCACAACCTGAATTGCCTCCAACCTACCCAATTCGTTTAGGTCAGCTTTGAATT
TCTCCGCTCTTCTATTACGAAATTTCAAACCTCTCTGATAAGGCTTGCCACTTGCCCAAACAAGCCTTTG
ATTAGCTATTGCTGAGTTAGATACTTTATCTGAAGAATCATACAAGGATAGCACTTTGATCATGCAAT
TATTAAGGGACAACCTTGACCTTATGGACCTCTGATATTTCTGAATCTGGTCAAGAAGATCAACAACAAC
AACAACAACAGCAACAGCAACAGCAACAACAGCAACAACAAGCTCCAGCTGAACAACTCAAGGTGAAC
CAACCAAATAA

YDR099W, 273 aa (SEQ ID NO 94)

MSQTREDSVYLAKLAEQAERYEEMVENMKAVASSGQELSVEERNLLSVAYKNVIGARRASWRIVSSIEQ
KEESKEKSEHQVELIRSYRSKIETELTKISDDILSVLDShLIPsATTGESKVFYKYMKGDYHRYLAEFS
SGDAREKATNSSLEAYKTASEIATTELPPTHPIRLGLALNFSVFYIEIQNSPDKACHLAKQAFDDAIAE
LDTLSEESYKdstLIMQLLRDNLTLWTSdISESGQEDQQQQQQQQQQQQQQQQAPAEQTQGEPTK

YDR134C, 701 bp, CDS: 501-701 (SEQ ID NO 97)

GGAGTTTTCTATTTTCAATTTGATGGCTGGGTTTGGAGCTGCAGGACACGCTGCAGTGGGGAAGCCCTTT
TAAATCCGCGAGTCCGGTCCGTGCTCACTTTTAGACGCGTGTTCATCGGCGTTCGGATGGTTTCCAGT
GAGAAAAGGGGCTACGCGTATGGTCGGTAGTCCCTTTTCAGGGACCAGTGCAGAGGGTGAATCAACGGCC
CCTTCACAGAAACCGCGCAGGAATTTTCTGGTGTTGTTATTTTTTTTTTCTTTGTACTTATCTCACTT
TTCTTTTCTTAATTTTTTTTTTGAATTTTTTGTGTACACTTTCCACAACATATAGGATGGTTTAGT
CATCTCTCGAAGTATATAAACCGTTGCTGGATCGTGGTTGTTCTTCATCGACTTCTCTCTGCTAGACTC
TCTTTTTTAAAAATTTTTTTCATAGAATAAAAAACCAAGGATAACAAACATCTTCTTTTCGTTTCGCTTCAA
ATAACTACAAATTAATAATGCAATTTCTTACCGTCGCTTCTATCGCTGCTATTGCCGCTGTTGCCCTCCG
CCGCTTCTAACATTACCACTGCTACTGTACAGAGAATCTACCACTTTGGTCACTATCACTTCTTGTG
AGGACCACGTTTGTCTGAAACAGTTTCCCCAGCTTTGGTTTCCACTGCTACCGTCACCGTAAATGACG
TTATCACTTAA

YDR134C, 66 aa (SEQ ID NO 98)

MQFSTVASIAAIAAVASAASNITTATVTEESTTLVTITSCEDHVCSETVSPALVSTATVTVNDVIT

YDR171W, 1628bp, CDS: 501-1628 (SEQ ID NO 103)

CTGGGGTTGGGTAAACAAGTGAGCAAGGGAAGTGAACATTTTAAGAAGAACAATAAAATAGCAAGAG
ATGGAATGGTAATGCTTGGCTCTCGAGAAGAGTAGCATAAAACGAGACTTGTTTAAACAGGATATGAC
ATACTTCAATTCAGCTTTCCCTATCAGCCGCTCGAGCAGTTATATAGGTGTGTTGCCGGAGTAATTTGG
CGGAGGCCAACAGTGGCTAGGCGGCAACGCCTGGAACACGCGCTTAAAGTTCTGGAAGGTTCCGGAAT
TGAGAACTGCTCAGGGGCGAATACAGGGGCGGCTTGGCGGCAGGGGGAGGCCTCTGTGAAGTTAGTT
ATATAAGACTTGTGTCATCGTTTTTTTTGATCCCGGCAGGAACCTATCTTTTATTCTCATACATACGGTC
AAGAAGTATAATTATACATAACATAGGGACAGTTTCAGGCAATTGTCCATATCCACACAAATTAAGAT
CATACCAAGCCGAAGCAATGAGTTTTTATCAACCATCCCTATCTTTTATGACGTTTTGAACGCATTAT
CCAACCAAACCTGGCCAGAGAGGGCAGCAAGGATATCCTCGCCAACCACAAAGGCCACAGAGATACCATC
CCCATTATGGACAAGTGCACGTTGGCGGGCATCATCTCGTCATCATCCATTGTATAGCAGATACAATG

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GTGTTCCCTAATACCTATTACTACCAGTTCCTGGACAAGCCTATTACTATAGTCCTGAATACGGTTATG
ATGACGAGGATGGTGAAGAAGAGGACCAAGACGAAGATATGGTGGGTGACAGCGGCACTACAAGACAGG
AAGATGGTGGCGAGGACAGCAACTCGAGAAGATATCCATCATATTACCATTGTAATACTGCCAGGAATA
ATAGGACCAACCAACAGGCAAACAGTTTAAACGACTTATTAACCGCGTTAATAGGTGTTCCACCATATG
AAGGCACTGAACCAGAAATTGAAGCAAATACCGAACAGGAGGGCGAAAAGGGAGAAGAAAAGGATAAGA
AGGATAAGTCTGAAGCACCCAAAGAGGAAGCTGGCGAAACCAACAAAGAAAAACCTTTGAATCAGCTGG
AGGAATCGTCGAGACCACCATTAGCCAAAAAATCTTCATCGTTTCGCTCACCTACAAGCGCCTTCCCCAA
TACCTGACCCGTTACAAGTATCCAAGCCTGAAACGAGAATGGACTTACCATTTTCACCAGAAGTGAATG
TCTATGATACCGAGGACACTTACGTAGTTGTTCTTTCGCTTACCAGGTGCTAACTCTAGGGCTTTCCACA
TTGATTACCATCCATCTTCTCATGAGATGCTCATCAAGGTAAGATCGAAGACAGAGTGGGCATTGATG
AAAAATTCTTGAAGATCACGGAATAAAATATGGTGCCTTTGAGAGAACCCTTAAATTTCCCGTGCTGC
CACGCATTAAGGACGAAGAAATTAAAGCTACTTACAACAACGGTCTACTACAAATTAAGGTGCCTAAAA
TTGTCAATGACACTGAAAAGCCGAAGCAAAAAAGAGGATCGCCATTGAGGAAATACCCGACGAAGAAT
TGGAGTTTGAAGAAAATCCCAACCTACGGTAGAAAATTGA

YDR171W, 375 aa (SEQ ID NO 104)

MSFYQPSLSLYDVLNALSNTGTGQRGQQGYPRQPQRQRYHPHYGQVHVGGHHPRHHPLYSRYNGVPNTY
YYQFPQAYYYSPYGYDDEDEGEEDQDEDMVGDSGTTTRQEDGGEDSNSRRYPSYHCNTARNNRNTNQ
ANSLNDLLTALIGVPPYEGTEPEIEANTEQEKEGEEKDKDKSEAPKEEAGETNKEKPLNQLEESSRP
PLAKKSSSFAHLQAPSPIPDPLQVSKPETRMDLPFSPEVNVYDTEITYVVVLALPGANSRAFHIDYHPS
SHEMLIKGKIEDRVGIDEKFLKITEKYGAFERTVKFPVLPRIKDEEIKATYNNGLLQIKVPKIVNDTE
KPKPKKRIAIEEIPDEELEFEENPNPTVEN

YDR399W, 1166 bp, CDS: 501-1166 (SEQ ID NO 129)

TCGTTTATCCTTTTTTGAACATGTCATCTGGCATCGTTAACAGTAAGGCCATCTGGAACATCAAGCAAGCAC
TCCACTTTTACGTCACAACCATAGTTGGTTAACTAAGAAAAGACAGTACATATTTCCCTTCCGAGTCAC
TTATTTTTTTTTTCTTCTGAAAAAATTAATTAGATTAATTTCAATTAATATCATTTCGCTTATCTGAC
TTCTTTTCATTTTTTTTCTCTATATTTTCGCGTTTACTAGGAAAGAAAAGGAAAAAAATTTTTCCCCCTC
CATCTGTCCCAAATCGGGTAGCGATGAGCTGCTATAGAATTTTCTATTTAAACATGTTTGATAAGCCCA
ATTTCCGTTAGATTTTGTTCCTTTCGAGTTTGGTTTGGCGTAACTTTTTTATTTTAGTCTCCATCT
AGCTGGAGTAATACGATGTAGTGCCTTGTAATCTTTCTTATTTTTATATTACCGTTCGTGTTTCATTATA
TCCATTACGTTCCCATATGTCGGCAAACGATAAGCAATACATCTCGTACAACAACGTACATCAACTAT
GTCAAGTATCCGCTGAGAGAATTAAGAATTTCAAGCCGGACTTAATCATTGCGTGGTGGTGGTT
TCATTCCTGCTAGGATCCTACGTACGTTCTTAAAGGAGCCCGCGTGCCAACCATCAGAATTTTTTGCTA
TTATTTTGTCTTTGTACGAAGATTTGAACAGTGTAGGCTCAGAAGTTGAGGAAGTTGGTGTTAAGGTTA
GCAGAACACAATGGATTGATTACGAGCAATGTAAATTAGATCTAGTCGGCAAGAAGCTTCTTATCGTTG
ACGAAGTCGATGACACCCGTACCACACTTCATTACGCTTTGAGTGAATTGGAAAAGGATGCAGCTGAAC
AGGCAAAGGCTAAAGGTATCGATACTGAAAAGTCTCCAGAGATGAAAACAACTTCGGGATTTTTGTTC
TACACGATAAGCAAAAACCAAAGAAAGCAGATTTGCCTGCCGAAATGTTGAATGACAAGAACCCTTATT
TTGCAGCTAAACCTGTTCCAGACAAGTGGTATGCATATCCATGGGAATCTACTGACATTGTTTTCCATA
CTAGAATGGCTATTGAACAGGGCAATGACATCTTTATTCCTGAGCAGGAACACAAGCAATGA

YDR399W, 221 aa (SEQ ID NO 130)

MSANDKQYISYNNVHQLCQVSAERIKNFKPDIIAIGGGGFIPARILRTFLKEPGVPTIRIFAILLSLY
EDLNSVGSEVEEVGVKVSRTQWIDYEQCKLDLVGKNVLIVDEVDDTRTTLHYALSELEKDAAEQAKAG
IDTEKSPMKTNFGIFVLHDKQPKKADLPAEMLNDKNRYFAAKTVDPKWYAYPWESTDIVFHTRMAIE
QGNDIFIPEQEHKQ

YDR418W, 998 bp, CDS: 501-998 (SEQ ID NO 131)

TGCACTGTGGATGTTTGGGTGTGTATTTTGCCTTTCATAACATACAGATATTTTGTTTAAGGAAGTGAA
ATAAACAATATCATAAAACAGGTACTTCATAGACCATAAAGCATAACCCAGATTATCCTCTTAGATAGC
AATGCTAATGTAAACAGAGATCCGTTTGCCTGACTTTATACTAATATGATATGCTACTTCGCTTTGTG
TTCGAGCAGCTGGCAGTCCCCCTTAGCCGCTTTTTTCCCTTTCCGAAGGTTTCCGCCTAAGCCCCCTG
GCTCTAGGCCGAGAAAATGTTAATGCTCCTTCTACGAGAAAATGCTTGTGCGCCACACCAGGACAGGTGC
TCGACGACGCTTCCGCTAATCTTTCTCAATGTTGTATCTTCTTTGGCGGTACATTACTAGTATGAAAAT
GGAATAAAAACAGTACCTAAATTATTTACTTACTTCCCGTTAAAGCAACCCCAAGTGCCCAATAGAAGG

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ATAAATCAATAGTCAATATGCCTCCAAAGTTTGTATCCAAATGAAGTTAAGTACTTGTACTTGAGAGCTG
TCGGTGGTGAAGATCGGTGCTTCCGCCGCTTGGCTCCAAAGATCGGTCCATTGGGTTTATCCCCAAAGA
AGGTTGGTGAAGATATCGCCAAGGCCACCAAGGAATTCAAAGGTATCAAAGTTACTGTCCAATTGAAAA
TCCAAAACAGACAAGCTGCTGCTTCTGTTGTTCCATCTGCTTCTTGGTCACTACTGCTTTGAAGG
AACCACCAAGAGACAGAAAGAAGGATAAGAACGTCAAGCATAGCGGTAACATCCAATTGGATGAAATTA
TTGAAATTGCCAGACAAATGAGAGACAAATCCTTCGGTAGAACTTTGGCTTCCGTTACTAAGGAAATTT
TGGGTACTGCTCAATCTGTCGGTTGTCGTGTTGATTTCAGAACCCTCATGACATCATTGAAGGTATTA
ACGCTGGTGAATTTGAAATTCAGAAAATAA

YDR418W, 165 aa (SEQ ID NO 132)

MPPKFDPNVYLYLRAVGGVGVGASAAAPKIGPLGLSPKKVGEDIAKATKEFKGIKVTVQLKIQNRQA
AASVVPSSASLVITALKEPPRDRKDKNVKHSNIGLDEIIEIARQMRDKSFGRTLASVTKEILGTAQS
VGCRVDFKNPHDIEGINAGEIEIPEN

YDR513W, 932 bp, CDS: 501-932 (SEQ ID NO 133)

TCTCCCTCTCCTGCCATATAACCCCACTGGTATTTTCCAATGCCTTATTGTTGGAAACCTGATCTTTAT
ACCATTCCTGCACCTTTCACAGGGTCATTGCCGTGGATAATACAAAACCTGAATTTGGACACCTGCTTGT
CACATGATGTAAATCTCCATATCTGTAATAGCTTCTAAATTGCCCTCCAATCGAATAGCAACTCGTCA
GTTGATCAAATGCCTCTCGGCAACTCATCGTTGTCGGATATTTTGTACTCATCCTTTCCTGTTTCTTCC
TCAAGCTGCTCTCTTTTACCCTAATAGAACCATCGCCTCCCTCTTGATTTATGCTAATACCACATCCAA
TAGCAGAACTATTACTAAGATCCGATATTTTCGGCCCCCTTCGCAAGGGGGCCCGCCGCACTTTCTTCAT
GAATTTTCATATAAAAAGTCCCAGGACGCCAAGAAAAGGTGCCCTCTTGATTAACGGACACTCCAATA
CTGTTATATATTGTTTCATGGAGACCAATTTTTCCTTCGACTCGAATTTAATTGTTATTATCATTATCA
CGTTGTTTGGCACAAGAATTATTGCTAAAAGATTTTATCTACTCCAAAATGGTATCCCAGGAAACAG
TTGCTCACGTAAAGGATCTGATTGGCCAAAAGGAAGTGTTTGTTCAGCAAAGACATACTGCCCTTACT
GTAAAGCTACTTTGTCTACCCTCTTCCAAGAATTGAACGTTCCCAAATCCAAGGCCCTTGTGTTGGAAT
TAGATGAAATGAGCAATGGCTCAGAGATTCAAGACGCTTTAGAAGAAATCTCGGGCCAAAAAAGTGTAC
CTAACGTATACATCAATGGCAAGCACATTGGTGGTAACAGCGATTTGGAAACTTTGAAGAAAAATGGCA
AGTTAGCTGAAATATTGAAGCCGGTATTTCAATAG

YDR513W, 143 aa (SEQ ID NO 134)

METNFSFDSNLIVIIITLFPATRIIAKRFLSTPKMVSQETVAHVKDLIGQKEVFVAAKTYCPYCKATLS
TLFQELNVPKSKALVLELDEMSNGSEIQDALEEISGQKTVPNVYINGKHIIGNSDLETLLKKNGLAEIL
KPVFQ

YEL009C, 1346 bp, CDS: 501-1346 (SEQ ID NO 139)

AGTTTCACTAGCGAATTATACAACCTACCAGCCACACAGCTCACTCATCTACTTCGCAATCAAAACAAA
ATATTTTATTTTAGTTTCAGTTTATTAAGTTATTATCAGTATCGTATTAAAAAATTAAAGATCATTGAAA
AATGGCTTGCTAAACCGATTATATTTTGTGTTTAAAGTAGATTATTATTAGAAAATTATTAAGAGAATT
ATGTGTTAAATTTATTGAAAGAGAAAATTTATTTTCCCTTATTAATTAAAGTCCTTTACTTTTTTTGAA
AACTGTCAGTTTTTTGAAGAGTTATTTGTTTGTGTTACCAATTGCTATCATGTACCCGTAGAATTTTATT
CAAGATGTTTCCGTAACGGTTACCTTTCTGTCAAATTATCCAGGTTTACTCGCCAATAAAAAATTTCCCT
ATACTATCATTAATTAATCATTATTATTACTAAAGTTTTGTTTACCAATTTGTCTGCTCAAGAAAATA
AATTAAATACAAATAAAATGTCCGAATATCAGCCAAGTTTATTTGCTTTAAATCCAATGGGTTTCTCAC
CATTGGATGGTTCTAAATCAACCAACGAAAATGTATCTGCTTCCACTTCTACTGCCAAACCAATGGTTG
GCCAATTGATTTTGTATAAATTCATCAAGACTGAAGAGGATCCAATTATCAAAACAGGATACCCCTTCGA
ACCTTGATTTTGTGTTTGTCTCTCCACAAACGGCAACTGCACCTGATGCCAAGACCGTTTTTGCCAATTC
CGGAGCTAGATGACGCTGTAGTGAATCTTTCTTTTCGTCAAGCACTGATTCAACTCCAATGTTTGAGT
ATGAAAACCTAGAAGACAACCTCTAAAGAATTGACATCCTTGTTTGACAATGACATTCCAGTTACCACTG
ACGATGTTTTCATTGGCTGATAAGGCAATTGAATCCACTGAAGAAGTTTCTCTGGTACCATCCAATCTGG
AAGTCTCGACAACCTTCATTCTTACCCACTCCTGTTCTAGAAGATGCTAAACTGACTCAAAACAAGAAAGG
TTAAGAAACCAAAATTCAGTCGTTAAGAAGTCACATCATGTTGGAAAGGATGACGAATCGAGACTGGATC
ATCTAGGTGTTGTTGCTTACAACCGCAAAACAGCGTTTCGATTCCACTTTCTCCAATTGTGCCCGAATCCA
GTGATCCTGCTGCTCTAAAACGTGCTAGAAACACTGAAGCCGCCAGGCGTTCTCGTGCGAGAAAGTTGC
AAAGAATGAACAACCTGAAGACAAGGTTGAAGAATTGCTTTCGAAAAATTATCACTTGGAAAATGAGG
TTGCCAGATTAAAGAAATTAGTTGGCGAACGCTGA

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YEL009C, 281 aa (SEQ ID NO 140)

MSEYQPSLFALNPMGFSPLDGSKSTNENVASASTSTAKPMVGQLIFDKFIKTEEDPIIKQDTPSNLDFDF
ALPQTATAPDAKTVLPIPELDDAVVESFFSSSDSTPMFEYENLEDNSKEWTSLFDNDIPVTTDDVSLA
DKAIESTEEVSLVPSNLEVSTTSFLPTPVLEDAKLTQTRKVKKPNSVVKKSHHVGKDDESRDLHLGVVA
YNRKQRSIPLSPIVPESSDPAALKRARNTAARRSRARKLQRMKQLEDKVEELLSKNYHLENEVARLKK
LVGER

YGL123W, 1264 bp, CDS: 501-1265 (SEQ ID NO 163)

TGGCTTATTCACTAAGGATTCCTTAAGGTTTTCTTAATAGTTTTCTACGTCGGCATGCGATTGTTTGGTT
TAGAAGACTGCTTTCTAAATATGGTTGGGTGTATTTAAGCTAGACCCATACACCCGCTCTATGGGATTA
TTTACTTGTGTTGAATTTTAAGATTTGTGATAATGGAAGTGGACGCAAAACATTTGATGGAAAACGCATGT
CATCATTAACGAGGTAACGTAGGTATCTGTCTGCTTGTAGTATTGCACGCAGCTTCCCAGGACGCCTAG
CTATTTTTTTCATCTATTCCCCTCTGTAGTAACGTAAAGATTTTCAAGTTTTTAATTCAGACTTTCTCTT
CCTTTGTTTCCAATTTCCCTTCTTACTGCTTGATACCTTTTCAATCCCAAAGAAACCGTGTCTTTATA
TATTGTCGATTGAAAGTTACCTACATCAACTTTCCGTGTTCATTCGACTATAACAAACAACCAATAA
GCTCAACTAATTAAGTAATGTCTGCTCCAGAAGCTCAACAACAAAAGAGAGGTGGTTTCCGGTGGCCGTA
ACAGAGGCCGTCCAAACAGAAGAGGACCAAGAAACACTGAAGAAAAGGGATGGGTTCAGTTACCAAAC
TAGGTAGATTAGTCAAGGCTGGTAAGATTACCACCTGAAGAAATCTTCTTGCCAGTCA
AGGAATTTCCAAATCATTGACACTTTGTGTGCCAGGTTTGCAAGACGAAGTCATGAACATCAAGCCAGTTC
AAAAGCAAACAGAGCCGGTCAAAGAACCAGATTTAAGGCTGTTGTCGTTGTTGGTGACTCTAACGGTTC
ACGTTGGTTTGGGTATCAAGACCGCCAAGGAAGTTGCTGGTGCCATCAGAGCTGGTATCATTATTGCCA
AGTTGTCCGTTATCCCAATCAGAAGAGGTTACTGGGGTACCAACTGGGTCAACCACATTTCTTTGGCCA
CCAAGACCACTGGTAAGTGTGGTTCCGTCTACTGTTAGATTGATCCCAGCCCCAAGAGGTTCTGGTATCG
TCGCTTCTCCAGCTGTCAAAAAGTTGTTGCAATTGGCTGGTGTGAAGATGTCTACACCCAATCTAACG
GTAAGACTAGAACTTTGGAAAACACCTTGAAGGCTGCTTTCTGTTGCTATTGGTAACACATACGGTTTCT
TGACTCCAAACTTGTGGGCCGAACAACCATTGCCAGTTTCTCCATTGGACATCTACTCCGATGAAGCTT
CTGCTCAAAAGAAGAGATTCTAA

YGL123W, 254 aa (SEQ ID NO 164)

MSAPEAQQQKRGFGGRNRRPNRRGPRNTEEKGWVPVTKLGRVLKAGKITTIIEIFLHSLPVKEFQII
DTLLPGLQDEVNLIKPVQKQTRAGQRTFRKAVVVVGDSNGHVGLIKTAKEVAGAIRAGIIIAKLSVIP
IRRGYWGTLNQGPHSLATKTTGKCGSVTVRLIPAPRSGIVASPAVKLLQLAGVEDVYTQSNKTRTL
ENTLKAFAIGNTYGFLTPNLWAEQPLPVSPLDIYSDEASAQKKRF

YGR209C, 815 bp, CDS: 501-815 (SEQ ID NO 187)

AACATCCAGACTTTTACGGGTGGCAACGGAACCAACGTATTTAGAGATTGTTTTTTGGTCAAGCGAGGA
ACCCCTGTTGGCAAAGTTGCCAGGTATATCATGGGTGGCGAGGTCACCATTGCAAGCATTGAAACCGTT
GGCGGCGTGAGAGTCAGTGAAGAAAGTCTTGTGAGCCCGGTAAGAATGACATACTCGGCTTCAAGATC
GCTCCAAGATCAGCATAACTTGAGTGCCAGTGAATATTAAGTAATCATCAAAGTATATGTGTAATTGTT
TATACTCTTAGTAAAGGATGCTCCCTACAAGGTGGCTCTTTTCTTACTAAGCGCGTTCAGTTTCCAGCC
AGCCGAAAGAGGGATATCAGTATATAAGAAAGCCATTGGGGGATGAAAAGCTGACAAGAGAATAACGA
GGACCAGTTTTTTATTTGTTGTCTAGCAAGAATTATACACGCACACATACACGAGAGTCTACGATATCTT
TAAATAACACATCAATAATGGTCACTCAATTAATCCGCTTCTGAATACGACAGTGCTTTAGCATCTG
GCGACAAGTTAGTCGTTGTTGACTTTTTTGCCACATGGTGTGGGCCATGTAAATGATTGCACCAATGA
TTGAAAAGTTTGCAGAACAATATTCTGACGCTGCTTTTTTACAAGTTGGATGTTGATGAAGTCTCAGATG
TTGCTCAAAAAGCTGAAGTTTCTTCCATGCCTACCCTAATCTTCTACAAGGGCGGTAAGGAGGTTACCA
GAGTCGTCGGTGCCAACCCAGCTGCTATCAAGCAAGCTATTGCTTCCAACGTATAG

YGR209C, 104 aa (SEQ ID NO 188)

MVTQLKSASEYDSALASGDKLVVVDFATWCGPCKMIAPMIEKFAEQYSDAAFYKLDVDEVSDVAQKAE
VSSMPTLIFYKGGKEVTRVVGANPAAIKQAIASNV

YHR039C-B, 1007 bp, exon1: 501-503, intron1: 504-665, exon2: 666-1007
(SEQ ID NO 197)

GTACATGCACCATTCGCTTCAACTGCGTCAGATAGTTGTAGTCCCTCTGGACATAAGCATTTTCGTTTCGT
GCTTGTCTGTCGTCGCCCTGTTTCAACGCCTCACTCGATATATACTCCTTAGGATCATGTGTTTGACCTG

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AGCAATTGTCCCTTGTCTTGTGCTTCTTGGAACTCCAAAGAGCAAGTTTGCACCAAACATCTTGGAC
ACTTGTATTTGAACTCTTTTATTCCGCATACACCACACAACACCGCCATACTTGCAAATTGCCACACCC
TTCCCTATTAAGTGGACTCCTATTCCAGCTCATCTCATCGAATATGAACTTTGACATCCACTATTATTA
CCGCGAATTTTTTTTTTTTTTCAATTTGTTACCCTGCCTTGGGTATCAAAAATTTTCATCTCTAAAAGGGA
GCGTGATAGATAAAGCAATCACACCTTAAACAATACATTTTTTTTTTTTCTGCAATCTCCAAAGTGTGC
AAGGTATACAAAGCAGAATGGTATGTGCCATTACATTACGTGTCAACACTTCTGTCTCTAACAAGCGTT
CTTACTAACATGAAAACTTTTTTAAACTGTGCTCTCTTGTGGACTGGTACCTCGTGACAAAGGTAT
TGGTTTTTTCATTGTTGCTCAGAACTATGTAATATTCTCTTTAGTCCCAAAAAACGGAATTGCCACCC
TACTACAAGCTGAAAAGGAAGCCCACGAAATAGTATCAAAGGCTAGAAAAGTACAGACAAGATAAGTTGA
AGCAAGCCAAGACTGATGCAGCCAAGGAAATCGACTCATACAAAATTCAAAAAGACAAGGAATTGAAGG
AGTTTGAACAAAAGAATGCCGGTGGTGTGGTGAATTGGAAAAGAAAGCAGAGGCTGGTGTGCAAGGTG
AATTAGCTGAGATTAAAGAAAATTGCAGAGAAGAAAAGGATGACGTTGTCAAATTTTGATCGAGACTG
TCATCAAGCCTTCTGCTGAAGTCCATATCAATGCCTTGTA

YHR039C-B, 114 aa (SEQ ID NO 198)

MSQKNGIATLLQAEKEAHEIVSKARKYRQDKLQAKTDAAKEIDSYKIQKDKELKEFEQKNAGGVGELE
KKAEGVQGELAEIKKIAEKKDDVVKILIETVIKPSAEVHINAL

YHR053C, 686 bp, CDS: 501-686 (SEQ ID NO 199)

AACTTCAACGATTTCTATGATGCATTTTATAATTAGTAAGCCGATCCCATTACCGACATTTGGGCGCTA
TACGTGCATATGTTTCATGTATGTATCTGTATTTAAACACTTTTGTATTATTTTTCTCATATATGTGT
ATAGGTTTATACGGATGATTTAATTATTACTTCACCACCCTTTATTTTCAGGCTGATATCTTAGCCTTGT
TACTAGTTAGAAAAAGACATTTTGTCTGTCAGTCACTGTCAAGAGATTCTTTTGTCTGGCATTTCTTCTA
GAAGCAAAAAGAGCGATGCGTCTTTTCCGCTGAACCGTTCCAGCAAAAAGACTACCAACGCAATATGG
ATTGTCAGAATCATATAAAAGAGAAGCAAATAACTCCTTGTCTTGTATCAATTGCATTATAATATCTTC
TTGTTAGTGCAATATCATATAGAAGTCATCGAAATAGATATTAAGAAAAACAACTGTACAATCAATCA
ATCAATCATCACATAAAATGTTTCAGCGAATTAATTAACCTCCAAAATGAAGGTCATGAGTGCCAATGCC
AATGTGGTAGCTGCAAAAATAATGAACAATGCCAAAATCATGTAGCTGCCCAACGGGGTGTAACAGCG
ACGACAAATGCCCCTGCGGTAACAAGTCTGAAGAAACCAAGAAGTCATGCTGCTCTGGGAAATGA

YHR053C, 61 aa (SEQ ID NO 200)

MFSELINFQNEGHECQCQCGSCKNNEQCQKSCSCPTGCNSDDKCPCGNKSEETKKSCCSGK

YHR055C, 686 bp, CDS: 501-686 (SEQ ID NO 201)

AACTTCAACGATTTCTATGATGCATTTTATAATTAGTAAGCCGATCCCATTACCGACATTTGGGCGCTA
TACGTGCATATGTTTCATGTATGTATCTGTATTTAAACACTTTTGTATTATTTTTCTCATATATGTGT
ATAGGTTTATACGGATGATTTAATTATTACTTCACCACCCTTTATTTTCAGGCTGATATCTTAGCCTTGT
TACTAGTTAGAAAAAGACATTTTGTCTGTCAGTCACTGTCAAGAGATTCTTTTGTCTGGCATTTCTTCTA
GAAGCAAAAAGAGCGATGCGTCTTTTCCGCTGAACCGTTCCAGCAAAAAGACTACCAACGCAATATGG
ATTGTCAGAATCATATAAAAGAGAAGCAAATAACTCCTTGTCTTGTATCAATTGCATTATAATATCTTC
TTGTTAGTGCAATATCATATAGAAGTCATCGAAATAGATATTAAGAAAAACAACTGTACAATCAATCA
ATCAATCATCACATAAAATGTTTCAGCGAATTAATTAACCTCCAAAATGAAGGTCATGAGTGCCAATGCC
AATGTGGTAGCTGCAAAAATAATGAACAATGCCAAAATCATGTAGCTGCCCAACGGGGTGTAACAGCG
ACGACAAATGCCCCTGCGGTAACAAGTCTGAAGAAACCAAGAAGTCATGCTGCTCTGGGAAATGA

YHR055C, 61 aa (SEQ ID NO 202)

MFSELINFQNEGHECQCQCGSCKNNEQCQKSCSCPTGCNSDDKCPCGNKSEETKKSCCSGK

YHR056C, 2999 bp, CDS: 501-2999 (SEQ ID NO 203)

ATGTATAGTTAAAGGTAAATTAAC TAGAGAACGTGGGAACAGTTCCGCACTGTGACCACCGGAACGTAC
GTCTGGTTAGCGCAGCATTAGTCCCAGTTACATCCGATTCAAAATGCAACAGCAAGTATTAATTGGGGA
AATCATATCATTTTGAATATAACCTTGGCGTCTACTAAGGATGGTTATACATCCTAGCTCGTGTAGTG
TGATATTTTGCAGGAATGATGCAAAGAGAGGAAGAACAAGAAGAGAGTTGTTGTTTTTAATGTATCTTA
GCAATTTATGAGAGGAGCATTTGTCGTTGTCTGCTGTGACTAGTGCGTAGCTTTGCCGTTTGTTTTTAAT
CATGATGGACATGCAAGTGAGAAAAGTGAGGAAGCCGCCTGCTTGCACCCAATGCAGGAAGAGAAAGAT
CGGGTGCGACAGGGCCAAAACCGATATGTGGGAATTGCGTCAAGTATAACAAGCCGGACTGTTTTTATC

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CAGATGGACCTGGTAAGATGGTCGCTGTGCCCTCTGCGTCCGGGATGTCCACGCACGGCAATGGCCAAG
GTTCCAACCATTTTAGTCAGGGAAACGGTGTAATCAGAAAAACGTAATGATTCAAACGCAGTATCCGA
TTATGCAAACGTCGATAGAGGCATTCAACTTCTCGTTCAACCCCTCTGTGGATACTGCGATGCAGTGGAA
CCAAGGCCGCTAGCTACCAGAATAATAACACCAATAATAACTGCTCCTCGTCAGAATAGTAGTACCG
TTAGTAGTAATGTTTCATGGAAACACTATTGTGAGAAGCGATAGTCCAGATGTGCCCTCCATGGATCAGA
TTAGAGAATATAACACACGATTACAACCTGGTTAACGCTCAAAGTTTTGACTATACAGATAACCCATACT
CTTTTAATGTTGGTATCAATCAAGACTCGGCCGTTTTTCGATCTAATGACTTCTCCGTTTACTCAAGAGG
AAGTATTAATCAAGGAGATAGACTTTTTTAAAAAACAAATTGCTTGATTTACAAAGCTTGCAACTGAAAA
GTTTGAAAGAAAAATCGAATTTAAATGCCGACAATACCACGGCAAACAAAATTAACAAAACAGGTGAGA
ATTCTAAGAAAGGCAAGGTTGACGGTAAAGAGCCGGATTTGATCATCAGACTTCAAGGACTTCTCAGT
CCTCACAAAAATACTTTACAGCGCTCACAATAACAGATGTGCAAAGTTTAGTCCAAGTGAAACCGTTGA
AGGATACCCCCAACTACCTTTTCACTAAAACTTCATCATTTTTTAGAGATCATTATCTTTTCAAGTTCT
ATAATATTTTGCACGATATCTGCCATATTAATCAGTTCAAAGTAAGTCCCTCCTAACAAATAAAAAATCACC
AACAAATATATGGAAGTTTGCAAAGTTAACTTCCACCAAAGCAATAATTATTGAGACACTAAACTCTG
AATCCCTTAACAATCTGAATATTGAAGAATTTTGCCAATCTTTGACAAAACCTCTTACTAGAATTTG
TTCATAACTCTTTTCCAAATGGTGATACCTGTCTTCATTCTCAACGGTCGATCTTCTTTTATCTCAAC
TGACCAAACCTAGGCGAATTAACCTGTGCTTCTACTGTTGTTAAACGATTCAATGACCCATTCAATAAGC
AGGCTATTAATAACCATGTTTTCGGCATTAAATGAATAATTGAGGTTGATTGCAAGCCAAATCACATTGA
TAAACCTGGAATATTATGACCAAGAGACAATCAAATTTATTGCCATCACAAAATTTTATGAATCTCTGT
ACATGCATGATGATCATAAATCAAGTTTAGACGAAGATTTGAGCTGTCTGTTAAGCTTCCAGATAAAAAG
ATTTCAAGTTATTCCATTTTTTGA AAAAATGTATTACTCAAGACATTCGCTTCTAGGTCAGTCTTCAT
TCATGGTACCCGCTGCTGAAAACCTATCTCCGATACCTGCCTCTATTGATACGAACGACATTCCTTTAA
TTGCTAACGATTTAAAATTACTGGAACGCAAGCAAAATTGATAAATATTCTGCAAGGTGTTCTTTCT
ACTTGCCAGTAAATTTAACCAAAATTGAAAGTCTGTTAGAAACCTTGACTATGGGCGTGAGTAATACAG
TAGACTTATATTTTCATGACAACGAAGTCAGAAAAGAATGGAAGACACTTTAAATTTTATCAATACCA
TTGTTTATACAAATTTTTTCTTTTTTGTTCAAAACGAATCCTCTTTGTCCATGGCAGTTCAACATTCTT
CTAACAACAATAAGACCTCGAACTCTGAAAGATGTGCAAAGGATCTGATGAAAATTATTTCTAATATGC
ACATTTTTTACTCAATAACATTTAATTTTATCTTCCCCATAAAGTCGATAAAGTCATTTTCAAGCGGCA
ATAATCGCTTTCATTCTAATGGTAAAGAATTTTTATTTCGCAAATCATTTTATTGAAATCTTACAGAATT
TTATAGCAATCACATTTGCTATTTTCCAACGTTGTGAAGTAATATTATATGACGAATTTTACAAAAATC
TTTCAAATGAGGAGATTAATGTTCAATTGCTATTGATTTCATGACAAGATTTTGGAATTTTAAAAA
TAGAAATTATCGTATCCTTTTTACGAGATGAAATGAATAGCAACGGAAGTTTCAAATCTATTAAAGGTT
TCAACAAGGTTTTGAATCTGATTAAATATATGCTGAGATTTAGCAAGAAAAACAAAATTTTGCGAGAA
ACTCTGATAACAATAATGTTACAGATTATAGTCAGTCGGCGAAGAACA AAAATGTTCTCTTGAAATTCC
CCGTTAGTGAACGAGAAATCTATTTAAATTTAAGGAGATTTTCAAGATTTTATGGAAGAGAAG
TTGTCCAAAGGAGTATAATTATTGACAAGGATTTGGAATCTGATAATCTGGGTATTACTACGGCAAAC
TCAACGATTTCTATGATGCATTTTATAATTAG

YHR056C, 832 aa (SEQ ID NO 204)

MVAVPSASGMSTHGNGQGSNHFSQNGVNVQKNVMIQTQYPIMQTSIEAFNFSFNPSVDAMQWTKAASY
QNNNTNNNTAPRQNSSTVSSNVHGNTIVRSDSPDVPSMDQIREYNTRLQLVNAQSFQDYTDNPYSFNVGI
NQDSAVFDLMTS

PFTQEEVLIDFLKNKLLDLQSLQLKSLKEKSNLNADNTTANKINKTGENSKKGKVDGKRAGFDHQ
SRTSQSSQKYFTALTITDVQSLVQVKPLKDPNYLFTKNFIIFRDHLYLKFYNIILHDICHINQFKVSPP
NNKNHQYMEVCKVNFPPKAIIEIETLNSESLNNLNIEEFLPIFDKTLLEFVHNSFPNGDTCPSFSTVD
LPLSQLTKLGELTVLLLLLNDMSMTLFNKQAINNHVSALMNNLRLIRSQITLINLEYDQETIKFIAITK
FYESLYMHDDHKSSLDEDLSCLLSFQIKDFKLFHFLKMYYSRHSLLGQSSFMVPAENLSPIPASIDT
NDIPLIANDLKLLETQAKLINILQGVPFYLPVNLTKIESLLETLTMGVSNVTVDLYFHDNEVRKEWKDTL
NFINTIVYTNFVQNESSLSMAVQHSSNNNKTNSERC AKDLMKIISNMHIFYSITFNFIFPIKSIK
SFSSGNNRHFHSGKEFLFANHFIEILQNFIAITFAIFQRCEVILYDEFYKNLSNEEINVQLLLIHDKIL
EILKKIEIIVSFLRDEMNSNGSFKSIKGFNKVLNLIKYMLRFSKKKQNFARNSDNNNVTDYSQSAKNKN
VLLKFPVSELNRIYLFKEISDFLMEREVVQRSIIIDKDLESDNLGITANFNDFYDAFYN

YJL138C, 1688 bp, CDS: 501-1688 (SEQ ID NO 223)

CTGTTGAATCATGGTAAAAGAGAAAATCAAAGCACGTTGACCTGGATATAACCTCAGTAGATCGAAAT
GCTTCGCAGAAGAGTACTGCAGAGAAACATGATATTGAGAAACCGACATCTAAGCCGCAATCTGCTTTT

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AAATTTGATTGGGAGTCTACGGATTATTTAGACCGCGTCCAAAGAGCATTCCCAAAGCCTGATACCTGA
TGCCATCCCTCTACCTCTTAGCTATCAATCATTCAACTAACTACTACATAGTATACATTAGCTGTACA
GTCGTACATCAGACGAATACAAAAGGCCGGGTGAAAGCGTTGATTTTGCGTACCTTTTTCTTTTTTC
GAAATTTTTTTATTTTTTTTTTCAGCATCATATATAAAAGAAATCTCATCTCAAGGAGAAGGAAACAGCA
GATCCCAATACACATAGTAGGAAAAAAAAGGTTTCGCTAAACAAAGGACTGGTGTGTACAAGAACTAA
TAAATAGTAATTGCAATATGTCTGAAGGTATTACTGATATTGAAGAATCCCAAATTCAAACCAACTATG
ACAAGGTCGTCTACAAGTTCGATGATATGGAATTGGACGAAAACCTGTTAAGAGGTGTTTTCGGTTACG
GTTTCGAAGAACCATCTGCCATTCAACAACGTGCCATCATGCCTATTATTGAAGGTCACGATGCTTTGG
CTCAAGCTCAATCTGGTACTGGTAAGACCGGTACTTTCTCCATTGCTGCTTTGCAAAGAATTGACACCT
CTGTCAAGGCTCCTCAAGCTTTGATGTTGGCTCCAACCTAGAGAATTGGCTTTGCAAATCCAAAAGGTTG
TCATGGCTTTGGCTTTCCACATGGACATCAAGGTCCACGCTTGTATCGGTGGTACTTCCTTTGTTGAAG
ACGCTGAAGGTTTGAGAGATGCTCAAATCGTCGTTGGTACTCCAGGTCGTGTTTTGACAACATCCAAA
GACGTAGATTTCAGAACTGACAAGATCAAGATGTTTCATCTTAGATGAAGCTGATGAAATGTTGTCTTCTG
GTTTCAAGGAACAAATCTACCAAATTTTACCTTACTTCCACCAACCACTCAAGTTGTTCTATTGTCCG
CCACCATGCCAAATGACGCTTTGGAAGTTACCACCAAATTTATGAGAAACCCAGTTAGAATTTTGGTTA
AGAAGGATGAATTGACTTTTGAAGGTATCAAACAATCTACGTTAATGTTGAAGAAGAAGAATACAAAT
ACGAGTGTGTTGACCGATTTATACGACTCTATCTCCGTTACTCAAGCTGTCATCTTCTGTAACACCAGAA
GAAAGGTGGAAGAATTGACCACTAAGTTAAGAAACGACAAATTTACCGTTTCTGCCATCTATTCTGATT
TACCACAACAAGAAAGAGACACCATCATGAAGGAATTCAGAAGTGGTTCTTCCAGAATTTTGATCTCCA
CTGATTTGTTGGCTAGAGGTATCGATGTTCCAAGTTTCTTTGGTTATTAACCTACGACTTACCAGCTA
ACAAAGAAAACTATATTTACAGAATCGGTAGAGGTGGTTCGTTTCGGTAGAAAAGGGTGTGGCCATCAACT
TTGTTACTAACGAAGACGTTGGCGCTATGAGAGAACTAGAAAAGTTCTACTCCACTCAAATTTGAAGAAT
TGCCATCCGACATTGCTACCTTGTGTAACCTAA

YJL138C, 395 aa (SEQ ID NO 224)

MSEGITDIEESQIQTNVDKVVYKFDDMELDENLLRGVFGYGFEEPSAIQQRAIMPIIEGHDVLAQAQSG
TGKGTGFSIAALQRIDTSVKAPQALMLAPTRELALQIQKVMALAFHMDIKVHACIGGTSFVEDAEGLR
DAQIVVGTGPRVFDNIQRRRFRDQIKMFI LDEADEMLSSGFKEQIYQIFTLPLPTTQVVLVSATMPND
VLEVTTKFMNRNPVRILVKKDELTLLEGIKQFYVNVEEYKYECCLDLYDSISVTQAVIFCNTRRKVEEL
TTKLRNDKFTVSAIYSDLPQQRDTIMKEFRSGSSRILISTDLLARGIDVQQVSLVINYLDPANKENYI
HRIGRGRFRGRKGVAINFVTNEDVGAMRELEKFYSTQIEELPSDIATLLN

YKL060C, 1580 bp, CDS: 501-1580 (SEQ ID NO 239)

TGGGTCATTACGTAAATAATGATAGGAATGGGATCTTCTATTTTTCTTTTCCATTCTAGCAGCCGT
CGGGAAAACGTTGGCATCCTCTCTTTTCGGGCTCAATTGGAGTCACGCTGCCGTGAGCATCCTCTCTTTCC
ATGACTTAACAACCTGAGCAGTAACCAATGGGAAAGCAGTAGCTTAGCGTTGCTCCAAAAAAGTATTGGA
TGGTTAATACCATTGTCTGTCTCTCTCTGACTTTGACTCCTCAAAAAAATAATCTACAATCAACAG
ATCGCTTCAATTACGCCCTCACAAAACTTTTTTCTCTCTCTCTCGCCACGTTAAATTTTATCCCTCA
TGTTGTCTAACGGATTTCTGCACTTGATTTATTATAAAAAGACAAAGACATAACTTCTCTATCAATT
TCAGTTATTGTTCTTCTTCTGCGTTATTCTCTCTGTTCTTCTTTTCTTTTGTTCATATATAACCATAACCA
AGTAATACATATTCAAAATGGGTGTTGAACAAATCTTAAAGAGAAAGACCGGTGTCATCGTTGGTGAAG
ATGTCCACAACCTATTCACTTACGCTAAGGAACACAAGTTTCGCTATTCCAGCTATTAACGTCACCTCTT
CTTCTACTGCCGTGCTGCTTTAGAAAGCTGCTAGAGACAGCAAGTCCCAATCATTTTGCAAACCTCTA
ACGGTGGTGCTGCTTACTTCGCTGGTAAGGGTATCTCTAACGAAGGTCAAAATGCTTCCATCAAGGGTG
CTATTGCCGCTGCCCACTACATCAGATCCATTGCTCCAGCTTACGGTATCCCAGTTGTCTTACACTCTG
ACCACTGTGCCAAGAAAGTTGTTGCCATGGTTGATGGTATGTTGGAAGCTGATGAAGCTTACTTCAAGG
AACACGGTGAACCATTATTCTCTCCCTCCACATGTTGGATTTGTCTGAAGAAACCGATGAAGAAACATCT
CTACTTGTGTCAAGTACTTCAAGAGAAATGGCCGCTATGGACCAATGGTTAGAAATGGAAATCGGTATTA
CCGGTGGTGAAGAAGATGGTGTAAACAACGAAACGCTGACAAGGAAGACTTGTACACCAAGCCAGAAC
AAGTTTACAACGCTTACAAGGCTTTGCACCCAATCTCTCCAACTTCTCCATTGCTGCTGCTTTTCGGTA
ACTGTCACGGTTTGTACGCTGGTGACATCGCTTTGAGACCAGAAATCTTGGCTGAACACCAAAAGTACA
CCAGAGAACAAGTTGGTTGCAAGGAAGAAAAGCCATGTTTCTTTGGTCTTCCACGGTGTCCGGTTCTA
CTGTCCAAGAATTCCACACTGGTATTGACAACCGTGTGTCAAGGTCAACTGGACACTGACTGTCAAT
ACGCTTACTTGACTGGTATCAGAGACTACGCTTTGAACAAGAAGGACTACATAATGTCCCCAGTCGGTA
ACCCAGAAGGTCCAGAAAAGCCAAACAAGAAGTTCTTTCGACCCAAGAGTCTGGGTAGAGAAGGTGAAA
AGACCATGGGTGCTAAGATCACCAGTCTTTGGAACTTTCCGTACCACCTAACACTTTATAA

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YKL060C, 359 aa (SEQ ID NO 240)

MGVEQILKRKTGVIVGEDVHNLFTYAKEHKFAIPAINVTSSSTAVAALAAARDSPKSPIILQTSNGGAAY
FAGKGISNEGQNASIKGAIAAAHYIRSIAPAYGIPVVLHSDHCAKLLPWFDMLEADEAYFKEHGEPL
FSSHMLDLSEETDEENISTCVKYFKRMAAMDQWLEMEIGITGGEEDGVNNENADKEDLYTKPEQVYNVY
KALHPISPNSIAAAGFNCHGLYAGDIALRPEILAEHQKYTREQVGCKEEKPLFLVFHGGSGSTVQEFH
TGIDNGVVKVNLDTDCQYAYLTGIRDYVLNKKDYIMSPVGNPEGPEKPNKKFFDPRVWVREGEKTMGAK
ITKSLETFRTTNTL

YKL097W-A, 779 bp, CDS: 501-779 (SEQ ID NO 245)

AGCTCCGAAGGGCAATTCCACAGGCACTCCGCGGGGGCCCGCCAAGGCCAAAAGGCGTGGAATATGCC
CGTTTTGGGGCCATAACACCCAGTACCACGGCCGGAACGGGCCATATAATAAGTTTTTCACTCTCAAGA
ATGGTAAACGTAAATAGGAACATCCCACTACCTAGAAATTGCGGAAATTTGCGCTTATCATTAGAAA
ATCTGGAACCGTCCTTTTTCTCTTTCTTGCATTTCCCTTTCCGTATTATTGCCATTCTTTAACTGCAT
TTGGGGAACCGTAGACCAAAAGCCAAACAGAGAAATGTAACGTTCTAAAAAAAACAACGAAAAAATT
GAAAAATAAGATACAATAATCGTATATAAATCAGGCTTCTTGTTCATCATTTTTCAATTCTCTTCTTGGC
ATCCCTTTTCTTATCTTTTGTCTTTTCTTCTCATAATCAAGAATAAATAACTTCATCACATTCGCTACA
CATCAACAAGAAAAAAATGCAATTCTCTACTGTCTGCTTCCGTTGCTTTTCGTCGCTTTGGCTAACTTTG
TTGCCGCTGAATCCGCTGCCGCCATTTCTCAAATCACTGACGGTCAAATCCAAGTACTACCACTGCTA
CCACCGAAGCTACCACCACTGCTGCCCCATCTTCCACCGTTGAAACTGTTTCTCCATCCAGCACCGAAA
CTATCTCTCAACAACTGAAATGGTGCTGCTAAGGCCGCTGTCTGGTATGGGTGCCGGTGCTCTAGCTG
CTGCTGCTATGTTGTTATAA

YKL097W-A, 92 aa (SEQ ID NO 246)

MQFSTVASVAFVALANFVAAESAAAIQITDGIQATTTATTEATTTAAPSSTVETVSPSSTETISQQT
ENGAAKAAVGMGAGALAAAML

YKL150W, 1409 bp, CDS: 501-1409 (SEQ ID NO 249)

CCCATCACATCGCATCACATCACATCACTCCCTATTCTGCCCTTTACAGCGCAAAGGAGTCGTGTGTGG
GTGTGTGCTCCTTTTGACGATCATAAGAGTCCATTTCTAGTATGCAAGCTGGTAACAATAGGTGAATGA
ATTAGGTTCAATTTGCGATGACCTTCAGTATCCCTCCACGCAATGCTAAACTATCCCCCTCATTATGACG
CCTATATCGTATAAGGAACCTGTTACCCCTGACAATTCAAACCTCAAAGGTCTAAGACCAACAAGCGT
AGGAACCTATCGCTCGGAGTGTTTCTCCGTTTGAAGAAAGAGAGAAATAAGGGCCCTTGATTGGTGCT
TGTCGAGAGAGGTACGTATATAAGAAATGCAGTTTGTCTCGCAATGCCCGCTTGTGTTAAGTACTCTTACC
TTTTCCCTCAATACTAACGTTTTGAAGCAGCAAACCTAACAATAGTATAACGTATATAGGTTAAATAA
TATTCGAAGTCAAAAACATGTTTTCCAGATTATCCAGATCTCACTCAAAAGCATTACCGATTGCTCTAG
GTACAGTTGCTATAGCAGCTGCTACCGCATTCTATTTTGCAAACCGTAACCAACATTCCTTTGTCTTCA
ATGAATCTAATAAAGTGTTCAAAGGTGATGACAAATGGATCGACTTGCCAATATCTAAATAGAGGAGG
AATCCCACGACACCAGAAGGTTTACTTTTAAGCTGCCTACCGAAGACTCAGAAATGGGGTTGGTCCTAG
CATCTGCTCTGTTTGTCTAAATTTGTACACCAAAGGGATCCAATGTGGTGAGACCATACTCCTGTGA
GTGATCTTTCCAGAAAGGGTCACTTCCAGCTGGTCTGCAAGCATTATGAAGGTGGTAAATGACCTCAC
ATTTATTTGGTCTTAAACCAATGACACCGTTTCTTTCAAGGGTCTTATTATGAATGGAAGTGGAAC
CTAATCAGTTCAAGTCAATCACCTTGTTAGGTGCCGGTACCGGTATCAACCCTCTGTACCAATTAGCTC
ATCATATAGTTGAAAACCCAAACGACAAGACCAAAGTTAACTTGCTATATGGGAACAAGACTCCTCAGG
ACATTTTACTAAGGAAGGAAGTGGATGCGTTGAAGGAAAAGTATCCTGACAAGTTCAATGTTACTTACT
TTGTTGACGACAAGCAAGATGACCAAGACTTTGATGGTGAAATTAGTTTCATCTCCAAAGATTTTATTC
AGGAGCATGTTCCAGGTCCAAAGGAAAGCACATTTGTTTGTCTGCGGTCCCCCACCATTTATGAACG
CTTACTCAGGTGAGAAGAAGTACCTAAGGACCAAGGTGAATTGATCGGTATCTTGAACAATTTGGGCT
ACTCAAGGACCAAGTTTTCAAATTTTAA

YKL150W, 302 aa (SEQ ID NO 250)

MFSRLSRSHSKALPIALGTVAIAAATAFYFANRNQHSFVNESNKVFKGDDKWLDPISKIEEESHDR
RFTFKLPTEDESEMGLVLASALFAKFVTPKGSNVVRPYTPVSDLSQKGHFQLVVKHYEGGKMTSHLFLK
PNDTVSFKGPIMKWKWQPNQFKSITLLGAGTGINPLYQLAHHIVENPNDKTKVNLLYGNKTPQDILLRK
ELDALKKEYPKFNVITYFVDDKQDDQDFDGEISFISKDFIQEHVPGPKESTHLFVCGPPPFMNAYSGEK
KSPKDQGELIGILNLLGYSKDQVFKF

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YKL156W, 1099 bp, exon1: 501-503, intron1: 504-853, exon2: 854-1099
(SEQ ID NO 251)

CGAAAGGTTTCGATCAAAGTTTGGCTCAATCACTGGACACTATTACTTCGAAAGCGCAGTGGGGTTAAC
AGAGACCGTGATGTCGTCAACAAGTATTTGAAGGAAAATGGTTACTATTAAGAAAAATCTCTTTTCTA
GCCATTTTGCCTTTTATATAGTCAAGTATCTATATGTGACAAATACTTCTTCTAAGCTTGGCCTTCTG
ATAGGCTTAGCTTGCAGTGGTTGCAAACATACATAAATCAACAAAAAGTACGGCTTAAAATTTTGGTA
TTCATTTATTTCAACCCGTGCACACTGGAAATAAATCTGTACATAACAGCATATTTTGTTTTGAAGAA
ATTTCTGTGTTTCTCCGATGTGGGAAGAATTTTAGGATCGGCTAAATTTTCGTAAAGTATCAGTAACCTG
GTATCTCTGTATAAGCGGAGTCTAATTTTCGATAACAAGCAACTTCATCGTAACACCTTCCAACAAAGCA
AAGATAGATATCCCAAAATGGTATGTTAGTATCCAATAAATGCAGCGCAACTGGACCAGTGAATAGAAC
AATACATATAGATAAGTCGCAAAAGAAAAGAATACATGTGGTGGAAAATTTTGCACCAAGAGAGGCAAG
AACTATGAAGAAAGACTTTTGAATATTTCAAGCGGTGCTACATATAGTGGATAAGATTTCAGGATGGA
CGTATGAGCTTACAGTTCATTGTAGGGGAATATAAAATTTCTGATGATGGCGAACTTCATTCCCAGCAAC
TCAAGCTATTGTTATTTTCTATTCTGCACCGAGATGAGGAGAAAAAGGAAGTTTACTAACAGTTAGA
TTTATTTCTTATTCTGTCTACAACAGGTTTGTAGTTCAAGATTTATTGCACCCAAGTGCAGCTTCTGAAGC
AAGAAAGCACAAATTAAGACATTAGTCCAAGGTCCAAGATCGTACTTCCTAGACGTTAAGTGGCCAGG
TTGTTTGAACATCACTACAGTTTCTCACACGCCAACTGCAGTTACCTGCGAATCTGCTCAACAAT
TTTGTGCACCCCACTGGTGGTAAGGCAAGCTTTCTGAGGGTACATCTTTCAGAAGAAAGTAA

YKL156W, 82 aa (SEQ ID NO 252)

MVLVQDLLHPTAASEARKHKLKTLVQGPRSYFLDVKCPGCLNITTVFSHAQTAVTCECSTILCTPTGG
KAKLSEGTSFRRK

YLR029C, 1115 bp, CDS: 501-1115 (SEQ ID NO 265)

TCGACACTTACTTAATATGTTTTGCCGCCCTTCATAAGAGGGTGTTCATAAAATTTATTGGGCAAGAAT
GAGATGGACTCGCACCCCTACATGACGTTTAAATATTTAGTGTTAAGGTTTCAGAACATGCACCAGGTGCG
ACATGTGTTGCGATTATCATGACAATGTCTCTATCCGAGATGCATTTGTAGTATCAATTGATGCGTATT
ATGACATGATTTACATAGCATACATCGTCAAACATGATATTATATCTTTTTTGTATAAATGTACGGAT
TTAAAGCTGTGCAATATATTTTCTGAAATTTCTTGGAGCTGACGCAAAATTTTCAAAGGTGCTAAAATT
TTTCAAGATTTCTCACTTTTGCTTGGTAACAAAGAATGATGGCATTGCATTTTACCACCGGTACATTT
AAGTGTCTATTTCTCACGTTTCTTTCCCTATCCTTAAGTAATCTTTTACAATCTAAGAAAACACGATC
AAACAAATAAATCAGCAATGGGTGCCCTACAAATATTGGAAGAATTGCAAAGAAGAAGCAATCTGATG
TTTTGAGATTTCTTGCAAAGAGTCAGAGTCTGGGAATACAGACAAAAGAATGTCAATCACAGAGCCGCTA
GACCAACTAGACCAGACAAGGCTAGAAGATTGGGTTACAAAGCTAAGCAAGGTTTCGTTATCTACCGTG
TCAGAGTTAGACGTGGTAACAGAAAGAGACCTGTTCCAAAGGGTGTACTTACGGTAAGCCAACCTAACC
AAGGTGTCAATGAATTGAAATACCAAAGATCCTTGAGAGCTACCGCTGAAGAAAGAGTTGGTCGTCGTG
CCGCTAACTTGAGAGTCTTGAACCTCTACTGGGTTAACCAAGATTCTACTTACAAGTACTTCGAAGTTA
TCTTGGTCGACCCTCAACACAAGGCTATCAGAAGAGATGCTCGTTACAACCTGGATCTGTGACCCAGTTC
ACAAGCACCGTGAAGCTAGAGGTTTACTGCCACTGGTAAGAAATCCAGAGGTATCAACAAGGGTCACA
AATTCACAACACCAAGGCTGGTAGAAGAAAGACCTGGAAGAGACAAAACACTTTGTCCTTGTGGAGAT
ACAGAAAATAA

YLR029C, 204 aa (SEQ ID NO 266)

MGAYKYLEELQRKKQSDVLRFLQVRVWVEYRQKNVIHRAARPTRPDKARRLGYKAKQGFIYRVRVRRG
NRKRPVPKGATYGKPTNQGVNELKYQRS LRATAEERVGRRAANLRVLNSYWVNQDSTYKYFEVILVDPQ
HKAIRRDARYNWICDPVHKHREARGLTATGKKS R GINKGHKFNNTKAGRRKTWK RQNTLSLWRYRK

YLR038C, 752 bp, CDS: 501-752 (SEQ ID NO 267)

GGAAAGCAAAGCTCTAAATGATAACTCTACAAAAAGTCAGAGAAATCTGTCACTAATTTATTGAAGGA
TGAAGAATTAATGCTTAAAGTCTTAGAGCTTTTGGTGACAAGTGCTGCAAACGCCACAGACCCAATTAA
AGCTACCGATTTCGTGGGACATGTGTTTCCAATTAATACGCTTACTCAAGGAATTAGACAGAGAAAAACA
CACACAATTGGTTCAAAAAGCACTCGAGAGATTCAAATAAATCTATATGACACCATGTATTCTTTACCA
TATAGCTTCATAACATTGACCAATCAATTTTTCAGAAATGCGTCGCGCGTAGTTTTGCCCGATATCCCCA
TCCCTTCAGGATCTTTTAAAGGTGATGAAAGATGCACCAGATAGAAAAGTTGCATTAAATGATTAGCA
GAGATATACAAATATTTTAGTAAGAATACATAAAGTATCTTTGCTTTCACAAATAGGAACAAGCACATA
AATACAGTATAATAGACATGGCTGATCAAGAAAACCTCTCCACTACATACAGTTGGTTTCGATGCTAGAT

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TTCCCCAACAAAACCAAACAAAGCATTGTTGGCAATCTTATGTGGATTATCACAAGTGTGTTAATATGA
AGGGCGAAGATTTTGCTCCGTGCAAGGTCTTTTGAAGACCTATAACGCCTTATGTCCCCTAGACTGGA
TCGAAAAATGGGATGATCAAAGAGAAAAAGGTATTTTCGCAGGTGATATCAACTCAGACTAA

YLR038C, 83 aa (SEQ ID NO 268)

MADQENSPLHTVGFDFARFPQONQTKHCWQSYVDYHKCVNMKGEDFAPCKVFWKTYNALCPLDWIEKWDD
QREKGIFAGDINS

YLR312C, 1697 bp, CDS: 501-1697 (SEQ ID NO 285)

CATCAATTAGGGCAAACCTTGAATAGTCAGCTAGGTCATATATTTAAATCAATTAGCCCTATGACTACA
TTAGGTTTATTGTTAGGTCTTTACGGCTGCATATTTGCTTTTCGCCGTTTCGGCGGGGTCTGCGACGATT
TCTGCGCGGTCTTGTATGGGTGGAGTTGACAGTTAACCCTCCGGACCCCTACCCCGGTGTGCCCCCGG
TCCATCTATCCATTTTGCGGTAACCCCTTTGCGCGACAGCTGCTTATCAAGGTACCTGGATCGAGCCAT
AAAAATTGATCTACACAGATGAGATGGGGCATTGGGATATATTATTAGTCGGAGTATCATTATAGTTAT
TCAGTTTATGCAGGTTACTGGCCAAACGTTTTTCTTCATTTGGAATAATCGTTTAGGAGCTACTGTTTC
CGGTATAAAGTAACAAGCACAGTAGCAGAGTAATACGCAGTGACGATAATAGAGACTAGTAAAAACAGTC
GAGTTGTGCGACCTAAAATGTCAGAAGAAGACGATCATCGAAGTCAGAAATATCTTTGGATAGTTTGCATGAAAGCTCCT
TTGCGAGGAGAGGACGACGAGGACTTCGATGCAGATGTCCTATCGAACACTAGCAGTGAAGAGTCTGCAC
AGATGAATCGTATTTACGATTTTAGAACATCTAATGAATTTAGTAATGCTGGAGTTAATATTGATCAAA
CTGGAGTTCCCACTATTTTACAGAGTCATTTGATACTTTGTCCGGCTCAAATGTTGGCGGAACGGTATTGC
CAAGTATGGAGGGGTGAAACTGAAGGATAGTACGATAAGGAATCTAGCACACTATCGGATCATATCA
TAGATAAAAGTGAGGGTAAATCTGCTAAATTGAAGATGTGGCATGTTATCATGCTATCTTCATTGCTTT
CCATGACCTTTTCATACCTCGCCCTCGAATATTCCCTGACTGGTGATGTGTTGGCAGGTTTTAAATCAC
AACAGTCATTACGTAATAATGAAAGGAAGCTGTTGTACGGCAATATCGATTTTGTGATAAAAAATCTT
ACGATTCATCAAGTGACTCTTTAAGTCAGTGGGCTCCTTCAGGAAAATACTACGTCGACTTCGACAATC
ATATTGCATACCCATTAAAGGATGATGACCTAATGGGCTGGAGACGATACAAAACAGACTTAGTTATTT
TATGGTATACAACAAAAGCTCGAATGAAAGACGGTTGGCACAAGAGAATTAACAAAATAAACGGAGGAA
GAATAAAGTTACACCTATTTCTCAAGAATCTTTTAAATCCGCTCAAGAAAGTTTAAGGGTATTGCATA
AAGAACAGAAACGCCGCTGGAAAAGGCTCTTTGTGCTACTTCATAATAAATACAGGCAATTTTCTCCAC
ATATTAAGGTTATTTTCGATCATTCTTGCCAAAAAGCAAAACAATGTTGGTCGGGATCCAGATTGCAGT
TGCGCAAGCTTCGTTTCAAGTCAATGAAACCATTCCGAGTTTTTCAGTTTAAGGTTTCGCAAAGATACCA
ACTGGTTTGTAAAGCAGCTGAAACGGTTCCGATTGAAATTACAGCATTTCGAGGATGTATAAAGCGATGT
CAGAATGCAGGAAAAAAATTATTTAAGTGCAACACTAG

YLR312C, 398 aa (SEQ ID NO 286)

MSEEDDHWNLVRLRLRKREGEEQSSKSEISLDSLHESSFAGEDDEDFDADVLSNTSSEESAQMNRIY
DFRTSNEFSNAGVNIDQTVPTISESFDTLSGSNVGGTVLPSMEGSKLKDSTIRNSSLSLSDHIIDKSEG
KSAKLKMWVIMLSSLLSMTFSYLALEYSLTGDLVLAGFKSQSLRNNERKLLYGNIDFVDKSYDSSSD
SLSQWAPSGKYVDFDNHIAIYPLKDDDLMGWRRYKTDLVILWYTTKARMKDGWHKRINKINGGRILHL
FLKNSFKSAQESLRVLHKEQKRRWKRLFVLLHNKYRQFSPHIKRYFDHSCQKAKQCWSGSRQLRLKLR
KSMKPFVRVQFKVRKDTNWFVKQLKRFLGLKLQHSRMYKAMSECRKKNYFKCKH

YLR414C, 1292 bp, CDS: 501-1292 (SEQ ID NO 293)

TAGTCAGCCACACATTGACGTACACTGTGAACAGCCTATTTCTTTCCATGTATCTCAGTGCCAGCTTA
TGAGAACTGTACAGCCTCCCACTTGACCCTCAGAGCCCTCTCCACTCCCCCCTCTTTCAACATCGCC
AGATAGCCCGCGTTGAATGGTGCAGGACAAACCCGGCTGGCCTGGCCAGGCAAAAAAGGACGCAGCAGC
CCTCGAGCGTTATTTCCAAATCGGGCGTACTATCAGCCAAGCCAGCTCGGTATTTTTCAGCGTTCTCG
CAGGAAAATTGGCTGAGAAGTATATACGCGAGAATGTTGCTCTTCCATGTCTCAGTAGTCAATGAGT
GTCCAGTGGTGTTCATTCTGGACCAGTTGTTTGGAGTAGAACTAAAAGAACTAGATCAAGATCATA
CAACGCTGCGCAGTAGTGAACCTTGATTAAAGCAATAGAGAACTATTAAGAAAAAAACAAACACATCAT
CGAAGGACGCTATAAGCATGAGGAATTTTTTACAGTTATTTTTCAGCTATATTTTTCGCTAGGAGCAC
TTATATTAGCCATTGTTGCTATGCGCAGGATCAACGAAAAATTACAGTCCCATAAAATAAAATTTACTGTG
CAGAATTGGATCTGTGCGCAGATGAAGGTATCGACGGTGCTCCCTCTTTGAGTTCTGCTACGCTATCTT
CGTTGGGCTGCCCTCATATATAAATATAGGGCTTTGGTCGTACTGTACAGTGGACTCCTCGCATAACA
TCCAATCATGTTCTTCGCCCTCACGGTATCCAGAATTTTAACCTATCGTCATTAGTGTATGACAATATCA

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ACAACAATGAGGCTCTGGAGCTTATGGATTCCGTGGCCAGTGTGTTTTGCCCGAAAACTAAAAAGTA
AAATGACATACTACAACAATTTGGTCAAGTGTATGTTTCATTACCATTCTTATTGGTATTGTCTTGACCT
TTGTGAATCTAGTGTTCAACGTATTGCGCTGGATCATCCACATAAGGCCGCTAACGTGGTTTGGTGCCCT
TTTTTTCATTTTTCGCCTTTGCCGCCCTATTAGTCAGTATAGGTTTCGTGTTTGGGCACTTACTCATACA
TCAAATACATCCTAAAGCATAACTATAGTGATTACGGTATTTCAATGAGCATTGGTAGGAACACCAGG
GTTTGATGTGGGGGGCTGTCGTGGAGCATTACTGAATTTTCATTCTATGGTGTAGCGTGAGATCGAGGC
CCACCGTCATCTATGCGAACGCTCCAATTGAGGAAAAACCATTGATTGTA

YLR414C, 263 aa (SEQ ID NO 294)

MRNFFTLFFAAIFSLGALILAIVACAGSTKNYSPINKIYCAELDLSQMKVSTVLPSSLSSATLSSSLGLPS
YINIGLWSYCTVDSSHNIQSCSSPHGIQNFNLSSLVYDNNINNEALELMDSVASVVLPEKLKSKMTYYN
NLVKCMFITILIGIVLTFVNLVFNVLRWIHIRPLTWFGAFFSFFAFAALLVSIGSCLGTSYIKYILK
HNSYDYGISMSIGRNYQGLMWGAVVGALLNFILWCSVRSRPTVIYANAPIEEKPLI

YMR251W-A, 680 bp, CDS: 501-680 (SEQ ID NO 317)

ATCCCGTTGAAGCAACCGCACTATGACTAAATGGTGCTGGACATCTCCATGGCTGTGACTTGTGTGTAT
CTCACAGTGGTAACGGCACCGTGGCTCGGAAACGGTTCCTTCGTGACAATTCTAGAACAGGGGCTACAG
TCTCGATAATAGAATAATAAGCGCATTTTTGCTAGCGCCGCCGCGCGCCCGTTTCCCAATAGGGAGGC
GCAGTTTATCGGCGGAGCTCTACTTCTTCTATTTGGGTAAGCCCTTTCTGTTTTTCGGCCAGTGGTTG
CTGCAGGCTGCGCCGAGAACATAGTGATAAGGGATGTAACCTTTCGATGAGAGAATTAGCAAGCGGAAA
AAAATATGGCTAGCTGGGAGTTGTTTTCAATCATATAAAAGGGAGAAATTGTTGCTCACTATGTGAC
AGTTTCTGGGACGTCTTAACCTTTTATTGCAGAGGACTATCAAATCATACAGATATTGTCAAAAAAAAA
AAGACTAATAATAAAAAATGAAGTTATCTCAAGTTGTTGTTTCCGCCGTGCGCTTCACTGGTTTTAGTAA
GTGCTGCTAACAGTTCTAACAGCTCAAGCTCAAAGAATGCTGCCCAACCAATTGCCGGTTTAAACAACG
GTAAGGTTGCAGGCGCCGCTGGTGTTGCTCTAGCTGGTGCTTTGGCCTTTTTGATTGTA

YMR251W-A, 59 aa (SEQ ID NO 318)

MKLSQVVVSAVAFTGLVSAANSSNSSSSKNAAQPIAGLNNQKVAGAAGVALAGALAFLLI

YNL030W, 812 bp, CDS: 501-812 (SEQ ID NO 323)

GTTTTGACACCGAGCCATAGCCGTGATTGTGCGTCACATTGGGCGATAATGAACGCTAAATGACCAACT
CCCATCCGTAGGAGCCCCCTTAGGGCGTGCCAATAGTTTCACGCGCTTAATGCGAAGTGCTCGGAACGGA
CAACTGTGGTCGTTTGGCACCGGGAAAGTGGTACTAGACCGAGAGTTTCGCATTTGTATGGCAGGACGT
TCTGGGAGCTTCGCGTCTCAAGCTTTTTCGGGCGCGAAATGCAGACCAGACCAGAACAAAACAACTGAC
AAGAAGGCGTTTAATTTAATATGTTGTTCACTCGCGCTGGGCTGTTGTTATTTCGGCTAGATACATACG
TGTTTGTGCGTATGTAGTTATATCATATATAAGTATATTAGGATGAGGCGGTGAAAGAGATTTTTTTTT
TTTCGCTTAATTTATTCTTTCTCTATCTTTTTCTCTACATCTTGTTCAAAGAGTAGCAAAAAACA
ATCAATACAATAAAATAATGTCCGGTAGAGGTAAAGGTGGTAAAGGTCTAGGAAAAGGTGGTGCCAAGC
GTCACAGAAAGATTCTAAGAGATAACATTCAAGGTATCACTAAGCCAGCTATCAGAAGATTAGCTAGAA
GAGGTGGTGTCAAGCGTATTTCTGGTTTGATCTACGAAGAAGTCAGAGCCGTCTTGAAATCCTTCTTGG
AATCCGTCATCAGGGACTCTGTTACTTACACTGAACACGCCAAGAGAAAGACTGTTACTTCTTTGGATG
TTGTTTATGCTTTGAAGAGACAAGGTAGAACCTTATATGGTTTCGGTGGTTAA

YNL030W, 103 aa (SEQ ID NO 324)

MSGRGKGGKGLGKGGAKRHRKILRDNIQGITKPAIRRLARRGGVKRISGLIYEEVRAVLKSFLESVIRD
SVTYTEHAKRKTVTSLDVVYALKRQGRPLYGFGG

YOL109W, 842 bp, CDS: 501-842 (SEQ ID NO 343)

GGAGGTCTGCTTCACGAGCGCGGTGTGCGCCTAGTATTGCCCGACGGTCCGGGTGCCTATCCCTAGAT
TTCGTCGTGCCCCGACCCAAATAGTTAAACGTGTGGTTTATGGGTGCACCAGGGCTTTATCGTGTTTAA
TATCGATGGCGATTTGTGCTCCAGTGTATTTTTGTATATCCAATTAAGGTTTCTTACCTAATTTTATT
TTTATCATCTTTAGTTAATGCTGGTTTGCTCTGTTTCTGCTGCTTTCTGTGCGGTTCTCCTCTTCTCTT
GTTTCTTCTGTTGTGCCCCATCGCCGATGGGCTTATATGGCGTATATATATAGAGCGAGTTTTTACGT
CGAAGATCATCTCAGTTTGCTTGATAGCCTTTCTACTTTATTACTTTTCGTTTTTAACCTCATTATACTT
TAGTTTTCTTTGATCGGTTTTTTTTCTCTGTATACTTAAAGTTCAAATCAAAGAAACATACAAAACACTAC
GTTTATATCAATTAATAATGTCTGAAATTCAAACAAAGCTGAAACTGCCGCCCAAGATGTCCAACAAA

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AGTTGGAAGAAACCAAAGAATCTTTGCAAAACAAGGGCCAAGAAGTAAAGGAACAAGCTGAAGCTTCTA
TCGACAACCTAAAAATGAAGCTACTCCAGAAGCTGAACAGGTGAAGAAGGAAGAACAAAACATTGCTG
ATGGTGTGCAACAAAAGAAGACCGAAGCTGCCAACAAAGTTGAAGAACTAAGAAGCAAGCTTCCGCCG
CCGTCAGTGAGAAGAAGGAAACCAAGAAGGAAGGCGGTTTCTTGAAGAAATTGAACCGTAAAATTGCTT
CCATTTTCAACTAA

YOL109W, 113 aa (SEQ ID NO 344)

MSEIQNKAETAAQDVQKLEETKESLQNKQVEVKEQAEASIDNLKNEATPEAEQVKKEEQNIADGVEQK
KTEAANKVEETKKQASAAVSEKKETKKEGGFLKKLNRIASIFN

YOR285W, 920 bp, CDS: 501-920 (SEQ ID NO 365)

ACTAGCAAGATGATCGTCAGATATGGTGATTTATTTCCCTGTGCATTGTACTTCAAAGATCATACAGCA
TACTAAGCGCTTTCCAGGGACACCTTCTGTGCGAAAAATATCAGAATTTTTCTTGATTAAACGCAGCATA
TTGAGTATATGAAATTAACGGGACACTGTGTGAAAAATTTGTAGTTGTACTTTTTTGTATCCCCTTTG
GTAGACATATGGACGAATTACTACTAAGATTGGCTTCCATAAGGCCCAAATCCAGATATCACCTACGGT
ATGTCCCTTTTCCCTACTTGCAATGACAAATAATTTGTTATTTATCTTGGAACCTATATAAGTTACATCTG
ATTGCTTTTGTATTTTTTTTGGAGAATATTATTACCCGCGGGAAGGAAGTAAGGGGAGAATTTTTGAG
GTGTATAAAAGAGAGTGGAGGCTTAATCAATCAAAGAATTCTTTCTCGTTTATTTTCAGGGTTTGTGAC
TAAGAAACGATATTAAAAATGTGGAAGGCCGTGATGAATGCTTGGAATGGAACCGAGAGTCAAAGTAAGA
ATGTTTCAAATATTCAATCTTACAGTTTGAAGACATGAAAAGAATCGTTGGAAGCATGATCCTAATG
TGGTTTTGGTAGATGTTAGAGAACCATCTGAGTACTCGATTGTTTCATATTCCTGCTTCCATCAATGTGC
CATATAGATCGCACCCCTGACGCATTTGCCCTTAGATCCCTTAGAATTTGAGAAACAGATTGGCATCCCAA
AACCTGACAGTGCCAAGGAGCTAATATTTTATTTGTGCTTCTGGCAAACGCGGGGAGAAGCTCAAAAAG
TCGCCTCCTCACATGGATATTCAAACACCTCACATATCCTGGCTCTATGAATGATTGGGTTTCTCATG
GGGTGATAAACTTGACTTATAG

YOR285W, 139 aa (SEQ ID NO 366)

MWKAVMNAWNGTESQSKNVSNIQSYSFEDMKRIVGKHDPNVVLVDVREPSEYSIVHIPASINVPYRSH
DAFALDPLEFEKQIGIPKPSAKELIFYCASGKRGEAQKVASSHGYSNTSLYPGSMNDWVSHGGDKLD
L

YOR327C, 848 bp, CDS: 501-848 (SEQ ID NO 369)

GTGTATTATTAAATACGAACAAAATAAAAAATATGCCGACCAATTCTGTAGTAGTACTGTACTATATTGAA
TATTAAGGGTTTTTCTGGTCTTAGCGTATCCCTTTTATCAGTCCGTGGAACAAAGCCACGGGCGGCTGTA
ACAATGACCATGGAATCATTCAGTCGCCCCATAAAGCGCATTCCACGGAGCGTTTTATAGTGATCTTGGTC
ACATGATATACGCGTGACTTTTTTTTTTATTTTTTCTCCCTGTCTTCCGCAAAAGTGGCTCAAAATCTT
CGGATTTTGGCATTATAGCGCAATGGTGCAGCGCAACCAAAACAAACACCAGTTGTGCGACCCAAAAGA
TGCAAAAGCGGGAGCCAGTTAGTTTTCTTCAAGTTTGGTTGAAACAGCCTTTAATATTTTATAGAA
AGGTAACTATCTGCTCAGTGAATAGTATCTGTAAGTCAGGCATACATTCGAAACACTTCCAAATACAA
AATAAGAACGCGCAACGATGTCGTCATCAGTGCCATACGATCCATATGTGCTCCAGAGGAGAGTAAC
CAGGCGCAAACCCAAATTTCCCAAAACAAGACTGCTGCTTTGAGACAAGAGATTGATGACACGGTGGGAA
TAATGAGAGATAATATCAACAAGGTTGCTGAACGTGGTGAAAGGCTAACATCCATTGAGGACAAAGCTG
ATAACTTGGCTATCTCCGCACAAGGATTCAGAGAGGGCGCCAACAGGGTCAGAAAGCAAATGTGGTGGGA
AAGATCTAAAAATGAGAATGTGTTTATTTCTTAGTTGTTATTTTACTAGTGGTAATTATCGTTTCCTA
TCGTCGTCCATTTTACGCTAA

YOR327C, 115 aa (SEQ ID NO 370)

MSSSVPYDPYVPPEESNSGANPN SQNKTAALRQEIDDTVGIMRDNINKVAERGERLTSIEDKADNLAI
SQGFKRANRVRKQMWKDLKMRMCLFLVVIILLVVIIVPIVVHFS

YPL037C, 974 bp, CDS: 501-974 (SEQ ID NO 377)

TCACGGCTGCTCTTCCCTCTTTTTTCGCATATTCTATTTTATCATCGACTTCCCTAATTTCGCACTCGTACC
AAAATGTTAAGCAGTATGGCGAAGAACGTGGCGCGCTGGAGTCGTGAATGTTTGGGTCTTTGATGATGG
ACTACGGTAGTAAGTATGTAGTAGTTGCAACTTCATATGTTCACTTCTGATCCAAGGAAGAGCGGTTAT
GAATTAATCTCTTGGCATGAGCGGACGGGTAAGGGGACACCGCCTTTTCTTCGATGGGAATCAGGGTAA

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TGGTATATGATGGATTATTGTGGAATCATTTAGTACGGCAGATGTTGAAAAAAAAAGCAGAAAATTTTT
GAATTTTTTTTCGTTGACATTGGAAGATTTCTAGTGGAAACAGCTGCAATTGCTTGTTAAGTAGTAACC
CCTCCTTTGTGACAAGAGAGCGAATATTCTTTCTAGGGAGGTTAAGAAATAGAATCTCACACCAGAC
GCGACTCATAATTCATAATGCCAATTGACCAAGAAAAATTAGCTAAGCTACAAAAGTTGTCTGCTAACA
ACAAAGTTGGTGGTACTAGAAGAAAGCTTAACAAGAAGGCAGGCTCTTCTGCCGGTGCCAACAAGGATG
ACACCAAGTTGCAAAGTCAATTAGCTAAGTTGCACGCTGTCACCAATTGACAACGTCGCCGAAGCCAAC
TTTTCAAGGACGACGGTAAGGTCATGCACCTCAACAAGGTCGGTGTCCTAAGTTGCTGCTCAACACAACA
CTTCTGTATTCTACGGTCTACCACAGGAAAAGAACTTGCAAGATTGTTCCAGGTATTATCTCTCAAT
TGGGCCCTGAAGCCATCCAAGCCTTGTCTCAATTGGCTGCCCAATGGAAAAGCACGAAGCCAAGGCTC
CAGCTGATGCTGAAAAGAAGGATGAAGCTATTCCAGAGTTAGTTGAAGGTCAAACTTTTGATGCTGACG
TCGAATAA

YPL037C, 157 aa (SEQ ID NO 378)

MPIDQEKLAQLQKLSANNKVGGRRLNKKAGSSAGANKDDTKLQSQLAKLHAVTIDNVAEANFFKDDG
KVMHFNKVGQVAAQHNTSVFYGLPQEKNLQDLFPGLIISQLGPEAIQALSQLAQMEKHEAKAPADA
EKDEAIPELVEGQTFDADVE

YPL079W, 1404 bp, exon1: 501-511, intron1: 512-932, exon2: 933-1404
(SEQ ID NO 381)

AAATAGGACGAAGAACTTTTTATATACGAGCATTTCCTAATTAGTAGGAAGCGGAAAATAATAATATAA
GAAAGTAAACGCAAAAGATAGGCTGACTGCCCTTCAATTCGACTAGGAGGTGAGGCGACATATTTGTCACC
ATTCAGTTACCGAGATGGTAGAGAGGTGGATGGCTCGGGTGAGCTTGATTGTACACTGCAGCAACGAT
GCTTTTTCTACCCATTTTATGAAGTTTAACATCCGTACCTTTCCACCTCCAAACATTTTTTGTAACTTC
GTCCTTTGAAAAATCAAGAAGTAATAGGTGTGCAGTATAGGGCCGCTTGAGCGCGCAATATCGGTGAGT
GAGGTAAGATCCATCCATACCTTAGCAAAATATGGTAGTGAGGAGGCCAACTGTATTGCGTTAAAGGCCAA
AAGGATTGGTATATACGAATGATTGGTAATTTGAAAAGTAGGTTTCGAATCAAAGAACTGAGACAGTC
AAGGACACTAAACAAAAATGGGTAAATCGTATGTCCATATAACTTCAAAATGAAAATATAGCAGTTGAA
ACATATCAATTAATTCATTATACATCTCCAATAAACATGTATGCAAGAGGAAAGCGTAAATATCTTCGA
TTTCGACAATACTTTGTCTACTGAACTAAAAATGAAAATGAAGTTGAATTTCTCAAAGGAATGTGATGCAA
GTTTCGTTAATTAATATGGTTTGTAGTGGAATTATCATAGTTTGTGATAGATACACACGAGGAGTAGTGA
GCAAAGCAAGTGCAACAGCAATGATATGTTAGCAGGAAAATAATATTATAAATTGGATATTGTGTGTTTT
TTTGATATATGTTTGTGCGAAGCTAATACAGAATGATTACTAACTGGAATTTAAAGCACAAATCATGCTC
TTGGATGATTGATCTATTAAAAAATTATAAACAGACATGGTTACAGATCTCGTACACGTTACATGTTT
CAACGTGACTTCAGAAAGCATGGTGCCGTTCCACATGTCCACCTACCTGAAGATCTACAAAGGTTGGTGAC
ATTGTGCGACATCAAAGCCAAATGGTTCTATCCAAAAGGGTATGCCACACAAGTTCTACCAAGGTAAGACC
GGTGTGCTCTACAACGTTACCAAGTCTTCTGTTGGTGTATCATCAACAAGATGGTCGGTAACAGATAC
TTGGAAGAGAGATTGAACTTGAGAGTTGAACACATCAAGCACTCTAAATGTAGACAAGAATTTTTTGAA
AGAGTTAAGGCCAATGCTGCTAAGCGTGCTGAAGCCAAGGCCCAAGGTGTGCTGTCCAATTGAAGAGA
CAACCAGCTCAACCAAGAGAATCCCGTATTGTCTCTACTGAAGGTAACGTTCCCTCAAACCTTTAGCTCCA
GTTCCATACGAAACCTTCATTTAA

YPL079W, 161 aa (SEQ ID NO 382)

MGKSHGYRSRTRYMFQRDFRKHGAVHMSYLYKIIYKVGDIVDIKANGSIQKGMPhKFYQGKTGVVYNVTK
SSVGVIINKMVGNRYLEKRLNLRVEHIKHSKRQEFLEVRKANAAKRAEAKFAQGVAVQLKRQPAQPRE
SRIVSTEGNVPTLAPVPYETFI

YBL109W 836bp CDS: 501 836 (SEQ ID NO 35)

CATCGCTTGATTTCGGCCTGCAAAAATAAAGTAGTCGGTACGTACTTTTCGTTTTCAATTTCCATGGTG
CACAGTATCTTAACTATCTGCTTAGTCGAGGAGAACCAGGATTCTGTTCGTTGCTCAGCCGCTTCGTGG
ATATTCTCTGGATACCTTAAACATGGACCTACGTTCCGCTCTCGAAAAGACCAATATAATAAAAAGTT
ATAAATTACATTTCCCTTATTAGGTATACGACCTCGCGCTTCGAAGTAGAGGAGCCCTTTTTGGCGTACC
TACATATGGCGCGTCAGACAGACAACTTCCCCAAAAATGTATTACCCCGCCGAATAAGAAAACAGAC
CCATTCAACCCACGACGTATCAAGTTACTTCCCTTGGTGCAATGTCCCACATATAAAAAAATTCCTTGACGC
TAGATCGTTGGACTAAAATCTGCGTCACAATCGCCTAAACAGGAAATATTGCCATTTTTTCGTACAAGGT
TACTTCTTAGATGCTATATGTCCCTACGGCCTTGTCTAACACCATCCAGCATGCAATACAGTGACATAT
ATATATACCTTAACACTACCTTAACCTACCTTATTTCAACCTTCCAACCTGTCTCTCAACTTACCT
CACATTACCTTACCTCTCCACTTGTACCCTGTCCCATTTCAACCATACCTTCCCAACCATCCATCCATC

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CCTCTACTTACTACCACCAATCAACCGTCCACCATAACCGTTACCCTCCAATTAGCCATATTCAACTTC
ACTACCACCTTACCCTGCCATTACTCTACCATCCACCATCTGCTACTCACCATACTGTTGTTCTACCCCTC
CATATTGA

YBL109W 111aa (SEQ ID NO 36)

MSLRPCLTPSSMQYSIDIYPNTTLLPYFNPSNLSLNLPSHYPTSPLVTLSSHSTIPLPTTIHPSTYYH
QSTVHNRYPPISHIQLHYHLPCHYSTIHHLLLTILFYPPY

YHR094C 2213bp CDS: 501..2213 (SEQ ID NO 205)

GCATTGAGTCAAAAGTTTTTCCGAAGTGACCCAGTGCTCTTTTTTTTTTCCGTGAAGGACTGACAAAT
ATGCGCACAAAGATCCAATACGTAATGGAAATTCGGAAAACTAGGAAGAAATGCTGCAGGGCATTGCCG
TGCCGATCTTTTGTCTTTTCAGATATATGAGAAAAAGAATATTTCATCAAGTGCTGATAGAAGAATACCAC
TCATATGACGTGGGCAGAAAGACAGCAAACGTAAACATGAGCTGCTGCGACATTTGATGGCTTTTATCCG
ACAAGCCAGGAACTCCACCATTATCTAATGTAGCAAAATATTTCTTAACACCCGAAGTTGCGTGTCCC
CCTCACGTTTTTAATCATTTGAATTAGTATATTGAAATTATATATAAAGGCAACAATGTCCCCATAATC
AATTCCATCTGGGGTCTCATGTTCTTTCCCCACCTTAAATCTATAAAGATATCATAATCGTCAACTAG
TTGATATACGTAAATCATGAATTCAACTCCCGATCTAATATCTCCTCAGAAATCCAATTCATCCAAC
CATATGAATTGGAATCTGGTCTGTTCAAAGGCCATGAATACTCCAGAAGGTAAAAATGAAAGTTTTACG
ACAACCTTAAGTGAAAGTCAAGTGCAACCCGCGTTGCCCTCCAAACACCCGAAAAAGGTGCTACGTAA
CGGTTTTCTATCTGTTGTGTTATGGTTGCTTTCCGTTGGTTTCATATTTGGATGGGATACTGGTACCATT
CTGGTTTTGTGCTCAAACCTGATTTTCTAAGAAGATTTGGTATGAAGCACCACGACGGTAGTCATTACT
TGTCCAAGGTGAGAACTGGTTTAATTGTCTCTATTTTAAACATTGGTTGTGCCATTGGTGGTATCGTCT
TAGCCAAGCTAGGTGATATGTATGGTCGTAGAATCGGTTTGATTGTGCTGTTGTAGTAATCTACACTATCG
GTATCATTATTCAAATAGCCCTCGATCAACAAGTGGTACCAATATTTTCATTGGTAGAATTATCTCTGGTT
TAGGTGTCCGTTGGTATCACAGTTTTATCTCCCATGCTAATATCTGAGGTGCGCCCCCAGTGAAATGAGAG
GCACCTTGGTTTTCATGTTACCAAGTCATGATTACTTTAGGTATTTTCTTAGGTTACTGTACCAATTTTG
GTACCAAGAATTACTCAAACCTCTGTCCAATGGAGAGTTCCATTAGGTTTGTGTTTCGCCTGGGCCTTAT
TTATGATTGGTGGTATGATGTTTGTTCCTGAATCTCCACGTTATTTGGTTGAAGCTGGCAGAATCGACG
AAGCCAGGGCTTCTTTAGCTAAAGTTAAACAAATGCCACCTGACCATCCATACATTCAATATGAGTTGG
AAACTATCGAAGCCAGTGTGGAAGAAATGAGAGCCGTGGTACTGCATCTTGGGGCGAATTATTCAGTG
GTAAACCAGCCATGTTTCAACGTACTATGATGGGTATCATGATTCAATCTCTACAACAATTAACCTGGTG
ATAACTATTTCTTCTACTACGGTACCATTGTTTTCCAGGCTGTGCGTTTAAAGTGACTCTTTTGAAACTT
CTATTGTCTTTGGTGTGCTCAACTTCTTCTCCACTTGTTGTTCTCTGTACACCGTTGACCGTTTTGGCC
GTCGTAACGTGTTGATGTGGGGTGCTGTGCGGTATGGTCTGCTGTTATGTTGTCTATGCCTCTGTTGGTG
TTACCAGATTATGGCCAAACGGTCAAGATCAACCATCTTCAAAGGGTGCTGGTAACTGTATGATTGTTT
TCGCATGTTTCTACATTTTCTGTTTTCGCTACTACCTGGGCCCCAATTGCTTACGTTGTTATTTTCAAGAT
GTTTTCCCATTAAGAGTCAAATCCAAGTGTATGTCTATTGCCAGTGCTGCTAAGTGGATCTGGGGTTCTCT
TGATTAGTTTTCTTACCCCATTTATTACTGGTGCCATCAACTTCTACTACGGTTACGTTTACGTTGGCT
GTATGGTTTTTCGCTTACTTTTACGTTCTTTTTCTTTCGTTCCAGAACTAAAGGTTTATCATTAGAAGAAG
TTAATGATATGTACGCCGAAGGTGTTCTACCATGGAAATCAGCTTCTGGGTTCCAGTATCCAAGAGAG
GCGCTGACTACAACGCTGATGACCTAATGCATGATGACCAACCATTTTACAAGAGTTTGTTTAGCAGGA
AATAA

YHR094C 570aa (SEQ ID NO 206)

MNSTPDLPQKSNSSNSYELESGRSKAMNTPEGKNESFHDNLSESQVQPAVAPPNTGKGVYVTVSICC
VMVAFGGFIFGWDGTISGFVAQTDFLRRFGMKHHDGSHYLSKVRTGLIVSIFNIGCAIGGIVLAKLGD
MYGRRIGLIVVVVIYITIGIIIIQIASINKWYQYFIGRIISGLGVGGITVLSPLMISEVAPSEMGRGLVSC
YQVMITLGIPLGYCTNFGTKNYSNSVQWRVPLGLCFAWALFMIGGMMFVPESPRYLVEAGRIDEARASL
AKVNCPPDHPYIQYELETIEASVEEMRAAGTASWGELFTGKPMFQRTMMGIMIQLQLTGDNYFFY
YGTIVFQAVGLSDSFETSIVFGVNFSTCCSLYTVDRFRRNCLMWGAVGMVCCYVVYASVGVTRLWP
NGQDQPSKSGAGNCMIVFACFYIFCFATTWAPIAYVVISECFPLRVKSKCMSIASAANWIWGFLISFFT
PFITGAINFYGYVFMGCMVFAYFYVFFVFPETKGLSLEEVNDMYAEGVLPWKSASWVPVSKRGADYNA
DDLMDHDDQPFYKSLFSRK

YBL099W 2138bp CDS: 501..2138 public: 1..2138 (SEQ ID NO 693)

CCCCGGGTGATGCAGTTGCGGCCGCGCCCTGGCCAATCAGATCCCTTTAAAAATGGGCCCGGTGCGCTTCT
ACCCCTTCACGCCTTTTACGCCTTTTTCGAATCTTGTATTTATTGTAATTATTAAACATTGGTCATATC
AAATTACATCAGACTTCAATTTTTCAATTCACTTTCTGAATAAGAGCCCTTCCCTTCATACAAGTAGA
GATATTATACTGTATAGCTCTTTCAATTGGTCTTATTAGATTGTCTCCATCTTTCCCATTTGACGTTGT
TACTCCCTCTCTTTTTTCGTTTTTAACTGATTTCTCATATATTCCCAAACAGGCATATATACTCGACGT
CAAGAAAGAAAAGAAAAGAAAACCTCATAAAAAATATAATCGAGAAGTTTTTTTCTCATCGCGAACC

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ATTAGTATAACAGATTGATCGTTCAGCTCTCATAACTATCGCAAGAACAGTAACAAAATAAATAAAAAA
AACACGCACATATAATAATGTTGGCTCGTACTGCTGCTATTTCGTTCTCTATCGAGAAGCTCTAATTAAGT
CTACCAAGGCCGCAAGACCTGCCGCTGCTGCTTTGGCTTCCACCAGAAGATTGGCTTCCACCAAGGCAC
AACCCACAGAAGTTTCTCCATCTTAGAGGAAAGAATTAAGGGTGTGTCCGACGAGGCCAATTTGAACG
AAACTGGTAGAGTTCTTGCAGTCGGTGATGGTATTGCTCGTGTGTTTTGGTTTTGAACAACATTTCAGGCTG
AAGAATTGGTCGAGTTCTCCTCTGGTGTAAAGGTATGGCTTTGAACTTGGAGCCTGGTCAAGTCGGTA
TCGTTCTTTTTCGGTTCCGATAGACTGGTTAAAGAAGGTGAATTGGTCAAGAGAACCAGTAATATTGTTG
ATGTCCCAGTCGGTCCAGGCCTTTTGGGTAGAGTTGTGCGACGCTTTAGGTAACCCATTATGATGGTAAAG
GTCCTATTGACGCTGCCGGTCGTTCAAGAGCTCAAGTCAAAGCACCAGGTATTTTGCCAAGAAGATCTG
TCCATGAACCAGTTCAAACCGGTTTGAAGCCGTTGACGCCCTGGTCCCTATCGGTAGAGGTCAAAGAG
AGTTGATTATTGGTGATCGTCAAACAGGTAAGACTGCTGTGCGCTTAGACACCATCTTGAATCAAAAAGA
GATGGAATAACGGTAGTGACGAATCCAAGAACTTTACTGTGTTTACGTTGCCGTTGGACAAAAAAGAT
CTACCGTTGCTCAATTGGTCCAACTTTGGAACAACATGACGCCATGAAGTACTCTATTATTGTTGTCAG
CTACTGCATCTGAAGCCGCTCCTCTACAATACTTGGCTCCATTACTGCGCATCCATTGGTGAATGGT
TCAGAGATAATGGAAGCAGCTTTGATCGTCTATGACGATTTGTCCAAGCAAGCCGTGGCATAACCGTC
AATTATCTTTGTTGTTGAGACGTCCTCCTGGTCGTGAAGCCTACCCTGGTGATGTCTTTTACTTGCATC
CAAGATTGCTAGAAAAGAGCCGCTAAGCTTTCTGAAAAGGAAGGTTCTGGTTCTTTAACTGCCTTGCCTG
TTATTGAAACCCAAGGTGGTGATGTCTCCGCTTATATCCAAACCAATGTTATTTCCATTACCGTGGTC
AAATATTCTTTGGAAGCTGAATTATTTCTACAAGGGTATCAGACCTGCCATTAACGTTGGTTTTGTCCGTTT
CTCGTGTGCGTTCCGCTGCTCAAGTTAAGGCTTTGAAGCAAGTCGCTGGTTCTTGAATATTGTTTTTGG
CTCAATACAGAGAAGTCGCTGCTTTTGTCTCAATTCGGTTCCGATTTAGATGCCTCCACCAAGCAAACCTT
TGGTTAGAGGTGAAAGATTGACTCAATTGTTGAAGCAAAACCAATATTTCTCCTTTGGCTACAGAAGAAC
AGGTTCCATTGATTTATGCCGGTGTTAATGGTCATTTGGATGGTATTGAACTATCAAGAATTGGTGAAT
TTGAGTCCTCCTTTTTGTCTATCTAAAATCCAATCACAATGAGCTTTTGACCGAAATTAGAGAAAAGG
GTGAATTGTCTAAAGAATTGTTGGCATCTCTAAAGAGTGCTACTGAATCATTTGTTGCCACTTTTTAA

YBL099W 545aa public: 1..545 (SEQ ID NO 694)

MLARTAAIRSLRSLINSTKAARPAALASTRRLASTKAQPTVESSILEERIKGVSDKANLNETGRVL
AVGDGIARVFLNNIQAELVEFSSGVKGMLNLEPGQVGIVLFGSDRLVKEGELVKRTGNIVDVPVGP
GLLGRVVDALGNPIDGKGPIDAAGRSRAQVKAPGILPRRSVHEPVQTGLKAVDALVPIGRQORELIIGD
RQTGKTAVALDITLQKRWNNGSDESKLYCVYVAVGQKRSTVAQLVQTLQHDAMKYSIIIVAATASEA
APLQYLAPFTAASIGEFWRDNGKHALIVYDDLQKQAVAYRQLSLLRRPPGREAYPGDVLYLHPRLLER
AAKLSEKEGSGSLTALPVIETQGGDVSAIYPTNVISITDQIFLEAELFYKGIRPAINVGLSVSRVGS
AQVKALKQVAGSLKFLAQYREVAFAQFGSDLDASTKQTLVRGERLTQLLKQNYSPATEEQVPLIY
AGVNGHLDGIELSRIGEFESSFLSYLKSNNHLLTEIREKGELSKELLASLKSATESFVATF

YDR504C 884bp CDS: 501..884 public: 1..884 (SEQ ID NO 695)

TAAAAGCCTTGCATATTGCTCAGAGTAAATTACAAGCGTTAAATGATAATTCAAATCTCAAATACAA
ATGACAGTTCTTCCAATAATTTTACGAATGCTGCAACTTATTCAAAGCCTAAATGAATATCAAGATTT
TAAACGCAGAATTCCAATTTGATAGAAAGGAATTAACGTTTTACTACGTTTGTGAGGAGAGAAATGATT
TTAGAGACTTGATAAAAGAGCTGTTCAAATATTACAAGACAAGAATTTGGTTGTGTGCCATCCCGAATA
ATCTGTCTATTGATTCTAAGTATTATGATAAACAACAAAAGAGCTGAAATTATATCAAACATAGTAA
AAAATTACAATGCTGAAGATTTAATGAATGTCAATGAGTTTTTCGCAGAACAGGGGGAATAACAGAGTTA
ATTTTGCACCTCCGTTGAACGAAATTGAACGACAACTTTCAGATTGCTGTGTATGAAGAATTAGTTC
ACGAATTATTTTCAATTAATGATCTGTTATTTCTTGTGTAACATATAAATTTTCTAAAAGAAAAGACAA
CCATTGGCCATTATTTTGTAAACATTTTTTCAATGTTTTTGTGTTTTGTTTTGTTTTGTTTTGTTTTTA
TTTTTGTCTACTTTTTTTATGTTATTTTGTGTTTTATCGTTTCTGTTTCGTTGTTTACCTATTTTCTGCCA
ATTCAATTTGGTACTATCTTTCTATTATCAATATTTCTTTCCCTTATGTTTTTTTCTATATGAAAAC
TCACAGGGAGAAATAGAAGAAATGTTTATTCTGTTTAACTTTGATAAAAATTACTTATACGTCTC
CCAATCATGGTTTCATGGTCACTGGTAAGGAAAAATTCGAAAAACTACGGGACTAA

YDR504C 127aa public: 1..127 (SEQ ID NO 696)

MICYFLVVTINFLKEKTTICHYFVNIFSLFLFVVFVVFIFVFFYVILFYRCSLFTYFPANSIWY
LSIINIFFPLCFFLYENFTGRNRRKCSLFLTLIKITYTSPNHGFMVTGKEKFEKL RD

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YEL032W 3416bp CDS: 501..3416 public: 1..3416 (SEQ ID NO 697)
TATCTACCGGCTGCAAGCAGCCGGTTCGGTGGCAAATCCGGCGCTTCCCCCTCAAAAAAAAAAAAAAAAAA
AAAAAAAAAGGGAACCTCAGAACGGGGGAGGTTGAAGAGCAGGCCAAGGGAAATATTAGTTTTGACCTA
TGTGGGAAACAGAATTTTCAATGAGTTATGGCAACTTGGCCGAGTGGTTAAGGCGAAAGATTAGAAATC
TTTTGGGCTTTGCCCCGCGCAGGTTTCGAGTCTGTCAGTTGTCGTTATTTTTCTCTTTTTTTTCAATTTCC
CTTGTTCGTCAGATCGAGGCGGTAGAAGAAACAATTACTTTTCCCTAAATGGGTAAAACTCGTGTTTTA
GGAAAAAAAAAGAAAAATTTGGTCAAACTCGAAAGATAGGTTCTTAATCTTCTTTCAAGTTGAAAAGGC
CTACGCTCTTTTTCCCTTGAAGCATTTTTCATCCTACTGCTCGTATTGAACTCCACTATAAGCGCACCAAAA
AGATACAAACGTCAATTATGGAAGGCTCAACGGGATTTGATGGAGACGCTACTACTTTTTTCGCTCCAG
ACGCTGTGTTTGGTGACAGAGTGGCGAGATTTCAAGAGTTTGTAGATACTTTCACCTCATACAGAGACT
CTGTAAGGTCCATACAAGTTTACAACAGCAATAACGCGGCCAACTACAACGATGATCAAGATGACGCAG
ACGAACGAGATTTGCTAGGTGATGACGACGGTGATGATCTTGAAGGAAAAGAAAAGCAGCATCGTCCA
CCTCATTGAATATACCTCCCTCACAGGATTATCATCTCGCTTGATGACTTGAGAGAATTCGACAGGTCGT
TCTGGTCCGGGCATTTTAGTCGAACCAGCATACTTCATCCCGCTGCCGAAAAGGCGCTTACTGACCTAG
CAGATTCATGGACGATGTTCCACATCCCAATGCCCTGTCAGTATCGTCTCGCCATCCTTGAAGCTTT
CGTTCAAAGGCTCATTTGGTGCACACGCATTGTCTCCTCGTACTCTAACGGCACAACATTTAAACAAAC
TGGTCTCTGTTGAGGGTATCGTAACCTAAGACTTCGTTGGTCAGGCCAAAGCTTATCAGATCTGTCCACT
ACGCGGCAAAAGACTGGTAGATTCCATTACAGAGATTATACAGATGCTACTACAACCTCACCACCCGCA
TCCCAACGCCCTGCCATCTATCCAACGGAGGACACTGAAGGTAACAACTAACACCCGAATATGGGTATA
GTACGTTTCATAGACCATCAGCGTATCACTGTGCAAGAAATGCCCGAAATGGCCCCCGCTGGCCAACTTC
CCAGGTCCATTGACGTCATTTCTCGATGACGACCTTGTGGACAAGACCAAGCCAGGTGACAGAGTTAACG
TTGTCCGGGGTATTCAAGTCGCTTGGTGTGTTGGTCATGAACCAAGTCCAACCTTAATACATTGATCGGGT
TCAAACTCTGATCCTAGGTAATACGGTGTATCCTCTCCACGCCAGATCCACGGGTGTCGCTGCGAGAC
AAATGTTGACAGATTTTCGATATAAGAAATATCAATAAACTATCCAAAAAAGGACATTTTCGATATCT
TGTCTCAATCTTTAGCGCCTTCTATTTATGGACATGACCATATAAAGAAAGCCATTTTATTGATGCTCA
TGGGAGGTGTGGAGAAAAATTTAGAAAATGGCTCGCATTTAAGAGGTGACATCAATATCCTAATGGTGG
GTGATCCATCCACTGCCAAGTCCCAATTGCTAAGGTTTGTGTTGAATACAGCATCACTGGCAATTGCTA
CTACTGGTAGAGGTTCTTCCGGTGTGGTTTGACCGCAGCGGTCACTACTGATAGGGAAACAGGTGAAA
GAAGACTAGAGGCTGGTGCCATGGTTCTTGCTGACCGCGGGGTTGTATGTATTGATGAATTTGATAAGA
TGACAGATGTGGATAGAGTCGCCATTTCATGAAGTAATGGAACAACAACCGGTGACGATTGCCAAAGCAG
GTATTCACACAACATTAATGCTCGTTGTAGTGTATTGCTGCCGCAAATCCCGTTTTTGGGCAGTACG
ATGTCAATAGAGATCCACACCAAAACATTGCCCCTACCGGACTCGCTGTTGTCTCGTTTTGATTTACTAT
TTGTTGTGACAGACGATATCAATGAAATCAGAGATAGATCCATTAGTGAGCATGTCTTAAGAACACACA
GATATTTGCCTCCAGGTTATTTAGAGGGTGAACCTGTGAGAGAGCGTTTGAATTTATCATTAGCCGTTG
GGGAGGATGAGATATAAATCTTGAAGAGCATTCCAACTCCGGGGCTGGTGTAGAAAATGAAGGAGAAG
ATGATGAAGACCATGTCTTTCGAAAAGTTCAACCCCTTATTACAAGCAGGTGCTAAGTTAGCAAAAAACA
AAGGTAACATAACGGTACAGAAATTCCAAAGCTAGTCACCATCCCATTTCTTAAGAAAGTACGTTCAAT
ATGCCAAGGAAAGGGTTATTTCCACAGTTAACACAAGAAGCCATCAATGTTATTGTGAAAAATTATACTG
ATTTAAGAAACGATGATAATACCAAAAAATCGCCCATTACTGCAAGAACTTTGGAGACTTTGATCAGAT
TAGCCACAGCTCACGCCAAAGTCAGGTTATCCAAACAGTCAACAAGGTGGATGCTAAAGTGGCTGCCA
ATCTACTAAGGTTTGCATATTGGGTGAGGATATCGGCAATGATATCGATGAAGAGGAAAGTGAATACG
AAGAAGCTTTGTGCGAAGAGGTCTCCACAGAAATCACCGAAAAAAGACAAAGAGTCAGACAACCAGCAA
GCAACTCTGGATCCCCAATCAAATCTACTCCAAGAAGGTCAACGGCATCTTCCGTTAATGCCACGCCAT
CGTCAGCACGCAGAAATATTACGTTTTCAAGATGACGAACAGAACGCTGGTGAAGACGATAACGATATAA
TGTCACCGCTTCCCTGCGGATGAGGAAGCTGAATTACAAAGAAGGCTTCAACTGGGGTTGAGAGTGTCTC
CAAGACGTAGAGAACATCTTCACGCACCTGAGGAAGGTTTCGTGCGGACCTCTTACCGAGGTCCGTACTC
CAAGATTACCTAACGTATCTTCTGTCAGGTGAGGATGATGAGCAACAACAGTCAGTTATTTCTTTTGACA
ATGTGGAGCCTGGTACCATTTCTACTGGTAGATTGTCTTTAATCTCAGGTATTATTGCGCGTCTGATGC
AAACAGAAATATTTGAAGAAGAAATCTATCCTGTGGCCTCTTTGTTCGAAAGAATCAACGAAGAATACT
CGGAGGAGGAAAAATTTCCGCTCAAGAATATTTAGCAGGTTTGAAGATCATGTGCGACAGAAATAACT
TAATGCTTGCTGACGATAAAGTTTGGAGAGTCTGA

YEL032W 971aa public: 1..971 (SEQ ID NO 698)

MEGSTGFDGDAITFFAPDAVFGDVRRFQEFLLDTFTSYRDSVRSIQVYNSNNAANYNDDQDDADERDLL
GDDDGDDLEKEKKAASSTSLNLPRIIISLDDLREFDRSFWGILVEPAYFIPPAEKALTDLADSMDD
VPHPNASAVSSRHPWKLSFKGSFGAHLSPRTLTAQHLNKLVSVEGIVTKTSLVRPKLIRSVHYAAKTG

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RFHYRDYTDATTTLTTRIPTPAIYPTEDTEGNKLTTEYGYSTFIDHQRTVQEMPEMAPAGQLPRSIDV
ILDDDLVDKTKPGDRVNVGVFKSLGAGGMNQSNSNTLIGFKTLILGNTVYPLHARSTGVAARQMLTDF
DIRNINKLSKKKDIFDILSQLAPSIYGHDIKKAILLMLMGGVEKNLENGSHLRGDINILMVGDPSTA
KSQLLRFVLNTASLAIATTGRGSSGVGLTAAVTTDRETGERREAGAMVLADRGVVCIDEFDKMTDVIDR
VAIHEVMEQQTVTIAKAGIHTTLNARCSVIAAANPVFGQYDVNRDPHQNIALPDSLLSRFDLLFVVTDD
INEIRDRSISEHVLRTHYRLPPGYLEGEVVRERLNLSLAVGEDADINPEEHSNSGAGVENEGEDDEDHV
FEKFNPLLQAGAKLAKNKGNYNGTEIPKLVTIPFLRKYVQYAKERVIPQLTQEAINVIVKNYTDLRNDD
NTKKSPITARTLETILRLATAHAKVRLSKTVNKVDKVAANLLRFALLGEDIGNDIEEESYEALSK
RSPQKSPKKRQVRVQPASNSGSPKSTPRRSTASSVNATPSSARRILRFQDDEQNAGEDDNDIMSPSPA
DEEAELQRRLLQLGLRVSPRRREHLHAPEEGSSGPLTEVGTPLPVPVSSAGQDDEQQQSVISFDNVEPGT
ISTGRLSLISGIIARLMQTEIFEESYPVASLFRINEELPEEEKFSAQEYLAGLKIMSDRNNLMVADD
KVWRV

YGR146C 1136bp CDS: 501..1136 public: 1..1136 (SEQ ID NO 699)
CTTTCAGTTGGGCATCTTTTTTTTTCACAATTAGGCCGCCCTTTTTTCCCAAATTGGCACTTGTTTGTA
CGATCTTTAGCTAGAACTTGGAGACCTGAAACGTGGTGATTCTTATATTTAAAGGAATACCGATCTTTT
CCGTTTCAACACCCCAATTGTGAGAATTTTATTTCTTGCATTTCGGAATTTAGATACATTCACATCC
ATACTTGGACACATATATATATACAATATAATCATTTGACACAGGCCATCGCCATTGAGTAACTGTCTT
TGAAGTGTCTAAAGAACTTAGAACTATAGTGTTGTCCCAAGAAGTTAAAAATTGAACACTTGTGAGAAT
TATAAACAGAGTAAGCAAAGAAAGAATAGAGAAACAATACTCCGCTACCGATTCTCCTTTTTTTTCTT
ATAAAAAAGCTCGAGAATAATTACTTTATTTCTTATCCCTCCACTCCTTTTCAAGTATTCTTTACCGATT
TGCATATCAATCATATAATGAGCACCGCATTCAACGATTACTGCACTGTTTGTGATCGTCTCATTCCAA
CATCTCCACAGAAAACGAACATTAATACCAGGAAGATCCAAAGGGACAATGAAACCAAGAGCAGTTTAC
AATCAAATAAGTTATATTGCTCCGAAGATTGTAAGCTGAAGGATTGCAACCCTCTTAATGAGAAATTAT
TATCCCACTTGCATAAAAAATCAAAAACCTTCTCATTGCGATAATCTCACTCCACCGCTTTCATATTCTA
AAAATTTAACTGCATCAAACCTCTTCGAGCCGACTACCTCACTATCTTCATCTCCGACATCTTCAACTA
TCCCCTTTGACGAGTTGGAGAAGCTAGAGTCCTTATTAATTTACCATTGCTGCTACCTCAGGATGGTA
TAGTCAATCCTAAGCAGGAGTCTAATCCTTCTCGTGTTGACGAATATGATGAAAATGAACATTATTTGA
ACTTAGCCGACTCTCTTAGACTCGATTCTAGTTACCAATTGCATTCAAAGGCACATTTGGGTTACGAAA
ACAACCTGCCACGATCAAACGATCTAATTGATGATCATTGATCTCAGATCAGATCATTGAGAATAACT
ACAACCTATGGTTTAGACTATCCTCCAGTTAA

YGR146C 211aa public: 1..211 (SEQ ID NO 700)
MSTAFNDYCTVCDRLIPTSPQKTNINTRKIQRDNETKSSLQSNKLYCEDCKLKDSNPLNEKLLSHLHK
KSKTSHSHNLTPPLSYSKNLTASNLFEPSTSLSSPTSSTIPFDELEKLESLLISPLLLPQDGIVNPKQ
ESNPSRVDEYDENEHYLNLADSLRLDSSYLHKAHLGYENNLPRSNLDIDHLLISDQIIENNYNLWFR
LSSS

YHR135C 2117bp CDS: 501..2117 public: 1..2117 (SEQ ID NO 701)
AGAGTATAACGAGTACATTAATGAGAAAGATTCAAGTAGAGCGCAGCGTCAAAACGCTGCCGCCGTTTT
AAGCAAGCTCGCCCATGACTTTTGGGAGAACGACTGTGTCAATTGACGAAGACATATTGCAAGATTGCTC
TGACGAAGAACAATCATGATTGCATCTCTTAATCGTTACACATACATACCTTCTACCTCTGTACTGTTA
CATATGCATTGACTTTACGATCTAATATAAATCCTTTTGATGTTACCCCGCCTGTGGGCTCGTCTCCT
TTCGTTTCTTACGATTTTTTCGCCGGAACAAGAAAAACAGAACAAAACAAATCAGCGATCGTATACAT
GGGTCTTTGATTTCTGCTTGCTTCTTACAAACAACAAACGCAAACCGTTTATTGAGTGCTCTGTGACTG
GTTTTCATGTGGATGCCATAGTAGAGAAAAGACACATACAAAATTTTCGCGCATTGCTGGCCCTTTTC
CTGCTCTCCTCTTCCCCATGTCCATGCCATAGCAAGTACCACTCTAGCAGTTAACAACCTCACCAATA
TAAACGGAACGCAAATTTTAACGTACAAGCAAACAAACAACCTCCACCACCAGGCTGTGACTCGCCCG
CAAGATCTTCGATGACCGCCACGACCGCCGCAACTCCAACAGCAACTCTTCAGAGATGACTCTACTA
TTGTGCGCCTACATTACAAGATCGGCAAAAAATAGGGGAAGGTTCTTTGGTGTGCTATTTGAAGGTA
CTAATATGATCAATGGCGTACCCGTGCGGATCAAATTCGAGCCAGAAAAACGGAGGCCCTCAATTA
GAGATGAATATAAAACATATAAAATCTGAATGGCACTCCCAATATCCCTACGCGTACTACTTCGGCC
AAGAAGGTTTGCACAATATCTTGGTCATTGATCTTTTGGGTCCCTCTTTGGAAGATTTATTTGATTGGT
GTGGAAGAAAATTTCTGTCAAACCGTTGTGCAAGTTGCTGTCCAAATGATTACTTTGATTGAAGACT
TGCACGCACATGACTTGATATACCGTGATATCAAACCAGACAATTTCTTGATTGGAAGGCCCGGCCAAC
CTGACGCAAACAACATCCATTTGATCGACTTCGGTATGGCCAAACAGTATCGTGATCCGAAAACCTAAAC

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AGCACATCCCATATAGAGAGAAAAAATCACTCAGCGGCACTGCCAGATATATGTCCATTAATACTCACC
TTGGAAGAGAGCAGTCCAGAAGAGATGATATGGAGGCCTTGGGTCACGTTTTCTTTTATTTCTTGAGAG
GCCACTTACCCTGGCAGGGTTTAAAGCTCCAAACAATAAGCAAAAATACGAAAAGATTGGTGAAAAGA
AAAGATCTACTAACGTTTACGATCTAGCTCAAGGCTTACCTGTGCAATTTGGCAGGTATCTAGAAATCG
TCAGAAGTCTTTCTTTGAAGAGTGTCCCGATTATGAAGGCTATAGAAAATATTACTATCTGTACTGG
ATGATTTAGGTGAAACCGCGGACGGCCAATATGATTGGATGAACTGAACGATGGCCGTGGTTGGGATC
TTAACATAAAACAAGAAGCCAAATCTCCACGGATACGGCCATCCAAATCCACCAAACGAAAAATCGAGAA
AACATAGAAAACAAACAGCTCCAAATGCAACAGCTCCAAATGCAACAGCTCCAACAACAGCAACAGCAAC
AGCAATATGCTCAAAAAAAGTGGAGCAGATATGCGCAATTCTCAATATAAAACAAAGTTAGACCCTACTT
CTTATGAAGCTTACCAGCATCAAACCCAGCAGAAATACCTGCAAGAACAACAAAAGAGACAGCAGCAAC
AAAAACTTCAGGAGCAACAACCTTCAAGAGCAACAATTGCAACAGCAGCAACAGCAACAGCAACAGCTAC
GTGCAACAGGCCAACCTCCATCTCAGCCTCAAGCGCAAACTCAATCTCAGCAGTTTGGCGCTCGTTATC
AACCACAACAACAACCTTCTGCTGCTTTAAGAACTCCTGAACAGCACCCAAATGACGATAATTCAAGTC
TAGCTGCTTCTCATAAGGGCTTTTTTCCAAAAATTAGGTTGTTGCTAA

YHR135C 538aa pulic: 1..538 (SEQ ID NO 702)

MSMPIASTTLAVNNLTNINGNANFNVQANKQLHHQAVDSPARSMTATTAANSNSNSSRDDSTIVGLHY
KIGKKIGEGSFGVLFEFTNMINGVPVAIKFEPRKTEAPQLRDEYKTYKILNGTPNIPYAYYFGQEGHLHN
ILVIDLLGPSLEDLFDWCGRKFSVKTVVQVAVQMITLIEDLHAHDLIYRDIKPDNFIIGRPGQPDANNI
HLIDFGMAKQYRDPKTKQHIPPYREKKSLSGTARYMSINTHLGREQSRRDDMEALGHVFFYFLRGHLPWQ
GLKAPNNKQKYEKIGEKKRSTNVYDLAQGLPVQFGRYLEIVRSLSFEECPDYEGYRKLLLSVLDLGET
ADGQYDWMKLNDRGWDNLNINKPNLHGYGHPNPNNEKSRKHRNKQLQMQLQMQQLQMQQLQMQQLQMQQLQ
TEADMRNSQYKPKLDPTSIEAYQHQTQOKYLOEQQKROQQQKLOEQQLQEQQLQEQQLQEQQLQEQQLQ
PSQPPAQTSQSQFGARYQPQQQPSAALRTPEQHPNDNSSLASHKGFFQKLGCC

YJL060W 1835bp CDS: 501..1835 public: 1..1835 (SEQ ID NO 703)

TAGAGCAGATTGTTTTGAGTAGGATTTAGGAATCAAGACCTCCATCTTTGTGCGATTATTCTCTAAATGT
AACGTAACCTCGTTTTGATAAGAGAATGTCTAATCGAAGAGAGTTAATAACTTAATAAGCTCTTTAAAAGA
ACGATGGCATTATCGTCTCCTATGCCAAGATAATTACTGGCTCAAAATTTGTTTACGCGTTCATAAACT
TTGATATCACTTTCTGGCGCACAAAGCTAACCTTTATGTAGTTCTTACGTAGATTCTTTTTAGCAAGTGC
CTGGTAGTGGTTATTACATAAATGTATCTTTTCATTTGATAACAATTTCTTCAGTAGCATGTCGTGTCT
AGCAGTGACGTAGAACTGTGGCTTTTTTGTGTGTCATTATGACAATCAAGATACCAAATTCAGTCATG
TTTAAAAGGGGAAGGTACGATAGAGATATATAAAGTGTTCATTTACTATAATTGCGTATAGAATCC
ATTGTTACTTGCTCTCAATGAAACAACGATTCAATTCGTCAATTTACGAACCTAATGTCTACTTCGAGAC
CGAAAGTTGTTGCCAACAAATATTTCACTTCTAACACTGCCAAAGATGTTTGGTCGCTAACCAATGAAG
CCGCTGCAAAGCTGCCAATAACTCCAAAAACCAAGGCCGTGAACCTTATTAATTTAGGCCAAGGCTTTT
TTTCATATTCCCCTCCTCAATTCGCCATTAAAGGAGGCTCAGAAAGCCCTAGACATTCCAATGGTCAATC
AATATTCTCCAACCTAGAGGTGACCTTCATTAATTAATTCCTTGATTAAAGTTGTATTCTCCTATTTATA
ACACAGAATTGAAAGCGGAAAATGTTACCGTAACAACAGGTGCCAATGAAGGTATACTTTCTTGCTTGA
TGGGGCTTTTGAACGCTGGCGACGAGGTTATTGTTTTTGAACCTTTCTTTGACCAATATATTCCAAATA
TCGAACCTTTGCGGTGGTAAAGTTGTTTACGTCCCATAAATCCTCCAAAGGAATTGGATCAAAGGAATA
CTAGAGGTGAAGAATGGACCATTGACTTTGAGCAGTTGCAAAAAGCGATTACATCCAAGACAAAAGCTG
TCATTATCAATACCCCTCACAACCCAATTGGTAAAGTTTTTCACGCGCGAGGAATTAACCACTTTAGGTA
ACATTTGCGTCAAGCACAACGTTGTGATTATATCTGATGAAGTCTATGAACACCTTTACTTCACTGATT
CTTTCACTAGAATTGCCACACTCTCTCCAGAAATTGGGCAACTAACCTTAACGGTCGGTTCTGCCGGTA
AATCGTTTGCTGCTACTGGTTGGAGAATTGGTTGGGTCTTATCCTTGAACGCAGAGTTGTTAAGTTATG
CAGCTAAGGCACATACAAGAATTTGTTTTGCATCTCCATCCCCTCTACAGGAAGCTTGTGCAAACTCTA
TTAACGACGCTTTAAAAATTTGGGTATTTTGAAAAAATGAGACAGGAATATATCAACAAATTCAAAATTT
TCACATCGCTCTTTGATGAATTGGGACTACCATATACAGCTCCAGAGGGTACATATTTTGTCTCGTTG
ATTTCTCTAAAGTGAAAATTTCCGAGGACTATCCCTACCCAGAGGAGATCCTGAATAAGGGAAAAGATT
TTCGCATTTCTCACTGGTTGATCAATGAATTAGGTGTGGTTGCCATTCCACCACTGAATTCATATCA
AAGAGCACGAAAAGGCTGCTGAGAATTTGTTAAGGTTTGCAGTTTGTAAGATGATGCTTATCTAGAAA
ATGCCGTAGAGAGATTAAACTACTCAAGGACTACTTATAA

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YJL060W 444aa public: 1..444 (SEQ ID NO 704)

MKQRFIRQFTNLMSTSRPKVVANKYFTSNTAKDVWSLTNEAAAKAANN SKNQGRELINLGQGFSSYSP
QFAIKEAQKALDIPMVNQYSPTRGRPSLINSLIKLYSPIYNTELKAENVTVTTGANEGILSCLMGLLNA
GDEVIVFEPFFDQYIPNIELCGGKVVPINPPKELDQRNTRGEEWTIDFEQFEKAITSKTKAVIINTP
HNPIGKVFRTREELTTLGNICVKHNVVVISDEVYEHLYFTDSFTRIATLSPEIGQLTLTVGSAGKSFAAT
GWRIGWVLSLNAELLSYAAKAHTRICFASPSPLQEACANSINDALKIGYFEKMRQYINKFKIFTSIFD
ELGLPYTAPEGTYFVLVDFSKVKIPEDYPYPEEILNKGKDFRISHWLINELGVVAIPPTFEFYIKEHEKA
AENLLRFAVCKDDAYLENAVERLKLKLDYL

YKL123W 881bp CDS: 501-881 public: 1..881 (SEQ ID NO 705)

AAAATTAATGGATGTAACACAAAATATTGGCATTGATCTTTTCATTGGAATTGGCGCGTTTAATGCCGC
ATATACAAGAACATATACGAGGGATGGTCTATTGGAAGACCCGGATAATGTTAGCTTCCGTGAAGCTCT
CTCTGAAGGCAAAGATATTGAAGTCGCCAAAGATCTTCAAAGAGTTCACGATCCACATGATGAAAGTGA
TGAAATGACGTCAGATGAGGTGAATTACATGTTAATTTGGGCCAAGTTGGGTTCGTCTTTATAGAAGC
CAATGTGAAAAAATATGCGTTTGGGAGTGTATATGGCCAAATTGGAATTCCTCCTGCGTATAATGGAAC
CGAGATCAAGAAGGATACTATTTTACAGAAAGGAGAAGAATTGCCACCAAGATATGCTGACACTGATAA
TTTCTTTGGTAGTATGAAGGTAAAGAAGGGTACCTCTAGGATAACGGCGCAAACCTGAAGCCCCCT
GTGGTCTGTTGGGACGTATGAAAGAATCTCTTCTAATTTGACAGAGAAAATAATGTTTACCACGACAG
TCTTGAAACCGACGATAACAACACCGATAACAATGTTAATAACAACGATGAGAACGCTGGTTGCAATGA
AAATTCGCCATTATTGGAAGATGATGGCAATAAAAGACCGGAAAATTCAAATACCCCCCGTGAAGTATC
AGATGGAGCTATCAATAAGAACCCTAGAAATAAATCTACTAAAAACGTCAAAGAAACAGAGGCAAATC
TTCTAAAAAGAAGAACAGATCGAGAAAATAAGAGACATTATGAATTTGGTTTTTTTTTACAATTTACGCA
TACACAATATATACATTCTACTAGCTTTTTTTTTTCTTCAATTCGATAGTTTAG

YKL123W 126aa public: 1..126 (SEQ ID NO 706)

MKESLLTLTEKIMFTTTVLKPTITTPITMLITTMRTLVA MKIRHYWKMMAIKDRKIQIPPVKYQMELSI
RTLEINLLKNVKETEANLLKRRTDRENKRHYEFGFFYNLRHNIYIPTSF FFFNSIV

YML028W 1091bp CDS: 501..1091 public: 1..1091 (SEQ ID NO 707)

GGTAAACGATAGGGTGATAACCGCTGTGATAAAGAACTTCGTGCTCTTTTGGGTACACTACTCCCCTA
TGTGAAGGAGAAGCTGGATGATATTGTTGCACAGAGAGCAAGGGACCGTGAGCAACCGGCTCCATCTGC
CCAACAGCAGGAAAACGAAGATGAGGCCCTCATAATCCCTGACGAGGAAGAACCACCGCCACAGGTGC
GCAACCTCATCTCTACATTCTGATGAAGACTAATTCGAATGCGATGTGGCCACGTTATATAATGCGTT
TAAGGTGTACGAAAACCCATGCTGTTCTGGCCCGTCGGTTTTCTGACAAAATTGCTTTTAGGGATTTT
TCGGTTTGGCTCGGGTTGGCAAAGTCGGCTGGCAACAACAGGACATATATAAAGGGAGGTAATTCGT
CAGATCAATGCCGAACCGTTCTCAACGGGCCTTCCCCTCGTTCAATTGCTCACAACCAACCACAACCTAC
ATACACATACATACACAATGGTCGCTCAAGTTCAAAGCAAGCTCCAATTTTAAGAAAACCTGCCGTGC
TCGACGGTGTCTTTGACGAAGTCTCCTTGGACAAATACAAGGGTAAGTACGTTGTCTAGCCTTTATTC
CATTGGCCTTCACTTTTCGTCTGTCCAACCGAAATCATTGCTTTCTCAGAAGCTGCTAAGAAATTCGAAG
AACAAGGCGCTCAAGTTCTTTTCGCCTCCACTGACTCCGAATACTCCCTTTTGGCATGGACCAATATCC
CAAGAAAGGAAGGTGGTTTGGGCCCAATCAACATTCCATTGTTGGCTGACACCAACCACTCTTTGTCCA
GAGACTATGGTGTCTTGATCGAAGAAGAAGGTGTCGCCCTTGAGAGGTTTGTTCATCATCGACCCAAAGG
GTGTCATTAGACACATCACCATTAACGATTTGCCAGTCGGTAGAAACGTTGACGAAGCCTTGAGATTGG
TTGAAGCCTTCCAATGGACCGACAAGAACGGTACTGTCTTGCCATGTAACCTGGACTCCAGGTGCTGCTA
CCATCAAGCCAACCGTTGAAGACTCCAAGGAATACTTCAAGCTGCCAACAAATAA

YML028W 196aa public: 1..196 (SEQ ID NO 708)

MVAQVQKQAPTFFKKTAVVDGVFDEVSLDKYKGKYVLAFLAFTFVCPTETIIAFSEA AKKFEEQGAQV
LFASTDSEYSL LAWNI PRKEGGLGPINIPLLADTNHSLSRDYGVLIEEGVALRGLFIIDPKGVIRHI
TINDLPVGRNVDEALRLVEAFQWTDKNGTVLPCNWTPGAATIKPTVEDSKEYFEAANK

YOL052C-A 686bp CDS: 501..686 public: 1..686 (SEQ ID NO 709)

TGGCCACTGAAAATTCCTGGCCAGACCACCCCTGAGCTAAGGGAGTTTAGCCGCTCAAGCTTTTATTTT
CTCTGATGTAATATATCACACACCCAGACACGGTTGCCAAGGCCCTGACGGAAGGCCGCTTCAAGGGAC
GGGGCAGTGGCTATCAGAAATACCTTAATATCATCAATATTTTTCATCAATCGCAAGGTGTCAAACATC
AATAAAGGATGATGCTCAAAGGTTTATGCCCGATGTTCTTCTAATCCCCTTTCTCTCTAAATAATCC

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TTTTTTTACTCTTCTTTTCCCCTGTTTCCATTTTGTCTTTTCTCACCCCTTATGGGACATCAATA
ATGCAAGTATGTTTATACATTTTATATAAATGTATATATAAATGCCATTTCTTACACATAACCTCCAT
TCTTTGGTTAATTCTTCTTCATTCTTTTTTTTTTTCATTCTGAAAAGCCCTCCAAGCAAGCACGCTAAT
TTAATATCGATTTAAACATGAAAGTATCACAAGTTTTTCTGCCATCTCTGTCTTCGGCCTCGCTA
CTAGCGTAAATGCTCAAAACGCATCCAACACCACGAGTAACGCTGCTCCTGCTTTGCACGCTCAAAATG
GTCAACTACTAAACGCCGGAGTCGTCGGTGCTGCTGTTGGTGGTCTTTGGCCTTTTTGATTTAG

YOL052C-A 61aa public: 1..61 (SEQ ID NO 710)

MKVSQVFISAVISVFLATSVNAQNASNTTSNAAPALHAQNGQLLNAGVVGAAVGGALAFLI

YOL099C 992bp CDS: 501..992 public: 1..992 (SEQ ID NO 711)

TGTCCAAATATGTTGATGAATTCTGTTTGCAAAGGGGAACAACTTCAATGAATTGTATTTGGAAAGGT
TGCAGAATGTTACCAAAACAGATCTGAAAAATGCCATGCAGAAATATTTTGTCAACATGTTTGATTCCA
ATAAAAGCGTTGCCTTTGTGAGCTGTCATCCAGCTAAATTGGAATCAGTTCAAGAATCTTTGAAACTC
AAGGTTTCACTGTGCGAAATAGAAGAGCTAGAAGATGACGATGACGAAATTGATAGTGAAGAAGACGAAA
ATGCGTGATACATGACCTCCATTTTCAGCTTCACTTTCAACACAGAAACAGTGCCTATTATCTGCATTTC
AATAAATAGCAAAAGGAGCATTGTCTCATTCTTTTTCGAATTCTGGGATTCTGCCTTACGGCGCTCTTTC
ATTTGATTGATCGAGAATTATTATTATATTTATATGAGTACTTGAAATTCCTCATATATTTATTTTAG
AGTATTTAAGTAGCTTGATGAAAACATTAGATAAAATTACTAATTACGACCTCTTCGATTTTGCAGATG
AGTTTTTGAAATTTGTTCTGTGTTTAGACCTAATCCCACGGTAACTTGTCTTTTGGCAATCCGTTAA
CTAATTTACTGGTTAACGGTACTGGAGCAGCGTGTTTTTTTGAATTTTGTTCCTGGCATTGATAAAGG
TTTCAAAAATTCTGCTTGATCTGTTGCTCTTAGCGCTATTAATCGATTGAGAAAACGAATTGTGCTTTG
AAATTGATGGAGATTGGCTATGCGTCCTGGGTTTTGGCGAAGGAGACTTGAAGTTGGAAGATCTTTAG
GTATGGCTCTTCCGGATGATGATGTTCTTCTTTCAATTACCTTTTGGTTTCTTTGCAACAGTTCTTTCT
CTATTTTATTTGTATTGCAATTAAGAATTTTTTTGAGAACAGTAAACAATTTGCTCGTGGTTTTTTTAT
CAGTGCTCAAAAGAAATGACTTGTA

YOL099C 163aa public: 1..163 (SEQ ID NO 712)

MKTLDKITNYDLDFDAEFLKFVPVFRPNPTVTCLFGNPLTNLLVNGTGAACFFEFCSLALIKVSKILL
DLLLLALLIDSENELCFEIDGWLCLVGFGEGLLEVGRSLGMALPDDVLLSITFWFLCNSSFSILFV
ELRIFLRTVNLLLVFLSVLKRNDL

YOL100W 3746bp CDS: 501..3746 public: 1..3746 (SEQ ID NO 713)

TTAACGATCGACTCGACACATTGTTGATGGAATAATTGGTCCCTAGTTAAACAGCGGAGAAATAGCCGC
CCAGGATAATCGGAGAAAAGTCACGTGCAAAAAGAAATCATATTCGACGAAATAAACTAGAATAACTTT
TGACGTTTAGCAATAATAACCCCAATGGAAGCGAACATTTCCCGATCCTTTTAGTTTTCTTTAAGGCG
CTATTGGCATTCTCTCAAAGCTTCCGCAACACAGAAATTATATATTACATTTCTGAGGCAGAGAAT
AGTTTTGACAACGAACTGTTAATATTTTACTCCAGTTACCGCCTTTGAAGTCTGATATTGGTGTACA
AAGGTACTTAGGGGTATTTAAGAACAAGAACTACATAAAATAGTTGCAAAAGGGGAAAACAAAAGTAAC
ATCTTGATGAACCGAGAAGCCACTAAGTATTTTTTAAAGCAAAAGAAATTAATCTCTCTTTTTTT
TTTTTCATTTCAACCAATGTATTTTGATAAGGATAATTCATGAGCCCTAGGCCGTTATTGCCAAGTG
ATGAGCAGAAGCTAAACATTAATCTTCTAACGAAAAGGAGAAATCTCGCATTTAGACCCCCATTATG
ACGCAAAAGCCACTCCACAAAAGCACTTTCGAATAGAAACGTTGGCGATTTACTTTTGGAAAAAGAA
CCGCTAAGCCTATGATTCAAAAGGCCTTGACGAATACGGATAATTTCAATTGAAATGTACCATAATCAGC
AGAGAAAAATCTTGATGATGACACTATTAAAGAAGTAATGATTAATGATGAAAACGGAAAAACTGTGCG
CTAGTACCAACGACGGCAGATATGACAACGATTACGATAATAACGATATTAATGACCAAAAAACTTTGG
ATAATATAGCGGGAAGTCCCCACATGGAAAAAAATCGAAACAAAGTAAAGATTGAACATGACTCTTCAT
CTCAAAAACCAATAGCTAAAGAGTCATCCAAAGCCCAAAAAATATAATCAAAAAGGGAATCAAGGACT
TTAAATTTGGTAGTGAATAGGTGATGGCGCGTATTCTACTGTAATGTTAGCGACGTCGATTGATACCA
AAAAGAGGTACGCCGCAAAAGTACTAAACAAAGAATATTTAATACGCCAGAAGTCAAAATACGTCAG
GCATAGAAAAAACCGCCCTTCAAAAGCTCAATAATTCTCTAGTGTTGTGCGATTATTTTCCACTTTTC
AGGATGAATCAAGCCTATACTTTCTCTTAGAGTATGCCCCAATGGGGACTTTCTTTCTTTAATGAAAA
AATACGGTTTCAATTAGACGAAACCTGCGCACGATATTATGCTGCGCAAATAATAGATGCCATAGACTACT
TACATTTCAACGGTATTATTTCATAGAGATATAAAACCAGAAAATATTCTTTTAGATGGAGAAATGAAGA
TCAAACTGACTGATTTTGGTACTGCGAAGTTACTGAATCTTACAAATAATAGCGTTTCGAAACCAGAA
ACGATTTATCAACAAGGTCGAAATCTTTCGTTGGAAGTGCAGAATACGTATCTCCAGAAGCTTTTAAATG

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ACAGTTTTACAGACTATCGTTGCGATATTTGGGCCTTCGGATGTATACTTTTCCAGATGATTGCCGGAA
AACCACCATTCAAAGCTACCAATGAATACTTGACTTTCCAAAAGGTAATGAAAGTTCAGTACGCCTTTA
CACCAGGTTTCCCACTTATTATCAGAGATTTGGTTAAGAAAATCTTAGTAAAAAACTTAGACCGAAGAT
TGACGATAAGCCAAATTAAGGAACATCATTTTTTCAAAGATTTGAATTTTAAAGACGGCTCTGTTTGGT
CAAAAACGCCTCCAGAGATCAAACCATATAAAATCAACGCCAAATCCATGCAGGCAATGCCAAGCGGAA
GCGATAGAAAACCTGGTGAAGAAATCAGTCAACACACTTGGCAAATCGCATCTAGTGACTCAAAGGTCAG
CTTCAAGTCCCTCTGTTGAGGAACTACTCATTCAACCCTATACAATAACAATACTCACGCTTCTACTG
AAAGTGAAATATCAATAAAGAAGAGACCCACTGATGAAAGAACAGCGCAGATACTTGAAAATGCAAGAA
AGGGTATAACAATAGGAAAAATCAACCAGGCAAGAGAACACCAAGTGGTGCAGCTTCTGCTGCCCTAG
CAGCTTCTGCTGCTTTAACCAGAAAACCATGCAAAGCTATCCAACCTTCTAGTTCGAAAAGTAGCAGGT
CAAGCTCTCCTGCGACAACATCAAGACCAGGAACCTATAAGCGTACTTCTTCTACAGAAAAGTAAACCAT
TTGCCAAATCTCCACCTTTGTCAGCATCAGTTTTATCGTCAAAAGTCCCAATGCCTCCATACACACCTC
CAATGTGCGCCCCCTATGACACCATATGATACATATCAAATGACACCTCCCTATACGACAAAACAGCAGG
ATTATTCTGATACCGCAATTGCCGCACCTAAGCCTTGTATTAGTAAGCAAAATGTTAAAAATAGCACAG
ATTCTCCCTTGATGAACAAGCAAGATATTCAATTGGTCCTTTTACCTGAAAAACATCAACGAACATGTAC
TAAGGACGGAAAAAATGGATTTTGGTTACCACAAATTACGATATCTTAGAGAAGAAAATGCTTAAACTAA
ATGGTTTCAATTGTTAGATCCTCAACTGTTTGGTAAGCCTAGACATACTTTTTTATCCCAAGTAGTAGGA
GTGGGGGAGAGGTTACAGGTTTTCGAAATGATCCAACCTATGACTGCTTATTCCAAAACAGAAGATACGT
ACTATTCGAAAAATATTATCGATTTGCAGCTCTTGGAAAGATGATTATCGAATTGAAGGAGGTGACTTAT
CGGAGTTGCTTACTAACAGAAGCGGAGAAGGTACAAATGCAATCAAAACAGCTCACCAATGAAAGACG
ATGATAAATCCGAATCTAACAATAAAGGAAGCTCTGTTTTTCTGGCAAGATTAAAAAATTATTTTACC
CTACCTCAGCAGCTGAAACGCTCTCTTCTCTGATGAAAAAACCAAGTACTATAAACGAACCATGTAA
TGACATCATTTGGAAGGTTTCTAGTATTTGCCAAGAGGAGGCAGCCAAATCCAGTTACAAATTTAAAGT
ATGAAGTAGAATATGACATAAATTTGCGTCAACAGGGTACCAAAATAAAGAATAATCATTTCCCTTGG
AAATGGGAACATAATCATATAGTTGTGATTGACACACCTTACAAGTCATTTCTTTTGAGCACTGATAAAA
AAACCACGAGCAAATTTGTTTACTGTTCTCAAAAAAATTTCTTAATTTCGAATACAAATAAAATAGAGAAAG
AACTGTTGCAAAGAAACCAAAAGGTAATTGAAAGAAGAACATCATCATCCGGAAGAGCCATACCTAAAG
ATCTTCCAACCTTCCAAGTCTCCTTCGCCAAAACCCAGGACGCATAGCCAATCTCCATCAATTTCAAAGC
ACAATTCGTTTTCTGAATCGATTAATAGCGCTAAGAGCAACAGATCAAGCAGAATTTTGAACCTTTA
TCAATGCCAAGGAACAAAATTCAAAAAAACACGCTGCTCCAGTACCGTTAACCAGTAAATTAGTTAACG
GATTGCCAAAAGACAAGTTACCGTGGGATTAGGTCTAAACACAGGAACAAATTTCAAAAACTCATCTG
CAAAATCGAAGAGGTCGTAA

YOL100W 1081aa public: 1..1081 (SEQ ID NO 714)

MYFDKDNSMSRPLLPSPDEQKLNINLLTKKEKFSHLDPHYDAKATPQRSTSNRNVGDLLLEKRTAKPMI
QKALTNTDNFIEMYHNQQRKNLDDDTIKEVMINDENGKTVASTNDGRYDNDYDNDINDQKTLDNIAGS
PHMEKNRNRKVIEHDSSSQPIAKESSKAQKNIKKGKIDFKFGSVIGDGAYSTVMLATSIDTKKRYAA
KVLNKEYLIRQKKVYVSIKLTALQKLNNSPSVVRLFTFQDESSLYFLLEYAPNGDFLSLMKKYGS
ETCARYYAAQIIDAIDYLSNGIHRDIKPENILLDGEMKIKLTDFTAKLLNPTNNSVSKPEYDLSTR
SKSFVGTAEYVSPPELLNDSFTDYRCDIWAFCILFQMIAGKPPFKATNEYLTFFQKVMKVQYAFTPGFPL
IIRDLVKKILVKNLDRRLTISQIKEHHFFKDLNFKDGSVWSKTPPEIKPYKINAKSMQAMPSSGSDRKL
KKSVENTLGKSHLVTQRSASSPSVEETHTSTLYNNNTHASTESEISIKKRPTDERTAQILENARKGINNR
KNQPGKRTPSGAASAALAASAALTKKTMQSYPTSSSKSSRSSSPATTSRPGTYKRTSSSTESKPFKSP
LSASVLSSKVPMPYPYTPMSPMPTPYDTYQMTPPYTTKQDYSDTAIAAPKPCISKQNVKNSTDSPLMN
KQDIQWSFYLNINEHVLRTKLDFTVNTNYDILEKKMLKLNGSLLDLPQLFGKPRHTFLSQVARSGGEVT
GFRNDPTMTAYSKTEDTYYSKNIIDLQLEDDYRIEGGDLSELLTNRSGEGYKCNQNSSPMKDDDKSES
NNKSSVFSGKIKKLFHPTSAEATLSSSDEKTKYKRTIVMTSFGRFLVFAKRRQPNPVTNLKYELE
YDINLRQOGTKIKELIIPLEMGTNHIVVIQTPYKSFLLSTDKKTTSKLFTVLKKILNSNTNKKIEKELLQ
RQKVIERRTSSSGRAIPKDLPTSKSPSPKPRTHSQSPSISKHNSFSESINSAKSNRSSRIFETFINAKEQ
NSKKHAAPVPLTSKLVNGLPKRQVTVGLGLNTGTNFKNSSAKSKRS

YOR302W 578bp CDS:501..578 public:1..578 (SEQ ID NO 715)

GTGTATGATGTAATCCATCACCCCCCTATAAAACACCTGTGCACCGCATATTTCCATAGCGCGTGACG
CTAAGTACAAGAAACAGCGAGGGGCCGTTAAGTGCAGGCTTTACCGAGGGCGCCGGCTGGCGCTTCCCG
TGGAAGGGTGTGTTGACTCATCATCGCATCGCATTACCTCATGATGAGTAAATAGTTGCGATTTCACTTA
TCACCTCTCGCGGAAAAAAAAGCGGATGACATGATATATAAGGCTCTCTCGTAAGACACTTAACTATCC

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AACGTTCATTAGATTATTCGGTCAATTTCTTTTTTCATGCCCCCTCCTTTTTCTTTTCTTTTCTTGACTC
GTCGTTTCTTTTTCTTTTTTTTTTTTTTTTTTTTTCTTCAGAACTATAACACATAGATACACTCGAACAT
CTAATTGTTTAAATACTGCAAAGAATACAAGGTAATCGACTCTTCTACATACCCTTTTTGCAGATTTGA
AATAAAAAAACATTATATGTTTAGCTTATCGAACTCTCAATACACCTGCCAAGACTACATATCTGACC
ACATCTGGAAAAC TAGCTCCCACTAA

YOR302W 25aa public: 1..25 (SEQ ID NO 716)
MFSLSNSQYTCQDYISDHIWKTSSH

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Figure 2**Candida spp. h mologues**

YBL002W_homolog 393bp public: 1..393 (SEQ ID NO 397)
ATGGCCCCAAAGCAGAAAAGAAACCAGCTTCCAAAGCTCCAGCTGAAAAGAAACCAGCTGCTAAGAAA
ACCGCTTCCACCGATGGTGC'TAAAAAGAGAAACCAAAGCTAGAAAAGAAACTTATTCCTCATATATATAT
AAAGT'TTTGAAACAAACACATCCAGACACTGGTATCTCCCAAAGGCCATGTCAATTATGAATTCGTTT
GTAAACGATATTTTCGAAAGAATTGCCACCGAAGCCTCCAAATTAGCTGCTTACAATAAAAAATCCACA
ATTTCCGCTAGAGAAATCCAACTGCTGTTAGATTAATTTTGCCAGGTGAATTGGCCAAACATGCCGTT
TCCGAAGGTACCAGAGCCGTCACAAAATACTCATCTGCTTCTAGTTAG

YBL002W_homolog 130aa (SEQ ID NO 398)
MAPKAEKKPASKAPAEKKPAAKKTASTDGAKKRTKARKETYSSYIYKVLKQTHPDTGISQKAMSIMNSF
VNDIFERATEASKLAAYNKKSTISAREIQTAURLILPGELAKHAVSEGTRAVTKYSSASS

YBL064C_homolog 732bp public: 1..732 (SEQ ID NO 399)
ATGAGAGACAAAAACAAACAAAAAATCTTTTTCGCCACGCACACTACCATGTGCGCAA
CAACCACATTTACGTCTCGGATCTACCGCACCTGATTTCAAAGCTGATACAACCTAACGGGCCTATTCTGT
TTTCACGAATACATTGGTGATAGCTGGGCTATCTTGTCTCACATCCCGCTGCCACACACAGTGTGTGT
AGCACCGAGCTTTCTGCGTTCGCACGACTCGAACCGGAGTTCACGAAGAGAGGGGTGAAAT'TGCTTGCA
ATTTAGCCGACCTGTTGAAGCAAATCCGACTGGATTGATGATATGGAAGATTTTAGCGGATCCAGG
GTCAAATTTCCAAATTATCGCAGACCCTGAGAGAAAAGTTGCTACCTTGTACGACATGATCGATCACCAA
GATGCCACCAATCTCGATGACAAAGGGCTTCAATTGACAATTCGTGCAGTGT'TATCATTTGATCCAAGT
AAGAAAATCAGATTGATCATGACCTACCCTGCCTCGACCGGTAGAAACACCGCTGAAGTATTGAGAGTA
CTCGACTCATTTACAGCTTGT'TGATAAAACAAAAGGTTATCACTCCAATCAATTGGGTTCCAGGTGACGAT
GTTCTTGTCCATATGGGTGTCCAGATGATGAGGCAAGAGTTTGT'TTCTTAAATATAGGGCTATAAAG
CCATATATTAGATTGACTCCGTTGGAAAAGGAAGACAAGTAA

YBL064C_homolog 243aa (SEQ ID NO 400)
MRDKKQTKKKKSFFFATHTTMSQQPHLRIGSTAPDFKADTTNGPISFHEYIGDSWAILFSHPAHTSVC
STELSAFARLEPEFTKRGVKLLAISADPVEANSWIDMEDFSGSRVKFPPIIADPERKVATLYDMIDHQ
DATNLDDKGLQLTIRAVFIIDPSKKIRLIMTYPASTGRNTAEVLRVLDLQLVLDKQKVITPINWVPGDD
VLVHMGVDPDEARVLFPKYRAIKPYIRLTPELEKEDK

YBR149W_homolog 981bp public: 1..981 (SEQ ID NO 401)
ATGAAATTAGCCACTGAAATTGATTTCAAACCTCAACAATGGTAAAACCATTCCCTGCCTTAGGACTAGGT
ACTGTTGCCCTCAAAGATCCTAAAGATGTTAAGGATCAAGTAATCACTGCTGTTAAAGCAGGATATCGT
CATATTGATACTGCTTGGT'TTTATGGTACTGAAAAATATATTGGTGAAGCATTACAAGAATTATTTGCT
GAAGGAATTATTTAAAGAGAAGATTTATTTATCACGACAAAATTTTGGCCATCATATTGGGCTAATCCA
GAAAATCTTTAGATGAATCTTTAAAGATTGCAACTTGATTATGTTGATTTATTTTACAACATTGG
CCAATTTGTTTACATGGTGATGAAAATGGATTACCGAAAATACCTAAGGATGAGAATGGTGAATTGATT
TATGATGATGATCCAAACCCCAATGGTACTAAATATATCGACGTTTATCATAAATTAGAGGATATTTTA
GAAACAACCACCAAAGTTAGATCAATTGGTGT'TTCTAATTATTTCAATTCCAAACCTTCGTCAATTATTA
CCTAAAGTTAAAAAACATATTCCTGTTTGTAAATCAAATTGAATATCATCCACAATTACCTCAACAAGAT
TTAGTTGATTATTTGACTAAAAATAATATATTGATTTCTTGTATTTCACCAAGTTGGTAGTTATGGAGCT
CCAGTATTGAAAATCCCATTAGTTAAGCAATTGGCAGAAAAATATCAAGTCACAGAGAATGAAATTGCT
GATGCTTATAATATTTTGAATGGTAGAGTTACATTACCAAGATCTTCTAATCTTGAAAGAATTAAACC
ATTATTAGATTACCACATTTGACTAAAGAAGAATTGGATGAATTGTATCAAGTTGGAGTTAAAGATCCA
CAAAGATATATTTGTGATCCTTGGGGGTATGGTATAGGATTCCGT'TGGTGGAAAGGCGATACTTTAAGT
AAAGAATTTGATTAA

YBR149W_homolog 326aa (SEQ ID NO 402)
MKLATEIDFKLNGKTIPALGLGTVASKDPKDVKDQVITAVKAGYRHIDTAWFYGTEKYIGEALQELFA
EGIIKREDLFITTKFWPSYWANPEKSLDES LKDLQLDYVDFLQHWPICLHGDENGLPKIPKDENGELI
YDDDPPTNGTKYIDVYHKLEDILETTTKVRSIGVSNYSIPKLRLQLLPKVKKHIPPVCNQIEYHPQLPQDD
LVDYCTKNNILISCYSPVGSYGAPVLKIPLVKQLAEKYQVTENEIADAYNINLNGRVTLPRSSNLERIKT
IIRLPHLTKEELDELYQVGVKDPQRYICDPWGYGIGFRWWKGD'TLSKEFD

YBR289W_homolog 1389bp public: 1..1389 (SEQ ID NO 403)
ATGAAACCAATGCAAAACGTTAAGGAGTGGTCAGAAAAATTGAAACAGGAAGGTAAAGATGTACCTCTT
GATTTGAAAGTGTATGAAGATTTGATTAGAAAGGATAAGGAATTTGTGGGTAAATTGAATAAACAGTTG
CATGACAACAAATTTATTATGGAAAATATTAACAGAGATATCAAGTCTTATAATCAAATCAAACAATTG

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AGGATGAATTCTATTGCGTTGTCCAACAAAGGACAGTATAATAACAGTATTTGGGGGGAAGGATATCAA
GGTTATGGCAATGGAATAACAACTCCAGTACAAAGTTATTTATTCCCAACAGGGATTTAACTGATAGA
ATCATCAATGAAAGAGTGATGAAAAACAAAAATAAACCAAAACATTATGTACCCATTTCGATTAGAGTTT
GACCAAGAAAGGGATCAATTTAAATTGAGAGACACATTTCTTTGGGATTTGAATGAAGAGATTATAAAA
GTGGAAGATTTCACTGCTCAATTGTTAGAGGATTATAAATTTATCTCCAAAGTTCATTATGAAACAATT
TTGTCATCTATTTAAAGAGCAGATTGCTGACTATCTGCAGAAACCTAGCAAAACAAATGGGTGAATTGAGA
ATTCCAATTAAGATCGATATCACCATTAACAATACACAATTAAGTACCAATTTGAATGGGATATATTG
AATAGCCAGGAAGGCGATGCAGAAGAATTTTCATCTTACATGTGCGACGAATTGTGTCTACCGGGGAGAG
TTTTGCACTGCCATCGCGCATAGCATAAGAGAACAATCGCAGATGTACTATAAAGCATTGAATATGGTA
GGGTACGGTTTTCGACGGTTCACCAGTACACGAAGATGAGATTAGAAATCATTTATTGCCACCTTTAAGA
TTAGTATCATCGGACTCTGGAATCGTGGATGATTTTTTCTCAATTTAAGAAACCCATCAAGTTTGCCA
GACTTTTACCTACGTTAGGTAAATTGTCCCAATTGGAAGTTGAAAGATTGGACAAGGAAATGGAGAGA
GAAAGTAGAAGGAAAAGAAGACACAATTACAATGAAGATCAGCAACAGGGTCTGGTCGAGGCTTCAGT
TCGAGAAGAATTGCAGCTCATGCTGGTAGGGGAAACACCATTCCCGACTTGTGAGACATACCCAAGACA
TTTAGGACGCCTGCCCCCTCATCCATATTGCCAGGTGCTGTTGATATGGGTGTACCTGAGGTGTATGAA
TATAATGAAGTTTAAATCAATAGAAGTCAAGTTAGGAATCCAGATTATAGACCGCCAACACCTATTCGT
GTTGAAATGAAGTACTAGTGGATTATAACCATGATCCAATTGAAGGTACTTTTATGGTTACAATCAAATTA
CCCGTATAA

YBR289W_homolog 462aa (SEQ ID NO 404)

MKPMQNVKEWSEKIKQEGKDVPLDLKVYEDLIRKDEKFGVGLNKLHDKNFIMENINRDIKSYNQIKQL
RMNSIALSNKGQYNNNSIWGEYQGYNGITNSSTKLFIPNRDLTDRIINERVMKNKNPKHYVPIRLEF
DQERDQFKLRDTFLWDLNEEIIKVEDFTAQLLEDYKFISKVHYETILSSIKEQIADYSQKPSKTMGELR
IPIKIDITINNTQLTDQFEWDILNSQEGDAEEFSSYMCDELCLPGEFCTAIAHSIREQSOMYYKALNMV
GYGFDGSPVHEDEIRNHLPLRLVSSDSGIVDDFFSILRNPSLPDFSPTLGKLSQLEVERLDKEMER
ESRRKRRHNYNEDQQQSGRGFTSRRIAHAHAGRGNTIPDLSDIPKTFRTAPSSILPGAVDMGVPEVYE
YNEVLINRTQVRNPDPYRPTPIRVENELVDYNHDPPIEGTFMVTIKLPV

YCR004C_homolog 597bp public: 1..597 (SEQ ID NO 405)

ATGGCACAAGGAAAAGTAGCAATTATCATTTATTCATTATATCATCATGTTTATGATTTAGCCTTAGCT
GAAAAGCTGGAATTGAAGCTGCTGGAGGTGTTGCTGATATTTATCAAGTTGCCGAAACATTATCTGAT
GATGTTTTAGCTAAAATGCATGCACCAGCAAAACCAGATATTTCCAATTGCAACTCATGAACTTTAACT
CAATATGATGCATTTTTATTTGGTATTCCAACCAGATTTGGTAATTTCCCTGCTCAAATTAAGCTTTT
TGGGATAGAACCAGGTGGTTTATGGGCTAAAAATGCTTTAAGAGGGAAATATGCTGGTGTTTTCGTTTCT
ACTGGTACTCCAGGTGGTGGTCAAGAACTACCATTATTAATAGTTTGGTACTTTGGCTCATCATGGG
ATTATTTATGTTCCATTTGGGTATGGATATCCTGGTATGACTGATTTAGAAGAAGTTCATGGTGGATCT
CCTTGGGGGGCTGGTACTTTTGCTTCAGGTAATGGGTCAAGAAAAGTTACTGATTTAGAAAAAGCTATT
GCTAAACAACAAGGTGAAGATTTCTTTAAACTGTCTTCAAATGA

YCR004C_homolog 198aa (SEQ ID NO 406)

MAQKVAIIIIYSLYHHVYDLALAIEKAGIEAAGGVADIYQVAETLSDDVLAKMHAPAKPDIPIATHETLT
QYDAFLFGIIPTRFGNFPQIKAFWDRGTGLWAKNALRGKYAGVFVSTGTPGGGQETIIINSLSTLAHHG
IIYVFPFGYGYPGMTDLEEVHGGSPWGAGTFASNGSRKVTDLKAIKQGEDFFKTVFK

YCR013C_homolog 450bp public: 1..450 (SEQ ID NO 407)

ATGATAACAATGTTACCATTTTCAGCAGATTTGACAGCAGCATCCAATAAGGATTTAGTACCGTTGGCG
AATTTTTCAAATTCGAAAACACCTGGTGGACCGTTCCAAACAATGGTCTTAGCTTTGGCAACAGCTTGT
TGGAAACAATTCGACAGATTTTGGACCACAGTCCAAACCCATCCAGTTGTCTGGAATACCTTCAGCATCA
GTAGCAGAAGAAGTTTTGGCATCTTTGTGCAATTTATCAGCAGTGACAAAATCAACTGGCAAGATCAAT
TCAACATTGTTTTTCTTAGCTTTTTCAACCAAGTGTTCAACGTTTTTAGCACCGGCTTCATCGAAAAGA
GAATCACCAATTGGCATTTTGTTCAGATTTTCTTGAAAGTGAAGGCCATACCACCACCAACAATCAAC
ATATCAACCTTGTCCAACAAGTTGTCAATCAATTGA

YCR013C_homolog 149aa (SEQ ID NO 408)

MITMLPFSADLTAASNKDLVPLANFSNSKTPGGPFQTMVLALATACWNNSTDFGPQSKPIQLSGIPSAS
VAEEVLASLSNLSAVTKSTGKINSTLFFLAFSTKCTFLAPASSKRESPIGILFKIFLKVKAIPPPTIN
ISTLSNKLIN

YDL147W_homolog 840bp public: 1..840 (SEQ ID NO 409)

ATGGATAGGAGTTGGGTAGTAGGTTGTGCCATAAAGGGTGGTTGTTTAGTTAGTTATGGCACATGTTGT
GGTAGTTTGATTTTTTTTTTGTGGTCCACACGACTGGCCAAACATTTATCAAAAAATCGAGTTCAACTTT
TTTTTTTTTCCAGTTCGCCACCACCACTACTTTTACCACCCTAACAACATGTCAAGAGAAGATCCA
ATTAAGGCTGAAAAGACTTTTCTGCTACTTTAGATGAACAATTTCCATTGATTGAAAAGATCTCTGAC

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TACAAGCAAGCATTAGATAAGTATCTTGTCTTGGAGAAACAACTCGTCAGTCTTCCGATTTGGCTTCA
TCAAAAAGAGTTCTCAACAAGATTGTTACTGCATTGGTTGATAATAACGATTGGGAGTATTTGAATGAC
TTGATAACTATCTTGTCAAAGAAACATGGTCAGTTAAAGTCGTCAATTCAGCATTATCAAAGATGTG
ATTGATAATTTGGATAAATTTGGATGAAAACAACAAGCAACAATTAGAGTTGAAGATGAAATTTGATTGAA
ACTATTAGAACAGTCACAGACAAAAAGATTTTGTGTAAGTTGAAAGAGCCATTGTTTCAAGACAGTTG
GCCAAAATTTATTTGAACAAATTGAATGATTTGGATAAGGCAGTGGAAATCTTGTGTGATCTACAAGTA
GAAACGTATTCGTTAATGCCATTCAAGTGACAAGATTGAGTATATCTTAGAACAAATTCAGTTGACTTTA
CAAAAGGGGGACTATGGCCCAAGCCAAGATTTTGTAGTCGAAAGATTTTATTAAATTCGTTGAAGAAGCTT
TGCCAAAGCTGA

YDL147W_homolog 279aa (SEQ ID NO 410)

MDRSWVVGCAIKGGCLVSYGTCCGSLIFFCGPHDWPNIYQKIEFNFFSSPPPTTFTTTNNMSREDP
IKAEKDFSATLDEQFPLIEKISDYKQALDKYLVLEKQTRQSSDLASSKRVLNKIVTALVDNNDWEYLND
LITILSKKHGQLKSSIQAFIKDVIDNLDKLDENNKQQLKMKLIETIRTVTDKKIFVEVERAIVSRQL
AKIYLNKLNLDLKA VEILCDLQVETYSMPFSDKIEYILEQIQLTLQKGDYGPSQDFESKDFIKIVEEL
CQS

YDR253C_homolog 1752bp public: 1..1752 (SEQ ID NO 411)

ATGCAAAATACTAACCGTAATAATAGTAATAGTAGTAAGAATAATAGTGATAATCATCATCAACAACAA
CAACGACAACGACAACAACAAGTTGATCAATATCAATCTATTACATTACCACCATTACAATATCAATCT
AATACTCACGAATCGATAGTATTACCTTCGCAACAACCTAAAAGAGGTCGATCTGAACATTTTAATTCA
CAATTTCCAACGTAATATAAAATTCAGACAGTGTTATTACCAAGTTCTCGTGATAATAATAACACCACA
AATATACCTTATACCTATAATTTTACCAAGTAGTACCAATTTCTAACAATCCAATTACTTCTAGTAGCAAT
TCAAGAATGTTTTTACCTTAATCTGTGAGTCCATTATATCCCGTGGTCACCACACCATTACAGCATTA
TCACCACCAACACAACACCATCAACAACAACAGCAACAATTACATAAAAAATTCAAAACATCAAATTCA
GGTTCCAATACTCCGATTACTGGTGGTGGGAATTGGATCTCCTAGTACTACTAGTTATTTAGCTAATTCT
GCTAATATCAGTTATAC TAGAAGTCAACCATTAAGAAGATAACAACCAACATCTTCCACAAC TAAGGAT
AATAATAACACGATAATTGAAAATGAAGACCAGAAGTTTTCGATTAGCAAAAGAAGCATTAGTAGCT
ACTGCCAAGGGAGTTAAGACGAATCATTTCCAATAATAATGGTAAATTTGGTAATAATACTTCTAAGATT
GATATTAAATAATCATAATAAGAACAACAACAACAAAAGTGATGGTAATGAAACCATACTTGATTCTACA
ATTGCAGATTTATTAAAGAAGATTACAATATGCTAGTGCTCCTCATGGTAATCCCATTGGCCAAATAAGT
GGACTTCAAAC TAATTTCTAAAGGATTACTTGAAGTACAAGATGAATAC TCTAATTTCCCTGATTTACAA
AACAATAATTTTTCAAAGTTAATAATGGTGATAATAATAATAC TAGTAATAGCAAGTTTAGTAATAAT
TATCATCATCCATCAGGTAATGAACCAGGATGGAATTTTTCATTTGATGAAGCATCAACGAAAACAACA
TCAAACAATAACGATCAACAGGAACAACAGGAACAGGAATAGGAGCAACAACCAATATAATATCAGAA
TCAGAATCGGAATTAAAAGTGAACGAGAATCAAGTATTGCCAATATAATCAATCCCTCAACAACAACA
ACTTCCACAACA ACTAATAAGAATAACAATAACACTTCATCATCTACTAAAAC TAGAAAATATTCTCAA
GATCCAACAAGAAAATTTCTTGTGATAAATGTCCCATGTCATTTTCGTCGATCATCAGATTTAAACGT
CATGAAAAACAACATTTAATATCCACCTAATATTTGTCAATTTTGTGGTAAAGGTTTGTCTAGAAAA
GATGCTTTTAAAAGACATATTGGGACTTTAATCATGTAAGAAGAAATGCTGATAAGAATTTATATATTGAA
AATTTAAATTTATTAAATAATTCAAGTCAAGATGATGATGAAGAGGAGGAGGATGAAGAAGAAGAA
GAAGGATTGGAACAGGATAGATTGTATAAGAAGAGGAGGAAGAGTAATAATAATCAATCAATATAAA
GAAGAAGGATTTGAACATAATGATGACGATGATGATGATGAAGAGGATGAAGTGAACGAGAATTT
CCAATTTATGGATATCAACAGAATTGA

YDR253C_homolog 583aa (SEQ ID NO 412)

MQNTNRNNSNSSKNNSDNHHQQQRQRQQQVDQYQSITLPLQYQSNTHESIVLPSQQPKRGRSEHFN
QFQRNINSRPVLLPSSRDNNNTTNIPIPIILPSSSTNSNNPITSSSNSRMFSPNPVSPLYPVVTPSSAL
SPPTQHHQQQQQLHKKFKTSNSGNTPTITGGGIGSPSTTSYLSANSANISYTRSQPLKDNNTSSTTKD
NNNTI IENEDQKFFRLAKEALVATAKGVKTNNHNNNGKFGNNTSKIDINNHNKNNNNKSDGNETILDST
IADLLRRLQYASAPHGNPIGQISGLQTN SKGLLEVQDEYSNFPDLQNNNFFKVNNGDNNNTSNSKFSNN
YHHPSGNEPGWNFLLEASTKTTSMNTRSTGTGTGIGATTNII SESESELKVKRESSIANI INPSTTT
TSTTTNKNNNTSSSTKTRKYSQDPTRKFPCKDCPMSFRSSDLKRHEKQHLTI PPNICQFCGKGFKARK
DALKRHIGTTLTKRNADKKLYIENLNYLNSSQDDDDDEEEDEEEEGLEQDRLYKKRRKSNNNNQIIK
EEGFENDDDDDDDEEDEVKREFPTYGYQQN

YDR276C_homolog 516bp public: 1..516 (SEQ ID NO 413)

ATGTGTTTATGTCTTTCGGATTTATTTCTTATTATTTCTTTCAGTATTATTCCCACCATTACCTGTTTGG
ATTAGAAGAGGATGTTGTTTCATGTGATTCATTAATTAATATTGCCTTATGTATTAGGATATTTCCCA
GGGTTAATTCATTTCATGGTATATAATAGCTAAATATTCTTCTTATTATTATCAACAACAACAACAACA
CGTAAAGATACCATTTATTATGTTTATCGAAGTGATTTAGAAAATCAAACACCAAGAAGAGATGGCAGA
GATGGGAGAGATGAATGTCATCATGACCACCACCACCACCATCATCATCACACCAGGCAGAAATCA
CAAAGTGCGGGATTAATAGTTTCTAATAATCATAATAATAATAATAATAACTATGGATCTGTGGTTGAA

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GGTTCATCATCATCGAATTTGACTCCTGTGGCTCCTATTCCTGTTGAAAATGGAGCTCCACCACCAGCT
TATACTGAGATTGATAATAAAACACAACATTAA

YDR276C_homolog 171aa (SEQ ID NO 414)

MCLCLSDLFLIILSVLPPLPVWIRRGCCSCDSLINIALCMLGYFPGLIHSWYIIAKYSSYYYQQQQQQ
RKDTIYYVYRSLENQTPRRDGRDGRDECHDHHHHHHHHNQAESQSAGLIVSNNHHNNNNNYGSVVE
GSSSSNLTPVAPIPVENGAPPPAYTEIDNKTQH

YEL039C_homolog 333bp public: 1..333 (SEQ ID NO 415)

ATGCCAGCTCCATTTGAAAAAGGTTTCAGAAAAGAAAGGTGCCACTTTATTTAAACTAGATGTTTACAA
TGTCACACCGTTGAAAAAGGTGGTCCACACAAAGTTGGTCCAAATTTGCATGGTGTTCGGTAGAAAA
TCCGGTTTAGCTGAAGGTTATTCTTATACTGATGCTAACAAGAAGAAAGGTGTTGAATGGACTGAACAA
ACCATGAGTGATTATTTGGAAAATCCAAAGAAATATATTCCAGGTACTAAAATGGCTTTTGGTGGTTTA
AAGAAACCAAAGGACAGAAACGATTTAGTTACTTATTTGAAGAAAGCTACTTCTTAA

YEL039C_homolog 110aa (SEQ ID NO 416)

MPAPFEKGSEKKGATLFKTRCLQCHTVEKGGPHKVGPNLHGVFGRKSLAEGYSYTDANKKKGVWEWTEQ
TMSDYLENPKKYIPGTMFAFGGLKKPKDRNDLVTYLKKATS

YER112W_homolog 321bp public: 1..321 (SEQ ID NO 417)

ATGTCAGCAGGTATTCCAGTAAGACTTCTAAATGAAGCACAAGGTCATATAATATCAATAGAATTGATA
AATGGAGATACATACCGTGGGAAGCTATTAGAAAATGAAGATAATATGAATTTATCCTTATACGAGGCA
ACTATAACACAAGGCAAATCGGGGAAAGTAAGTCATATGGACCAAGTGTATATAAGAGGGTCAATGATT
AGATTTATATCTGTGCCTGATATTTTAAAGAATGCTCCTATGTTTTTATGAAACCTGGAGATAAACCA
AAACCTCCAATAAGGGGCCCTCCACCAAAAAGAAAGAGAGTATGA

YER112W_homolog 106aa (SEQ ID NO 418)

MSAGIPVRLLEAQQGHIIISIELINGDTYRGKLLNEDNMNLSLYEATITQKSGKVSMDQVFIRGSMI
RFISVPDILKNAPMFFMKPGDKPKPIRGPPPKRKRV

YFR010W_homolog 1239bp public: 1..1239 (SEQ ID NO 419)

ATGGTTTTAGGCACTCCAGACAAGAATTTGCCTTCAAAGCCAGTTGAAAAACAAGTTTTCTCGAAGAT
TTGAATAAAAAATCAATTGGTTAAAGTTAGTAATGAACCTAGTGGGTTGACCAATTTAGGGAACACTTGT
TACTTGAACCTCAAGTTTACAAACAATATTCCATATTGATGATGTGAATAACAGGTTGAAAGATTACACT
TTTGGTGGAGCCAATCAAGCCAATAGTGCCTTTGTGTTGTCATTGAAAAGTATGTTCCAGCAAATGTCTG
AAAAACAAGAAGTTATAACTCCTTCTACATTTCTTTCTCTTTTCAGAAGATCTTATCCTCAATTTGCT
GAACAACAAAATGGTATTTATAACAACAAGACGCCGAAGAAGCATTTCCTCAAATTTGAGCTCTTTG
AGAAGCGAATTGAAAATAGATGATGTGTTCAAAATTACATTTAACACCAAGACTCAATGCTTGGCTATT
CCAGAAGATGTACAGAAGGTTTGAAGAAGCATATAAATGAATTGTCATATCGGCGTCAAGACCAAT
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GTCATTACTCATGCTGGATCATCTGCCGATGGTGGTCATTATAAAGCATACGTCAAGGATCCAACAGAC
TTGGATGGCGAGAGATGGTGGTTATTTAACGATGATAAGGTGAGCTCCGTAAACAAAGAAAAGATCGAA
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YFR010W_homolog 412aa (SEQ ID NO 420)

MVLGTPDKNLPSKPVEKQVFLEDLKNQLVKVSNESGLTNLGNTCYLNSSLQITIFHIDVNNRLKDYT
FGGANQANSFVLSLKSMFQQMSKKQEVITPSTFLSLFRRSYPQFAEQQNGIYKQDAAEEAFSILSSL
RSELKIDDFKITFNTKTQCLAIPELVTEGFEEAYKLNCHIGVKTNFLRDGLLAGLKETIEKHNSTLNA
DTEYETTKTITRLPKYLTVHFIRFFWKRDINKSKILRKVQFPFELDLAEMLDVSIKADKVSNRDITRK
VEKDNLDMIRDFKTKNDTSLTPLEQQEEDMKITSIKSKFKDDLNSALPNVDFNTTENPSSVYELNA
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YFR052W_homolog 834bp public: 1..834 (SEQ ID NO 421)

ATGTCCTTTACAAAACTCACTGCAGAAATATACTCACTATTTGGAAAAGGAGATTATCAAGGTTGCCAA
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ACCGATAAAAACCAAATTAATGATTTGAGAATTGCCCAAAGAATTTTGAAATTGGAGCATTATCGTCA
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GAAACCAATGTTGATAACCAATCGGTTATAAGAATTTATTAGGGTACGCTGAACAAATCGAATCCATC
GTATAA

YFR052W_homolog 277aa (SEQ ID NO 422)

MSLQKLTAEIYSLFGKGDYQGCQQLLAPIKLELVKHDLLVPLPSNTTDKNQINDLRIRIAQRILEIGALSS
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YDAQQDKYLQFPINLESNLMEGNYIKIWKLLKEEKNLPCQEYTHFVDTLINALRFEIAKSLEKTYDSIP
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V

YGL080W_homolog 354bp public: 1..354 (SEQ ID NO 423)

ATGTCATCATTTTAAAAAATTCAGTATTTTATTTTCAAAACAATCCCTTAGATATGTCTGTACAAC
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GCAGTTACTCCTCAAATTTATTTATTTGGGTGTCAATTTGTTAATGAATTGGCACAATTGAGTCAA
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CAAAATTGA

YGL080W_homolog 117aa (SEQ ID NO 424)

MSSFKKFTDFLFSKQSLRYVCTTHFWGPVSNFGIPIAAILDLKKDPDLISGPMTGSLILYSLVFMRYSM
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YGR070W_homolog 4146bp public: 1..4146 (SEQ ID NO 425)

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CAAGCATTTATAGAACAACAACAACCACCACAACCACAACAATATCCGCAAGACGGCCAA
GCTCATACAAAAACCCACCAATCAATAATCGTTTTCATCAATCACAACCACCACAACCTGCGCCATCAA
TACATCCCATCCAAACAAGAACAATGCAACAACCTTACCCAACCTGCCGAACAATAATCAACACTTT
CCTCCACCACAGGAAAGATCATATAGTTTTTTCATCGACTATGGATCCTGGCTCACCTAGCAAAATGACG
CCACCTAATTTTTTCAAAAGGAACCAATCATTTTTCTGGCTACCAACAACCACCACCACAACAACAG
TATCCGCAGTCACCCCATATAAGGCATATAACCAACAACCCACACTCACCAGGTGGACTTCAACAGCCA
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GATGATCCTGGATATCAACTACAACCACTGGCAATTCATACACACCCACCACAACAACAACAACAA
CAACAGCCTCCACTCCAGACACGTAGACAACCTCGTAAGGCCCTTCGAGCAACTTGCCCCCAATTCAA
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AATATTATTCCTGATTACCAAAGAGAAACATTTATTCAAACCTGTGTTTGGGGGAGTGCCTGATTGTGTTG
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ACATAA

YGR070W_homolog 1381aa (SEQ ID NO 426)

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AQKFHFDVTYNHRLRDSVHEIYAFNNVYNDVDFNEENGAGSVSNGENSALNSKHGSFLDSSTQLQNA
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TIMPHRYHGSLSVSDTSIRPQRAESNYIGNTLNSSSTPKFQLNFFGLGSNQVHASLFADDLTIQNVLSQ
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YGR132C_homolog 966bp public: 1..966 (SEQ ID NO 427)

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MSRRYDSRTTIFSP EGRLYQVEYAQEAISNAGTAIGILSP EGVVLACEKKVTSKLLDDDGSAEKLYIIN
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KIHTVGADPGKSILAEPESLNNSTEGYLVGEGYDFIPDVLNRKYVDDWIKTDDAESFKLARRIIREEG
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GKTIKDLVAGKAPVVTVTLSDTVAKTFDLLQSNQFDQLPVLNNSGRLVGLITLSKILKSLSTKKIQTNN
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YHR138C_homolog 384bp public: 1..384(SEQ ID NO 433)
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YHR138C_homolog 127aa(SEQ ID NO 434)
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YHR179W_homolog 1212bp public: 1..1212(SEQ ID NO 435)
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YHR179W_homolog 403aa(SEQ ID NO 436)
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NELAYISLVEPRVQASWDIAKENQVGSNEFILKHWWKQVIRAGTYAHELNKINEDINNDRTLIAFSRFF
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YIL074C_homolog 1392bp public: 1..1392(SEQ ID NO 437)
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TCTGTCTTGGCTGAAGCTATGGGTATGAATGTTATCTATTATGATGTCATGACCATTATGCTTTTAGGT
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GCTACTCCAGAAACCAAGAATTTGTTGAGTGTCTCCACAATTTGCCGCTATGAAAGATGGTGTCTTACGTT
ATAAATGCTTCTAGAGGTACTGTTGTTGATATCCAGCTTTGGTTCAAGCCATGAAAGCCGGAATAAT
GCTGGTGGCGCTTTAGATGTTTACCCTCATGAACGACAAAGAAATGGTGAAGGTTTATTTCAGTGAATG
TTGAATGAATGGGCCAGTGAATTTGTGTTTCATTGAGAAATGTGATTTTGACTCCACACATTGGTGGTTCT
ACCGAAGAAGCCCAATCTGCTATTGGTATTGAAGTTGGTAATTCATTGACCAAATACATCAACGAAGGT
GCCTCTCAAGGTGCTGTTAACTTTCCAGAAAGTTTCATTGAGACCATTAGATTTGGATCAACAAAATGTT

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GTCAGAGTATTATATATCCATCAAAAACGTTCTGGTGTGTTGAAAACGTGCAACAATATCTTATCCAAT
CATAACATTGAGAAACAATTCTCCGATTCTCAAGGTGATATTGCTTACTTAATGGCCGATATTTCTGAT
GTTGATATCAGCGATATACAGTCATTATATGAACAATTAGAACAAACTCCATATAAAATTGCTACTCGT
TTGTTGTATTAA

YIL074C_homolog 463aa (SEQ ID NO 438)

MSSPQQIVNSFQQALNLSGSPNAVSTSPQSFLSQYVPSKPAKALKPFKTGDILKILLLENVNQTAINIF
KNQGYQVEFYKSSLPEDELLEKIKDVHAIGIRSKTKLTEKILKAAKNLVVIGCFICGTNQVDLEFAAKS
GIAVFNSPFSNSRSVAELVIAEIIITLARQLGDRSIELHTGTWNKVSAKCWEIRGKTLGIVGYGHIGSQL
SVLAEAMGMNVIIYDVMTIMSLGNSKQVESLDELLKKADFVTLHVPATPETKNLLSAPQFAAMKDGAYV
INASRGTVVDIPALVQAMKAGKIAGAALDVYPHEPAKNGEGLFSDSLNEWASELCSLRNVILTPHIGGS
TEEAQSAIGIEVGNLSLTKYINEGASQGAVNFPEVSLRPLDLDDQQNVVRVLYIHQNVPGVLKTVNNILSN
HNIEKQFSDSQGDIAIYLMADISDVIDSDIQSLYEQLEQTPYKIATRLLY

YIR037W_homolog 486bp public: 1..486 (SEQ ID NO 439)

ATGTCCTCAATTTTACGAATTAGCTCCAAAAGACGCCAAAGGTGAACCATATCCATTTGAACAATTGAAA
GGGAAAAGTTGTCTTATCGTCAATGTTGCTTCCAAATGTGGATTCACTCCTCAATACAAGGTTTAGAA
GAATTGAATAAGAAATTTGCTGATCAACCAGTACAAATCTTGGGTTTCCCATGTAATCAATTTGGCCAC
CAAGAACCAGGTAGTAACGAAGAAATTTGGATCATTCTGTTTATTGAACACGGTGTACATTCCCAGTC
TTGGATAAAATTTGAAGTCAATGGTGACAATACCGATCCAGTTTATAAATATTTGAAATCACAAAAGAGT
GGTGTTTTGGGATTGACCAGAATTAATGGAATTTTGAAAAATTTCTTGATTGACCAAAATGGTAAAGTT
ATTGAAAGATTCAAGTTCATTGACTAGTCCAGAAAGTATCGGTACCAAGATTGAAGAATTGTTGAAGAA
TAA

YIR037W_homolog 161aa (SEQ ID NO 440)

MSQFYELAPKDAKGEYPFPEQLKGKVVLIWVASKCGFTTPQYKGLEELNKKFADQPVQILGFPCNQFGH
QEPGSNEEIGSFCSLNYGVTFPVLDKIEVNGDNTDPVYKYLKSQKSGVLGLTRIKWNFEKFLIDQNGKV
IERFSSLTSPESIGTKIEELLKK

YJR096W_homolog 849bp public: 1..849 (SEQ ID NO 441)

ATGTCATATCGATTAAATCAAACCTCAATTCGGTCATACCATTCATCAATTGGATTAGGATGTTATGAT
ATCCCAAGAAATAAAACGGTTTCGGTAGTTTATGAAGCTTGTAAGTTGGATATCGTCATTTTGATACT
GCAGTGTGTATATGGAACGAAGAAGTCAATGAAGGTATAAGTAAATCTTACGAGAGAACCCCAAT
ATACCAGATCTGAGTTTATACACCACAAAGCTTTGGAATAATCAATTGGGTACTTCAAGCACTAAA
CAAGCCATTTCAACAATGATGGCTCAAGTTGGTGATAAATTAGAATATATTGATTTATTATTGATTCAT
TCTCCATTACCAGGTAAGACCAAACGTTTAGAAAGCTGGAAAGTTTTCGAGGATGCTGTGGAAAAAGGA
TGGATTAAAAACATTGGGGTTTCTAATTATGGTAAACATCATATTGAAGAATTGTTGACCAATGCAACG
ATCCCTCCAGCTGTCAATCAAATTTGAAATAGTCCTTGGTGTATGAGACAGGATTTAGCTACTTGGTGT
TTAAGTAAAGGTATCAATGTTGAGGCATATGCACCATTAACCCATGGTAACAAATTACAAGTCAACAAT
ACTGAATTTCAAGAAATTATGCAAAAGTATAAATCAAGCTGCTCAAATATTGATTAAATGGTCAATTA
CAAAAAGGTTATATACCATTACCAAAAAACAAAACCTCCATCTCGATTAAAGGAAAATCTTCTGTTGAT
GATTTTGAATTGACTAATGAAGAAATTAAGGCTATTGATCAACCTGATGCTTATGAACCAACAGATTGG
GAATGTACTGATGCTCCATAG

YJR096W_homolog 282aa (SEQ ID NO 442)

MSYRLIKLNSGHTIPSIGLGCYDIPRNKTVSVVYEACKVGYRHFDTAVLYGNEEVIEGISKFLRENPN
IPRSEFFYTTKLWNNQLGTSSTKQAISTMMAQVGDKLEYIDLILLHSPLPGKTKRLESWKVLQDAVEKG
WIKNIGVSNYKHHIEELLTNATIPPAVNQIEISPWCMRQDLATWCLSKGINVEAYAPLTHGNKLQVNN
TEFQEIMQKYNKSAAQILIKWSLQGYIPLPKTKPSRLKENLSVDDFELTNEEIKAIQPDAYEPTDW
ECTDAP

YKL196C_homolog 603bp public: 1..603 (SEQ ID NO 443)

ATGAAGATTTATTACATTGGTATTTTAAGATCAAGTGGAGACAAGGCTTTAGAGTTAACTTCAGCCAGA
GATTTATCACAGTTTTCCTTTTTCGAAAGAAATGGGGTATCCCAATTCATGACTTTTTCGCAGAAACC
GTATCCCAAAGAACTCAACCTGGACAGAGACAAAGTGTTGAAGAAGGTAATTATATTGGTCATACTTAT
ACCAGATCAGAAGGAATTTCTGGTATCATTATAACGGACAAAGATTACCCTGTAAGACCAGCATATACA
TTAATAAATAAAATCTTGAAGAATATTTATCATATGCATCTTAAATCTGATTGGGAAAAACATTGATAAA
GCAAATGAAACTTTACAATATGGACAATTAGAAGCATATTTGAAAAAATATCAAGATCCCACTCAAGCT
GATTCAATCATGAAAGTTCAACAAGAATTAGATGATACTAAGGTTGTTTTACACAAAACCTATTGAAGGG
GTTTTACAAAGAGGAGAGAAATTAGATTCATTGGTTGACAAATCAGAAGCATTGTCAAGTTCTTCAAGA
ATGTTTTATAACAAGCAAAGAAAACCAATCTTGTGTGTGATTATGTGA

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YKL196C_homolog 200aa(SEQ ID NO 444)

MKIYYIGILRSSGDKALELTSARDLSQFSFFERNVGSQFMTFFAETVSQRTQPGQRQSVEEGNYIGHTY
TRSEGISGIIITDKDYPVRPAYTLINKILEEYLSLHPKSDWENIDKANETLQYGQLEAYLKKYQDPTQA
DSIMKVQQELDDTKVVLHKTIEGLVLRGEKLDLSVDKSEALSSSSSRMFYKQAKKTNSSCCVIM

YKR076W_homolog 771bp public: 1..771(SEQ ID NO 445)

ATGGATGACAAAGGGTGGAGATTTCCTACAAAGGAAGAATTGAAGACATTAACAACTGAAGACGACATT
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GAATACGAGGGAAGATTACAGTTCCAGTATTGTGGGACAAAAAGAAGGTACAATCGTAAACAATGAA
TCTGCTGAAATCATCAGAATGTTGAATACTGAATTCAATAGTATTTTGCCAAGTGAATATGCCGAAGTT
GATCTTGTTCCTCAAAAGACTTAGAATCTCAGATTGATGAATTGAACAGCTGGATTACGATAATATTAAC
AATGGTGTATTATAAAGCTGGATTTCATCCAAGCAAGAGGTGTACGCCAAAGAATGTCAAAATGTGTTT
GATCATTTTGGACAAAGTGGGAAGCCATTTTGGAGAAAAACCACAATGGGTCCAAGAAGGGAGAATTTTGT
TTGGGCAACCAATTGACTGAAGCAGATATCAGATTGTACACAACAATTATTAGATTGTATCTGTCTAC
GTTCAACACTTTAAGTGTAAATATTGGTACAATCAGAACTCACTATCCATACATCCACAATTGGCTCAGA
TTATTGTATTGGAAGATTCTTGGTTTCCAAGAACTACCAATTTTCGAGCACATCAAGTACCACTACACC
AAATCTCATATCAAGATTAAATCCATACGGTATAACACCATTGGGTCCAGTACCAATATTTTACCATTG
GAAGAAAAGTAA

YKR076W_homolog 256aa(SEQ ID NO 446)

MDDKGWRFPKTEELKTLKTEDDISLGTDPDHNYDFSRLRELYFKAEPYEGFRFTVPVLWDKKEGTIVNNE
SAEIRMLNTEFNLSILPSEYAEVDLVPKDLSEQIDELNSWIYDNINNGVYKAGFASKQEVYAKECQNVF
DHLDKVEAILEKNHNGSKKGEFLLGNQLTEADIRLYTTIIRFDPVYVQHFKCNIGTIRTHYPYIHNWLR
LLYWKIPGFQETTNFEHIKYHYTKSHIKINPYGITPLGPVNPILPLEEK

YKR092C_homolog 1287bp public: 1..1287(SEQ ID NO 447)

ATGGGTGAGTGTGGCTGGGGAGAGGGAATATTTAGCAGCCAGAGGAAAAAGAGACCAAGATTCGTTTTT
GGGCTCATCTCTCTCTCTCTCTCTCTTACTCACACAAAAGAAGAGCTACGATTAAAGTTTGGCCAAATGGG
TTGGAAAAAAATTTTTTTTTTAAATTTCTTTTTTTCACCTCTTAAAGAGTCAATTATTACAACACTACTACCA
ATAGCAAAGTAGTGTCCAATACTCAAGATTAGTTTTAGCTTATATTAAATGATTATGTTTCCAGAAAT
GAAGAAATTGTCAAAGTTGAAGAAGGCATTATCGAAATCTTAGCAGGCAAAGAATTACCAAAAGTTTCT
AAACAGTTGGAATCCATTATTGATGAAGTGGAAAATCAAGAAAAGAAAAGCAAACCAAGAAACTCATCA
TCTGATAGTGAAGACTCTTCATCTGAGAGTGAAAGCTCCACTTCGGACAGCGAAAGCTCCTCCTCAGAT
AGCGACAGCTCTTCCCTCAGACAGTGAAAGTTCTTCCCTCAGACAGTGAAAGTTCTTCATCAGACAGTGAA
GACAGCGATGACGAGGAAGACAAGGAAGACAAGGAAGCAGAAAAGATAACAAAGACAGCGAAGACAGC
GAAAACGAAAAAGTGGAAAGAAGACAACAAAGACACCAGCTCTGATTCAAGTTCCAGTTCCGACTCAAAA
TCTGATTTCAGACTCAGACTCAAGCTCCAGCTCTGATTCAAGTTCTGACTCTGATTCAAGTTCTGATTCC
GACTCCAGCTCCAGCTCTGATTCCGACTCCAGCTCCAGCTCTGATTCCGATTTCAGACTCAGATTCTGAT
AGTGACAGTGACGACAATTCCCTCAGAAAGTAGTTCTGAAGACGAAGAATCATCTAGTGATTTCAGAAATCC
AAAGAGGAACAAAAACAACCAGAAGACAAGAAAAGAAAGCACACAGATGATATCAAAGAAGAAAAACCA
GTTAAAAAGTTCAAAAACGAGTCAGAAATCATCAGCATCATCTTCTACTGATTCAATTCCTGCAACTCCA
GAACCAGAAATTAAGCCAGGCCAAAGAAAACATTTTTCTAGAATAGATAGAAGTAAAGTTGTTGAA
AATTCAGTATTACAAGACAATACTTACAAGGGAGCTGCAGGAACCTGGGGAGAAAAGGCTAGTGAAAAA
TTATTACAAGTCAGAGGTAAAGATTTACAAAGAATAAAAAATAAATGAAGAGAGGAAGTTATAAAGGA
GGTAGTATCACTTTAGCTAGTGGGTCCCTATAAATTCGAAGATTAG

YKR092C_homolog 428aa(SEQ ID NO 448)

MGECGWGEGIFSSQRKKRPRFVFLISLSLSYSHKRRATIKVCPNGLEKNFFNFHLLKSQLLQLLP
IAKMSSNTQDLVLAYINDYVSRNEELSKLKKALSKFLAGKELPKVSKQLESIIIDEVENQEKKSKPRNSS
SDSEDSSSESESSTSDSESSSSSDSDSSSSSDSESSSSSDSESSSSSDSESSSDDEEDKEDKEAEKDNKDS
ENEKVEEDNKDTSDDSSSSSDSKSDSDSDSSSSSDSSSDSDSSSDSDSSSSSDSDSSSSSDSDSDSDSD
SDSDDNSSSESSSEDEESSSDSESKEEQKQPEDKKRKHTDDIKEEKPVKKFKNESSASSSTDSIPATP
EPELKPQQRKHFSRIDRSKVNFEVSVLQDNTYKGAAGTWGEKASEKLLQVRGKDFTKNKNMKRGSYK
GSITLASGSYKFED

YLR043C_homolog 312bp public: 1..312(SEQ ID NO 449)

ATGGTTCACGTTGTCACTGAAGTTAACGAATTCCAAACCTTTTAAAGGAAAACAACTTAGTTATTGTT
GACTTTTTTGGCACTTGGTGTGGTCCATGTAAATGATTGCTCCATTATTAGAAAAATTCAAAATGAA
TATTCTAATATTAATTTTTGAAAATTGATGTTGATCAATTGGGTTCTTTAGCACAGAATATAATGTT
AGTTCTATGCCAACTTTGATTTTATTCAAAATGGTGAAGAAGTCAATCGTGTCAATGGTGCTAACCCA
GCTGCTATTAAACAAGCTTTGGCTTCTCTTGCTTAA

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YLR043C_homolog 103aa (SEQ ID NO 450)

MVHVVEVNEFQTLLENLIVDFVFATWCGPCKMIAPLLEKFQNEYSNIKFLKIDVDQLGSLAQEYNV
SSMPTLILFKNGEEVNRVIGANPAAIKQALASLA

YMR273C_homolog 4938bp public: 1..4938 (SEQ ID NO 451)

ATGTCACTGCCTAACACGTCATTCCATAGCGATTCAAATTTTGAATCAGCTGTACAAGATCTTGAACAA
GAGAAGAAAATGGTGGCAGCCTTAAAGAGACTATCTATAGGTCATATGATGCAATATGATCCCGACTTG
CCACCAGGCAGTATGGATGATATTGATCCCTTTGCAACAATAACAACAACAGCAATACCGCTAGTAAC
AATAACCACTATAATGGTCATACCAGAGATCACACCAGCAACAACAACAATACACACAATCATTCTCCC
AACTCAAATTTGAACCACCATCGTGGTCAAAGTCCTTATGATGAAGATTTAATTCCACAGAATATCCAC
AGATCACACTCAACTCGATCAGATCAAAATCACATTCAACTTCTCCTTCTACTTTCGCCTCAACACAAG
CAACAACAACAACAACCGCAACCTTTCCACATGAACACAGACTCCTCCATATAACAATACCA
AGCCAGTCAAGAGACGTAGTTTTTACGACAATCCAGCGTGTGACGTGAGAAAGTCACGATATTTTT
TTCGATGCCGAGGATGAAGTTTATGATAGTTTATCCCTTTGTGTGGGTACCAGCTAACTCTCATCT
CAAGTGAATCCTGAATCGTTCAAGAGTTTAAATCAAACCTCAAGTGAAGAGATATTGGAAGAAAGCTA
TCTCGAAAGTCAACTATTTCAAGAAAGTCAACTTTATCACGCAGCTCCTCAACCAGTACCAAAGAGACA
TTAGCCCCAGAACAGAAATAAGTCCAGAACTGGAATGTGATGTGTACCTCCTTCTCCAGTAAGAAAA
TCTTCCTTGGCTTAACCAATGATGGTCAACAATAAAGAGACGTTTCTCGAAATCGTCGTCTCCGGTT
TCTTCAACTTCTCCACAAAAGATCCAGCTAAGAGAGAATCTTGGTACTTCAACAACCTCAAAAAGTAC
CTGAATCCATCATTTGCGAGAGCTAACTTCAGAATTGGAGCAGTTGTCAAAAATGGCGGGGATGGACAAG
AATGACGCAGTAACTTTGGCAAGAATTTGTGGGCACAATCATTGGGGTATACAGATGTGGAATAATTA
GCATTTGACGAATTAGATAGTTCAACAACAACCGCTACTGCAACAACACCCAATTCAGTGGGTCTCCA
GGAAGTTATGACTCTGCAACCCACCTCGCACCACGACCTTGCATTTACAACAACGATTACAACATCAA
TTTCAACAAGCTCAAATCAAGGCAGAAAGGGAGGCAGAAAGATCGACAAGACATCAACAAGCGAACA
CAGTGGCCAGTATCGAATGACGATAGTCACAAATCTGTGTCACAGTTGACAGCAAGTGAGGGAGGTTCT
ACTGCTAATGCTTTTACCAGTGCTGGGAGTGGTGTGCTGACTTTGCCTTGAAACGAAGTAGAAGAATGAT
TACCGGAAAAGGAAACAGATTCGAAACAAAAGACTTCGAATAATTCGCCTCCTACAAGAAAGTACAAT
GTCCGGAATTTCCAGTTGTTATTTAACTACAAGAAACAGTAGATTCTCCTTCGCTGTACCTTCACCT
TCACCATCTACATCTCAAAGCATGATGGGTACAGGGTGAAACACAAGAAATCTCAAAGCCATTGGAA
CAGCATTTGGCTAACCAATGATGGATGGTTAGATATGTACATAACCCGTATCCCACTGCTTCAACC
ACTATTGATTTTCACTCGTATGGGTGCTAAGAAATCAGCCAGACAATCACTTAGTCCAGAGAATGCAATG
GATGGCAGATCTCGAACAAGCCCGAAAACAAGACTCATCGTGGCTATCTGCATCAAGAAAGGTCTCAT
CCTTATCATCAACAACCACAGCCTCAAGTGCAACCTCAAACCCGCCAACAACCTTCCACCAGCACAACA
GCTCATAGACAATCGACGAGACAAACCCACAATCATCCGAGCACAGGAGTTGAAAAGCATCACCGACAG
GATAACAAGCGTGTAATGCTGTGAGCTTCTAATACAGACATAAATGATTTTATGGCTCAACTGAATCAA
TTTCAAGCTAATGGAACAAGAAACCATCGATATGACAACCTCCATAAAAAGGATAAGACTGCATTTTGG
CCAAATGAAGACCACCAACGTAAGTCCCATTTCGACAGAAATTCAAATGTAAGAAATTTGTCTTCTCG
TCTCAACAGCATTTACATCAACCGTATCTGACAACCTTCTGTGCGCCCAAGTCACGTCAACTACATCAA
AATTTAGACAAGTTGAGATCCGAGATCAATGAATTTAAGGAAAGCTTGAATAAATCGGAATTACCTGGT
GAGGAATCAAAAAGAGAACACAGACTGCGTCACGACCAGCACCACCAACAACGACAACGACCAGCACCA
TCACAGCACCAACTTGAGCCTCGCAATTACAACCAATGACCGTCACCAAGACAACAGCATGAACAT
GTACAACCCCAACAAGTCCAGCCCTTACAGTCAGATCACTAGTTTGTATCAGTTATCAAGATTTAAGC
GTTGAAGATCAATTGGGTATTGAACAGGAAGCATTGAGAGAATTAGGCAAGGAAAAGGGCATTTCAT
GAGATTGATATAGATGATGCATTTGATGAAAATTTAAANNTCTGCCATCAATGAACGACATGGCTCT
CAATTCACACTTGATCATGACATTTTGGACAGCTTTAATTTGGTAGATAATCAGTTGGTTGGATCTGCA
GATGAAGGAATTGATAATTTGAAGGGTAAGAATGAAATACCCGTTGGGCGACAACAACCACAACAACA
CGTCAACAACCAAGAGCTGCTTCGCCACCATCTCACAGCAGTACTTGGGGCATGATGAATTGCACTTG
CAACAAGGTAAAGATACAAATAAAAAAGTTGGTCTCGTTTAAGTATTGATACATTGCAGAACAAGCCT
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AATATAGCCGACAAATCATCTACTGCGGGTACCCCCAAAACAAGAAAGGAGACCAAGTTAAACGAAA
TTATTCAATAAAGACCCATAATTTGGAGATTATAGACTCTGATAACTATAAGGAAAAAATGGGCATTGAG
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GCAATGATACATCTGAAAATGAAGGGCCCAAGAAATGAAAAAGAAAAAGTCGTGGGGCTGGTTGCCG
GAGCGTTCTGCCAGTGCCCTCGTCTGCAGATATCAACAATTTGCCCGCTTTGCCCTTGTGATAAACTACCT
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GATCTTGAACGTGAATTGGAACACGAACCTGAACCTTGAACCTTGAGTTGGAGCTGGATCTTGAGTTTGAT
TACGAGCAACAAGAAAGCACCAGATGCTTCAATGGTAAATGATTCAAGCTTTGCAAGTTGATTCTATC
TCTATGAAGTCGACAGACAAGGAAACGTGCTTTCCAAATTTTCAAGAAAAAGGCAAGGTACCAGGT
TCAAGCTCACAGTCAGTATTTTCAATTTGAATCAAAAAGTTTCAAGGGCCAGCGTCAGATGAATCGGAC
AACGACGCGAAACTGATCAAAAAGAGGGCAACAATAGCAGCAGGTTATTCAAGAAAGAAATCAAGGGCC
AAATTTGTCAGAACAAAGAGAATTCAGTGAATAAGGAAAGCTTCGACCTTTGAATTTAGTGTCAAACGAA
TCGACAGCAGATCGAGGAGAAAGAGAATTTGCGACAAAGTAATGGCACTCGTAAGGCAGAAAGAGTTGAG

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AGTCAAGAGCAACAGGAGGAACAGTTCCCTGTAACCTCGTCGCCGATACATCAATTCAACATTGAACAT
CTCAAAGACGACTTTGTCACTCTTGGGGAGAAGGACGATGTTTTAGATTCTGGTACTGATGACTTGGTT
GAAGATGTAAGATCTCGTAACATTCAGAGCACAATAGTTATTGTTGATGAGGATGAAACTCCTATTCAA
AATAACAATGATAACAAAGATTTGGGGATGCTAAAAGTTGACGAATTGTCCAAAAAGAAATCAATTAGC
AGGAAAAAACGGAACAATATGCAAAAGAAGAACCTTTCTACTGAACTTACTGATACAAACAAAGAGGTA
GTAGAGGAGGTTCTTGCAACTGAGCAAAGTGTCAAACCAAGCCAAGGGGAAGATCTTTTGTCTAAGAAT
GAAGATAAAGAGAAATTAGATATCCAAGAAAAGTTGAAGAAATCAATAAAACGTACATCAAGGGCCAAC
CAGCCTATTGAGTTTACTGATTCAGCCTTTGGGTTCCCTTGGCCACCACCATCTCAATCAACTTTAGTG
ATGCTTGACTACAGATTTCCAGTTCATGTTGAGCGTGCCATTTATAGATTGTCACACTTGAACTTGCT
AACCTTAAGCGTTCACTAAGAGAGCAAGTTTGTGTTGTCGAATTTTATGTATGCCTACCTCAACTTAGTT
GATCATACATTACATTTAGAGCAACAAAATATGAGCAGTGAGGATGGCGATCAGATGGAACGTGACGAC
GACGAAGAAGAAGAAATGACTGACACTGATGAGAAAGCATGATTTTTGGAGAGAGTAATATTGCCGAT
GACGATGATCTTTATTCCTGAAGAAGCAAATGGTGATTTCGATTGGGATTAACCTTAGATATGGATGGTTTA
CATAGGAAACAGCATCATCAATCTGGAATCGAAGTATAG

YMR273C_homolog 1645aa (SEQ ID NO 452)

MSSPNTSFHSDSNFESAVQDLEQEKKMVAALKRLSIGHMMQYDPLPPGSMDDIDPFANNNNNNSNTASN
NNHYNGHTRDHTSNNNNTHNHSNPKLNHHRGQSPYDEDLIPQNIHRSHSTRSRKSHSTSPSTSPQHK
QQQQQQPQPPFHEPQTPPYNKSPSPVKRRSFYDNSSLTSESHDIFFDAEDEVYSSSPLLWVPANSH
QVNPESFKSLIKTQVEEILERKLSRKSTISRKSTLSRSSSTSTKETLAPEPEISPESECDSVSPSPVRK
SSLSSSSQQNQNEVDVRKSSSSVSSTSPQKDPAKRESWYFNNSKRYSNPSLRELTSLEQLSKMAGMDK
NDAVTLARTLSAQSLGYTDVEKLAFFDELSSQTTATATTPNSSGSPGSYDSANPPRTTTLHLQQLQHQ
FQQAQIKAEREAERSTRHQSEQQWPVSNDSSHKSSSQLTASEGGSTANAFTSAGSGADFALKRSRRTD
YRKKETDSKQKTSNNSPPTRKYNVRNSQLLFNYKKPVDSPSSSPSPSPSTSQSMGHRVKHKKSKQKPLE
AALANPMDGSDMSHNPYPTASTTIDFSRMGAKKSARQSLSPENAMDGRSRTKPKENKTHRGYSHQERSH
PYHQQPQPPQVQPPQTRQQLPPAQQAHRQSTRQTHNHPSTGVEKHHRQDNKRVMSASNTDINDFMAQSNQ
FQTNGTRNHRYNLHKKDKTAFLPNEDHQRKSHSTRNSNVRNLSSSSQQLHQPYSTTSVAPKSRQLHQ
NLDKLRSEINEFKESLNKSELPGEEKREHRSRHDQHHQQRQRPAPSQHQLPRNYNHNDRHQRQHEH
VQPPQVQPLQSDTSFDISYQDLSDVEDQLGIEQEALRELGKEKGHSHEIDIDDAFDENLKKSPINERHGS
QFTLDHDLDSFNLVDNLVGSADDEIDNLKGKNEIPVGRQQPQQRQQPRAASPSSQQYLGHDELHL
QQGKDTNKKVGPRLSIDTLQNKPIHPEETATGFGMNALPSPTLHLDSEQNSTPGHSRKASNSASYDDYY
NIADKSSTAGTPKTKKETKVKTKLFNKDPNLEIIDSNDYKEKMGIIETSNNKKLKKKSFGLLSTTSVG
ANDTSENEGPKKLKKKSWGLRERSASASSADINNLPLPLDKLPTRSFSPNETSTDQHQKHDLENGS
DLERELEHEPELELELESDFDYEQQRKHQDASMVNDSSFAVDSISMKSTDKENVLKSKFFKKKAKVPG
SSSQSVFVSFESKSGASVDYESDNDAKSIKKKGNSSRLFKKKSRAKLSEQENSVNKEKLRLNLVSNE
SQTIEEKENLRQSNGRKAERVESQEQEEQFPVTSSPIHQFNIEHLKDDFVTLGEKDDVLDSDGTDLDV
EDVRSRNIQSTIVIDEDETPIQNNDNKLGLMVKDELKSKKSI SRKKRNNMQKKNLSTELTDTNKEV
VEEVLA TEQSVKPSQGEDLLSKNEDKEKLDIQEKLKKSIRKTSRANQPIEFTDSAFGFPLPPPSQSTLV
MLDYRFVHVHVERAIYRLSHLKLANPKRSLREQVLLSNFMYAYLNLVDHTLHLEQQNMSSSEDGDQMERDD
DEEEEMTDTDEKDMIFGESNIADDDDLIPEEANGDSIGINLMDMDGLHRKQHHSQSGIEV

YNL112W_homolog 1332bp public: 1..1332 (SEQ ID NO 453)

ATGTCATACAATAACGGAGGATATAATAATAGAAACGGAGGTAGTTACGGTGGAGGCTACGGCGGTGGT
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GATCAAGGTGGATACAGAGGTGGAAGATTCACTGGTGGTGGCCGTGGTGGTGGTAGATTTAATGATGCT
CCAAGACAAGAATTAAC TGCTCCACAATGGGATTTAGAACAATTGCCAAAATTTGAAAAAATTTCTAT
TCAGAACATCCAGATGTTGCTGCCAGATCTGATAGAGACATTGAACAATTTAGAAAAGAAAATGAAATG
ACAGTTAAAGGTCATGATATCCCTCATCCAATCACTACTTTTATGATGAAGCTGGTTTCCAGATTATGTT
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TTGAGTGGTAGGGATATGATTGGTATTGCCGCCACTGGTTCGGTAAAACCTTTATCTTATTGTTTACCA
TCTATTGTCCATATTAATGCTCAACCACAATTACAATATGGTGATGGTCCAATTGTTTTGGTTTTAGCA
CCAACAAGAGAATTGGCAGTGCAAATTCAACTGAATGTTCCAAATTTGGTAAATCATCAAGAATTAGA
AACACTTGTGTTTTATGGTGGTGCACCAAAAGGTCCTCAAATTAGAGATTTAGCCAGAGGGGTTGAAATT
TGTATTGCCACTCCAGGAGATTAAATTGATATGTTGGAAGCTGGTAAACTAATTTGAAAAGAGTCACT
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ACTAGAGATTATTTGAACGATCCTATTCAAGTCACCATTGGTTTATTGGAATTGGCTGCTTCTCATACT
ATTACTCAATTGGTTGAAGTCATTGATGAATTTTCCAAGAGAGATAGATTAGTAAAACATTTGGAATCC
GCTTTAAATGAAAAGATAACAAAATATTGGTTTTTGTCTTCTACTAAAAGAAGCTGTGATGAAATCACC
ACTTATTTAAGATCAGATGGTTGGCCAGCATATGCCATTCACTGGTGATAAAGAGCAAAATGAAAGAGAT
TGGGTTTTAGATGAATTCAGAAAGGGTAAAACCTTCTATTATGGTTGCAACTGACGTTGCTGCTAGAGGT
ATTGGTATGTATAATTTTTAA

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YNL112W_homolog 443aa (SEQ ID NO 454)
MSYNNGGYNNRNGGSYGGGYGGGSRGGRDGYSGGGRGGGYGGGDRDQGGYRGGGRFSGGGRGGGRFNDA
PRQELTAPQWDLEQLPKFEKNFYSEHPDVAARSDRDIEQFRKENEMTVKGHDIPHPITTFDEAGFPDYV
LQEVKDQGF PKPTPIQCQGWPMALSGRDMIGIAATGSGKTL SYCLPSIVHINAQPQLQYGDGPVILVLA
PTRELAVQIQTECSKFGKSSRI RNTCVYGGAPKGPQIRDLARGVEIC IATPGRLIDMLEAGKTNLKRVT
YLVLEADRMLDMGFEPQIRKIVDQIRPDRQTL MWSATWPKEVQQLTRDYLDNPIQVTIGSLELAASHT
ITQLVEVIDEF SKRDLRVKHLESALNEKDNKILVFASTKRTCDEITTYLRSDGWPALAIHGDKEQNERD
WVLDEFKRGKTSIMVATDVAARGIGMYNF

YOL151W_homolog 1032bp public: 1..1032 (SEQ ID NO 455)
ATGTCAACACCAATTACTGTTATTGTTTCTGGAGCCACAGGATTTATTGCTCAACACGTTGTTAAACAA
TTATTAGCTAAAACTATCAAGTCATTGGTACAGTTAGATCAACAGCCAAAGGTGATCATTATTAAAA
TTATTTCAACAATCCACAAAACCTTATCTTATGAAATTGTTGAAGATGTTGGAACATAAGGTGCCTTTGAT
AAAGTATTACAAAAACATGGAGAAGCAAAAGTGTTCTTACATTTAGCTTCACCATTCCATTTTAATGTG
ACTGATGTTGAAAAAGAATTGTTATTGCCTGCTGTTGATGGTACTAAAAATGTATTACAAGCAATTTAT
AATTTTGGTAACAATATTGAAAAAGTGGTTATCACTTCATCTTATGCTGCCATTAGTACCGCTTCTAAA
GAAGCTGATAAAAAATGCAATTATTACAGAAAAGGATTGGAATGAAATCAGTTGGCAAGATGCTTTACTT
AATCCAGTTAATGGATATCGTGGATCCAAAAAATTTGCTGAAAAAGCTGCTTGGGATTTTATAAAATCT
AATGATAAATGTTAAATTTTCATTGTGCGACAATTAATCCATCATTGTATTGTTGGTCCACAATCATTGGT
TCAGAAATTAACAAAGTTTAAACACTTCTAGTGAAATCATTAAATCTATTTTGAAATTGAAACCAAT
GATTC AATTCCTGCGTCAAAAGGAGGTTGGGTTGATGTAAGAGATGTTGCCAAAGCTCATATCATTGCC
TTTGAAATGAGGATGCCAAAAATCAAGAATATTGTTGAATTCAGGTAGATTTACATCTCAATCACTT
GTTGATATTATTAATGATAAATTTCCAGATTTGAAAGGGAAAATACCAGTTGATGAACCAGGTTTCAGAT
AAATCTGTTATTGCTGAAAGTTTGGCTACTATTGATGATACCAAATCTCGTGAATTATTAGGATTTGAA
TATTATAACCTTGAACAATCAGTTTATGATACTGTTGAACAAATTGTTAATGCTCATAAGTTGTAA

YOL151W_homolog 343aa (SEQ ID NO 456)
MSTPITVIVSGATGFIAQHVVKQLLAKNYQVIGTVRSTAKGDHLLKLFNPNQNLSEIIVEDVGTKGAFD
KVLQKHGEAKVFLHLASPFHFNVTDVEKELLPAVDGTKNVLQAIYNFGNNIEKVITSSYAAISTASK
EADKNAIITEKDWNEISWQDALLNPVNGYRGSKKFAEKAAWDFIKSNDNVKFSLSTINPSFVFGPQSFG
SEIKQSLNTSSEIINSILKLPND SIPASKGGWVDVRDVAKAHIIAFENEDAKNQRIILLNSGRFTSQSL
VDIINDKFPDLKGKIPVDEPGSDKS VIAESLATIDDTKSRELLGFEYNNLEQSVYDTVEQIVNAHKL

YOR286W_homolog 546bp public: 1..546 (SEQ ID NO 457)
ATGTTTGCATTTAAAAATCTACTACTTCAATTCTCAAAACAGTGGTCGCCCAACATCATCTCGTTAT
TTATCCACCGTCACATTAAGATCAATCCCAAGAACATTCCATAATGCCACTAAAGTTTCATTATTCAAT
GGATTAAGAACTACACCAAGATTTTATAGTGTATTGACTGAATCTCCAGAGGCAAAAGTATATAAATAT
GCCGATGTTAAGGATGTGGCCGTACACCCTGAAAACACCCTGATTCTGTTTTAGTGGATGTTAGAGAA
CCAATGAATTTGGAGATGGTCATATACCAGGAGCTTTGAATATTCCATTTAAAAGTAGTCCCGGCGCA
TTGGATTTGTGAGAAGAAGATTTCCAAGAACATTTTGGATTTCTTAAACCAAGTACTGATAAAGAATTG
ATTTTCTATTGTCTTGGAGGTGTTAGATCTACTGCAGCTGAAGAATTGGCCAATACTTTTGGTTATAAG
AAAAGAGGAAATTATCTTGGAAAGTTGGGAAGATTGGGTAAAACATGAAAATAAAAAGAACTAA

YOR286W_homolog 181aa (SEQ ID NO 458)
MFAFKKSTTSILKTVVAPTSSRYLSTVTLRSIPRTFHNATKVSLFNGLRTPRFYSVLTESPEAKVYKY
ADV KDVAVHPENHPDSVLVDVREPTEFGDGHIPGALNIPFKSSPGALDLSEEDFQEHFGFPKPKSTDKEL
IFYCLGGVRSTAAEELANTFGYKKRGNLGSWEDVWKHENKKN

YPL078C_homolog 702bp public: 1..702 (SEQ ID NO 459)
ATGTCCATGATCAACAGAATTGCATTGAGAAGTGCTCGCCAGCCATGGGAATGGCTTTCCGTCCAGCC
CCAATTTGGTTTGAGATACTTGTCTGCTCCAGCTGACCCAAAACAAAAGGCCAATTCATCATTGATGCA
TTACCAGGTAACAACCTATTATCTAAGACTGGTGTTTTGGCTACTTCAGCCGCTGCTGCCATCTATGGT
ATTTTCCAATGGATTATTTATTATACACGATGAACCAATTTTGGCTTGTCACTTTTGCAAGTTTCACAGCT
TTGGTTCGCCAAATTCGTTGCTCCTTTATACACTGAATGGGCGGATGGTGAAATCAAAAAAGTCAACGAT
ATATTGAATCAATCTAGAACTAACCATATCGAAGCCGTTAACAAGAGAATTGAAACCGTTTCAGAAATTA
AAAAACGTTGTTGCAACCACTGAAGATTTGTTTGGCTTTATCTAAAGAAACCGCTCAATTCGAAGCTGAT
TCATTTGAATTAACAAAAAATTTGGCTGTTTCTCAGGAAGCTAAATCTGTTTTGGACTCTTGGGTTAGA
TTTGAACAACAACAAGACAATTGGAACAAGAACAATTGGCCAAAGAAGTCATTGATAAAGTTGACAAA
GAAATTGCTAATCCAAAATTCGAAGACAAGTATTGGCTGAATCTCTTAACGAAATCGAAAAATTTGTTT
GCTAAAAACTAG

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YPL078C_homolog 233aa (SEQ ID NO 460)

MSMINRIALRSARPAMGMAFRPAPIGRLRLYSAPADPKQKANSIIDALPGNNLLSKTGVLATSAIIY
ISNGLFIIHDETILLVTFASFALVAKFVAPLYTEWADGEIKKVNILNQSRTNHI EAVNKRIETVSEL
KNVVATTEDLFALSKETAQFEADSFELKQKLAVSHEAKSVLDSWVRFEQQQRQLEQEQLAKEVIDKVKD
EIANPKFQDKVLAESLNEIEKLFKN

YPL085W_homolog 2490bp public: 1..2490 (SEQ ID NO 461)

ATGTTGTCCTTAAAGTTGAAACATGCATTGACTTTAGCTGATTATGGATTGATCAATGAATCACAGAGA
TATATTGATCATATTAATTCTAGTATCAAGACATTGGGTAACAAATCACCTTTTGTACGCCTAATTTG
CTTCATGAGTTTCAGAAATTGATTATGAGAATCACTGAAGTTGGATCTGGAGATGATCAAAACAACCTGG
TTTTCCGGTAAGATTAGTCGAGTCAATCTTGATAAGATCTGGGGACAAATTGATAAAATTTATTGTTGGT
GGAGATGAAC TGAAAAATGGTAACAATAACGATGGTAAATGGAACTGGCAATGGAACTGGTAGTGTGTTTC
AATAAAATTTAGCCCTTCCGTGTCGAGAAATGCATCAAGTGTGAATTTACACAATTATGTACAACTTCA
ATGATTAGGCAACCATCACATTTACCATATCAACCACAACAACACCGCAACCGCAACAGCAATTATTG
GATCAAGTTCACATTGAAAGAAAACCTACAACCTGGATTCACTCCGCAACCAACCACTTAGTTGGTCAT
CCATCAACGACATCAGTTAATAAAATATCTTCCAAGTATTAAATCGAGTCCCTCGTCAAGCACAACCTGAAT
AAGTTTGAAAAATATGCCCCAAGCAACAATTCATCTCATATAATCTTAGTCTTGTGTAAGAAAGGTC
GCTGTTACTAGTGTGATGGTCCCTGAATACCCTCACCACCAACCAACAGAGATCAATGCGTCAACA
GTTCCCGTGCCACTTCCACCACCAACCAACCGGTAAGCATGCCACAACATGTATCTAGGTCCTCCACGT
AGCCATCAACTGCACCAACCAACCAACATTTACCACCACTGCATTCACATCATGTTCAACAACCATCTAGA
GATCGGTCAACCATTAGCGACACGAATCTACCCTTATAGCAATAGTGTGGCGGACAAATTTCTACTACG
TCAGTGGGTTCTATTTCTTAGTCAAATACCACCTTGGTCGACAGACTCATGGGAAACAACCTTCTATTTCA
AGTGTAAATTTCTGGAGATAGTATTGCAGCAGTTGGTTTAGGAGAACAAAGAGAATGTTTTACCCCCATCA
ACCGGACAAACAGGGAAAAACAGCTACAAGTGAAGTGAATAGAAATGAGGAAGGTTATGGATTGTTGGGGT
CACTATCATCATGATCAACCTGAACTATAACGGAATCTCCAGAATTAAGAGGCTTACAACAACCAACAG
TCCAGTGAAGCAGAAATTAGTAAAGACATTTCAAATGATGTAGCATTTGGATAGTGCTAAGATACCAGAA
GCTTCACAGGAACCAAGAAAGAAACGGACGAATCAGGTAATGTGGCAGCTGCTCCACCACCTCTACCT
GCTCCAGTTGCACCTCC TAGAAAAACAAATCTTCTAGATCTAATCCATATGCTCCATCTACAGATATT
GGTGTATCAGTAATGCACCATCAGCAATAGGACAAACACCTAGTGGGAAACCAAGTGTGAGAAAATCA
GGATCAAGAACTAACAGATATGGACCAACCAACCAAGGAGTTGGTAATAAACAACCAACTATTGTATGTTTCG
CCACCTTCTGCTACTAATAATAC TGGTAATGAAGATTCCATTAGTATGTTTTCCTATGGTGCCTATCAA
AATGAGTCTAGTCTCCACTCAAGCAACCGTCACAATTTGATCAGACTGCAGTTGCATCTGCCCTGCT
CCACATCCATTACAACCACAATTTGGCGGTTCCAGAAAGAGTTCCAACTAAAAATGTCGCCAATATTGAT
GATAGTTTTGATGAAAAATAGTTTAGCAGCTGATACATTAACAACCTTACAATAATAATATGGTAAATAAA
CCATATGGACTGTCAACCAATGGACCAACTGTTGCAACTAATGGACCTGGATCAGTTACTCTGACACCT
TTGATTTTAAATCAAGGTTCTGCAATATGAAATTTATCAAAATCTCAGTACTATTAGTGTCACTGGAAC
GGAGCCGGAAC TGTACTGGGACTGGTGGAGCATTCGATGGATTTCCTATACCAGGATCACCTGATGAA
ACTACTCGACCAAAATTTCTATATTTGGTGGTCATACTAGAGGATTATTTCTTCAAGATTATCAGAATCA
CAAAGTGATTATATCAACAATATGCAATTGCTGATGATACAGTTGGTGATTATATTCCTATTATGGAA
GAAGATGATGAAGATGATGAAGATGAACAAGCTAAGCAACAGAAACAAAAAGAAAAAGAGGCACAAGAA
CAAGAATTGAAGAGAAAGCAGGAACAACAACAACAAAGCTGCAGCAAGAAATAACAACAATAGTGGC
GGTGGTGGTGGCAAAATCTTTAGCTTATTCCGGTGGTGGTAAATAATAAGAAACAAGATAATGATGCT
AAAGTTTATAAAGCTCATTTAGGACAAAGAATACTTTTGTATGATGAAAAATTGAAACGTTGGATA
GATTAA

YPL085W_homolog 829aa (SEQ ID NO 462)

MLSLKLKHALTLADYGLINESQRYIDHINSSIKTLGNKSPFVTPNLLHEFQNLIMRITEVSGDDQNNW
FSGKISRVLNLDKIWGQIDKFIVGGDESKNGNNDNGTGNCGSGSVFNKFPSPSVSRNASSVNLHNYVQPS
MIRQPSHLPYQPQQQPQQQLLDQVHIERKPTTGFTPQPPLVGHPPSTTSVNKYSPSIKSSPRQAQSN
KFEKYAPSNNSSHHNL SLVEERSAVTSADGPEYPHHQHQQSINASTVPVPLPPPTPPVSMPQHVSRSR
SHQSHQPPPTLPPSHSHVQPPSRDRSPLATRIYPYNSNSVGGQISTTSVGSIPSQIPLGRQTHGKQPSIS
VISHGDSIAAVGLGEQENVLPSTGQTGKTATSEVNRNEEGYGFGGHYHHDQPETITESPELRGLQQPQ
SSEAEISKDINSNDVALDSAKIPEASQEPEEETDESGNVAAAPPLPAPVAPPRTKSSRSNPYAPSTDI
GAISNAPSAIGQTPSGKPSVRKSGSRTNRYGPPPGVGNKQPTIDVSPPSATNNTGNEDSISMFSYGAYQ
NESSPPLKQPSQFDQTAVASAPAPHLPQLAVPERVPTKNVANIDDSFDENSLAADTLTYNNNMVNK
PYGSSPMGPTVATNGPGSVTSTPLILNQGSANMKLSNLSTISVTGTGAGTGTGTGGAFDGFPIPGSPDE
TTRPNSIFGGHTRGLFSSRLSESQSVLYQQYAIADDTVGDIPI MEEDDEDEDEDEQAKQKQKEKEAQE
QELKRKQEQQQQKAAAKNNNNSGGGGGKFFSLFGGGGNKKQDNDKAVYKAHLGQKNTFVYDEKLKRWI
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YPL190C_homolog 396bp public: 1..396 (SEQ ID NO 463)
ATGCCAAGTACAAAAAGATCATCTACTGAATACTCCCATAAAGACTCTAAAAAGAAAGTCAAACCTA
GATTATGTAAATCTCAAACCATCACAAACGTTATATGTCAAAAATCTAAATACCAAATCAATAAGAAA
ATTTTATTGCATAATTTGTACCTATTATTTCTGCATTTGGAGATATCATTTCTATAAATCTACAGAAT
GGTTTTGCCTTTATAATATTTAGTAATTTAAATCTGGCTACATTGGCGTTGAGAAATTTGAAAAATCAA
GATTTTTTTTGACAAACCACTTGTATTAAATTATGCTGTCAAGGAATCTAAAGCTATTTCTCAGGAGAAA
CAAAACTACAAGATGAAAATGATGAAGAAGTGATGCCACTGTATGAATAA

YPL190C_homolog 131aa (SEQ ID NO 464)
MPSTKRSSSTEYSHKDSKKKVKLDYVNLKPSQTLVYVKNLNTKINKKILLHNLVLLFSAFGDIISINLQN
GFAFIIFS NLNSATLALRNLKNQDFDKPLVLNYAVKESKAISQEKQLQDENDEEVMPSE

YBR112C_homolog 3243bp public: 1..3243 (SEQ ID NO 465)
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AACGGTGGACTACATGCAAGTGGGGCTCCTCCAAATTCCCATGAAGCAGCAGCTATTGCTCAGCAACAA
CAACAACAGCAGCAACACCACAATGGTCCTGGTATGATTGTTGCCGAGCTGCAGCTTCTGCTAACCAA
CAAGCTGTCCAAGCCAGAGCCCAACAACAACAACAGCAGCAACAACAGCGATTACCTAGTTTACAGCTGCT
CTTAATGAAACTACAGTATCAACTTGGTTAGCCATTGGTTCATTAGCCGAGAGTTTAGGTGACATTGAA
CGTGCGCAGCTTCTTACAATTCCGCTTTGAGACATTACCAAATAACCCAGATATTTTAGTCAAAATA
GCAAATACATACCGTTTCAAAGATCAGTTTCTTAAGGCTGCTGAATTGTATGAACAAGCTCTTAATTTT
CATGTTGAGAATGGTGAACTTGGGGATTATTGGGTCAATTGTTACTTGTATGTTGGATAATTTGCAAAGA
GCTTATGCTGCTTATCAACGTGCATTGTTTTACTTGGAAAACCTAACGTTCCAAAATTGTGGCAGCGA
ATTGGTATTTTATATGACAGATATGGCTCATAGAAATATGCTGAAGAAGCCTTTGTGAGAGTTTGGAT
TTGGATCCAAATTTGACAAGGCTAATGAAATTTATTTCCGTTTAGGGATCATTTATAAGCATCAAGGT
AAACTACAACAGCATTAGAATGTTTCCAATACATTTTGAATAATCCACCACACCCATTAACCAACCA
GATGTTTGGTTTCAAATTTGGTTCAGTGTATGAACAACAAGGATTGGAATGGTGTAAAGGATGCTTAT
GAAAAAGTGTTACAGATTAATCCTCATCACGCTAAAGTTTTGCAACAATTGGGATGTCTTTATTCCCAA
GCAGATCAAATCCATCAACACCAGCTAATGGTGTGCACCACCACATAAGCCATTCCAACAAGATTTG
ACCATTGCTTTAAATATTTGAAACAATCTTTGGAAGTTGATCAAAGTGATGCTCATTCATGGTACTAT
TTGGGTAGAGTAGAAATGATTAGAGTGATTTACTGCTGCTTATGAAGCTTTCCAACAAGCTGTCAAT
CGAGATGCAAGAAACCCAACCTTTCTGGTGTTCAATTGGTGTTTTGTACTATCAAATAAGCCAATATCGT
GATGCATTGGATGCTTATACCAGAGCCATTAGATTAAATCCTTATATCAGTGAAGTATGGTATGATTTG
GGGACTTTGTATGAGACTTGTAAATAATCAAATTAGTGATGCATTGGATGCATATAGACAAGCAGAAAGA
TTGGATCCAAATAATCCTCATATAAAGGCAAGATTAGAACAATTGACAAAGTATCAACAAGAAGGTAAT
ACTCACCCACCTCAACCACCGCCAAGTTCTCAACAACCTAGATTACCTCAAGGAATGGTTTTGGAAAGT
ACTCAACAACAACAGCAACAACAACCACCACCTCCACAACAACAACAACAACAACCACTTCAACACCAA
CTGCAACTGCAACCTCAACCACAGCAACCACCTCAAACCCAATCAACAACCACTGTTACTTCAACCA
TCTTCATTGCCTCCTCAACAATCCAACCATTAATCAACAAGCTGCAAGCCTTTAGTGAATCAACAA
CAAAGTCCACCACCACCTCACTTGATGAACCTGGGACAACCGGGCAACAACCACAACAATTGCCACCA
CATCTTCCACCACATACCCAGCAACCTTCTCAAATTCAGAAAAGCCTCCAACCTCAAGAACCAACCAT
TATCAACCACCTCCACCTCCACAACATCAACAGCAATCGCAATCGCAACCGCAACCTCCACACCAACCT
CAACACACTCAAAATCAACTGCCTCAATTAGTCAATTGGCACCACACCATTTAATCCTCCAGCTAAG
CCACATGGTGCACCTCAACAAGAAGTGGTTTACCGGATTTATTACACAACCTCTGCTAATATCATATCA
GCTCCATCACAAGTACCTCAACCACAACAACAATATCAACAACCACATATTGCACCTGTTAGACAAGAA
CAAGTTAACCATGTTCCCTCAATTTATCTGGCTCCTAGACCAACTGAGACAACACTTCTCAAATCAAC
AACCCAAATGAGTCAACCACAACAAGTTCACAACCTCAAAAAGGAGGAACCTAAACCAGAGGCTACT
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ACTACACCTGCTACTTCAACCCTGCAGATGCTGTGCCAGTATCTGTGTCTCAAGTTGGTGAAGCACC
AATGTTGTTCAAGAGAAGAAAGTTCCGGACACCGAGCAGATCGTTTCAAGTTGAAAAACCCGTGGAG
TCACAACCAGAAGTTACACCAGCTCCAACACCAGCTCCAGCTCTTGCAACAGCACCACCTGAACCTGCA
CCTACTGATAAGGACGTTGTAATGGCTCCAAGTAAAAGTGCAACACCTGTTTCTCAAAGTATTGTGGAA
CAGAACACCAGAGTATCTGAAGCTACAAGGCAACAGCAATCCAATGGTAAACATGATTAGAAAGACAAG
AATGATGAAGAAAAAATTTTAAAGAGGCCAATGTTGAAACGACTACTGAATCTGTACCAGTTAAACCA
CCTGTTGAGAAAGAAAATGAAAAAGTTGAGGTACCACCGCCACTGGAACAACCAAGTTCAGAAAAGAGA
GAAAAAGAAAGTCAACGGATCAATTAAGAAACCATTTGGAAAATGAAAGTAAGGTTGATATTCCTCAATTC
TCATCAAATATCACAGCTCAAAATGAAGAAGCAAAATCTGGAGAAGAACTAAAAAAGATACAACCAAG
ACAAGTCCAGCAAAACAAGGGGAAGTTAAGGAAGTAATACCATCATCTACAGAACTGTATCAAAACCA
GATGTTGAAAAAGACAATAAAGAGAAAGACAAGATGAAGATGAAGTGATGGCTGATGAAGATGACGTC
AAAAAGATGAAAATCCAGAACCTCCAATGAGAAAGATTGAAGAAGATGAAAATTATGATGATGAATAG

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YBR112C_homolog 1080aa (SEQ ID NO 466)
MYATAHTIKQQQQQQQHPPLNGGLHASGAPPNSHEAAAIAQQQQQQQHHNGPGMIVAAAAASANQ
QAVQARAQQQQQQQRLPSSAALNETTVSTWLAIGSLAESLGDIERATASYNLSALRHSPNNPDILVKI
ANTYRSKDQFLKAAELYEQALNFHVENGETWGLLGHCYLMLDNLQRAYAAYQRALFYLENPNVPKLWHG
IGILYDRYGSLEYAEEAFVRVLDLDPNFDKANEIYFRLGIIYKHQKLOPALECFQYILNNPPHPLTQP
DVWFQIGSVYEQQKDWNGAKDAYEKVLQINPHHAKVLQQLGCLYSQAESNPSTPANGAAPPHKPFQDDL
TIALKYLKQSLEVDQSDAHSWYYLGRVEMIRGDFTAAYEAFQQAQVNRDARNPTFWCSIGVLYYQISQYR
DALDAYTRAIRLNPYISEVWYDLGTLYETCENNQISDALDAYRQAERLDPNNPHIKARLEQLTKYQQEGN
THPPQPPSSSQPRLPQGMVLESTQQQQQQQPPPPQQQQQQQLQHQSQSQPQPQPQTQSQPSLLQH
SSLPPQIQPLHQAAKPLVNQQQSPPPHLMNLGQPGQQPQQLPPLPHTQQPSQIQEKPTQECPH
YQPPPPQHQQQSQSQPQPPHQPHQHTQNSPQLAQLPPHNSNPPAKPHGAPQQTGLPDLHNSANIIS
APSQVPQPPQQYQPHIAPVRQEQVNHVPSIYAPRPTETTLQINNPNESTTTQVPQLKKEPKPEAT
VSAPVPEAIKVQDQVTIQESAPAAAAAVSAPASAPVGDIKTDTVSTTTTATSTTADAVPVSVSVQGEAP
NVVQEKKVPDTEQIVSQVEKPVESQPEVTPAPTAPALATAPTEPAPTDKDVVMAPSKSATPVPQSIVE
QNTRVSEATKAPESNGKHDLEDKNDDEEKILKRPTVETTTESVFPVNPVEKENEKVEVPPPSEQPSSEKR
EKEVNGSIKKPLENESKVDIPQFSSNITAQNEEAKSGEETKKD'TTKTSPAKQGEVKEVIPSSTETVSKP
DVEKDNKEKDKDEDEVMADDDVKDENPEPPMRKIEEDENYDDE

YDR145W_homolog 1536bp public: 1..1536 (SEQ ID NO 467)
ATGGAAAGGTTCAATCAAATTAGACAAAACTCACTGAAGTTCAAAGGAGGGTTTCAGTTGTTGGAACAA
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GCAAAGTTCCAACAGTATCAAAAAGTAGGGATTTATATTAGAAATCAGTTGGTTCTTCAAGCTAAAGCA
CAACAACAGAGACAATTGCAACAGCGACAGCAACAACAGCAACAGCAACAGCAACAGAATAACAATCTA
AAATCAGCTCAGAACCAGAACCAGAATCAAAACCAAAACCAAAACCAAAACCAAAACCAAAAC
CAATATCAAGGAGTGCAATCTGCTGGACAAACACCTCAGCAACAGAGCTTTTCGCCACAGTTGCAGGCT
GTACAACAACAACAATTTATGGGCAACCTGCAACAACAACAGCAGCAGCAACAACAACAACCTTAGAAAT
GCGAATAAAAGTGCACCTTCAAGGTCAAGCTCCTTCACAGGCGCCAACTCCTTTACCTGTTCCGCCAACA
CCTCAGAGTCAACCTACAGCACAAGCGGGTGTGTGCTTCACAGGCAGCTACACCAGGATTTTCGAGCTTCT
CAACCCACACCATCGCAAACTTCGAGAATCGGATCAGCTCTACAACAAGGGCACCAAGTCGACAGGCA
TCTTCTACACCGCAATCTCAATTCCAACCACCTATACCCTGGAGAGTCGACATCCTTCTGCAACTACA
TCAGAAAAGCCACTTCCCAACAACCTGGAAGCGGAACAGCGAAGAGTCTAGTGTGCTGCTACTCTCT
GCTCAGAATAATGGCACTGTAAGTGGCCGGTCTGCATCACCTGTTGCAACTACTACAGATAGTGCTACA
ACTGGACGCTCAGGAACCTCCCAACAACAATCAAGGTCACGATCTGGATCATCGTTGAATTTGGCTGGC
ATTACACGTCAGTCTGTCCCATCATTTGCCAATTTTCGAGTTCTATTAAATGTAAGACAGCCACAATCACC
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ACAAGAAAAATACAACCTAGTAATAGTTATAGTCAGAAAGTACAAGGTGTCGAAGTTTCGAAAGCTGTG
AATGATGATAATGCTTAA

YDR145W_homolog 511aa (SEQ ID NO 468)
MERFNQIRQKLTEVQRRVQLLEQTKKTGNTPEQIQQIDKEIIECKAKFQQYQKVGIIYRNQLVLQAKA
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VQQQFMGNSQQQQQQQQQQLRNANKSALQGQAPSQAPTPLPVRPTPQSQPTAQAGVASQAATPGFRAS
QPTPSQTSRTGSALQQRAPSRQASSTPQSQFPPLPSESRHPSATTSEKPLPQQPGSGTAKSPSVAATP
AQNNGTVTARSASPVATTTDSATTGRSGTPQQQSRSRSGSSLNLAGITRQSVPSLPISSSINVKQPTIT
TFNSINDTRPSLTGGAANPMSILLDTPAITKLPTFDIEGDTGVIDSSTSGRVLNKRKLGLDLINTIGVDE
GDGKTSIDGNVEEFLDLADEFIHSVTSFACRLAKHRKVDSEARDVQLHLDKNWNKI PGYAMDEIRN
TRKIQPSNSYSQKVQGVESKAVNDDNA

YDR154C_homolog 333bp public: 1..333 (SEQ ID NO 469)
ATGATGTCGTTCCAAAGACTGCTGAAAATTTTCAGAGCTTTATGTACTGGTGAAAAAGGTTTTGGTTACA
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GTACTGGTGGTAAAAGTATTTACGGTACCAATTTGCTGATGAAAACCTTTGTCAAGAGACATGACAGAC
CAGGTTTGTGTTCTATGGCCAATGCTGGTCCAAACACCAATGGTTCCCAATTCCTTATTACCACCGTTC
CATGCCCATGGTTGGATGGTAAACACGTTGTTTTCGGTGAAGTCACTGATGGTTTTAG

YDR154C_homolog 110aa (SEQ ID NO 470)
MMSFQRSSKISELYSVKKVLVTKVLFSTESSHNSCFKVVISPTLTVSVKVFTVFNLSMKTLSRDMTD
QVCCLWPMVSVQTPMVPNSSLPFFAHGWMVNTLFSVKSSMV

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YDR216W_homolog 4257bp public: 1..4257 (SEQ ID NO 471)

ATGATTTTACCAACTCACCAGAGTCAATACCTTAATTATTTTGTCAACCCAGTTTAAATGACTGAGTCC
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GCGCCTACTCCCGCCTCGACTACCAAGAATTATAAGCACAAAAACAGAATACCAATACTGGAACATCC
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TTATTTGTTTGTCAAGTCTGTACAAGAGCATTGTCTAGGTTAGAACATCTACGTAGACATGAAAGATCA
CACACAAAGGAAAAACCATTTAGTTGTGGTGTGTGTCAACGGAAGTTTAGTCGTCGAGATTTATTGCTA
AGACATGCACAGAAATTACACGCTGGCTGTACTGATGCAATAACAAGATTAAGAAGAAAATCAATTAAG
AAATCTCAGGATGGGGACGATGATGATGACGATGATGACGACGATGAAGAAATGGCAAATTTCTGAAGAC
GAAAACGATCATGATGAATCGGGCAATGCAAGCACAAAGAATGGTAAAAAGGATAAAAAAGATCCACCA
CCGGAGTTCAATTTAAATTTATTCAATCTGAAACAAAAGCCAACTAAAGCGAACACGACAAAGTCAAAA
GTGGCTAAATTATCAACAACGACATCAAGGAAAAATTAACCAATCCTACGAGAAAAAACTCCAGCTCT
TTGCACAAAGCAGGTTCTTGATCAACGTCAAAAGGCTGCCGTTAATACAAAAATTTGTATCAAGTACCAAA
ATTGTATCAGGTACCAATAGTGGAGTGTGATAACTCCAACAAGGTCTAGAAGAGGTGCATCATTTTCT
GCTCAATCGGGTGCCAACTATGCCATCAACATACCTGAGTTTAAATGATATATATCCACAATCTGATAAT
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TCAGCAGATCATGTAACACCTCCAGTAAACGTAGTCAGCATGGGTCAATTTTCTCATCATCAACATTTT
TCAGCTACCGATATGGGACAAACAAGATCCGAAAGTGTAAACAGTTTAAACATCCATTTGATGGTTCC
TACATGATGCCAACGGTAACAATAAGCAATCAAGAAATCCAAATGGTGTGCTGCTCATCATCATCAT
CAACAACAACAGCAGCACCAGCAGCACAATCATCAACATCAACCAATCAGTCTCTGCTCGGGTTATCG
AGAAATGACATGTTAAGTGAAGATCACTATGGCTATTCAATTTATGATATCCCGGAGAATATTCTCAAT
TTCCCAATGGATTCTATATCAACAACCTTCAATGCAATGTCTTCCGGCCCAATTCAAAATTTAAACCA
TTATTCGCCTTACACACAAGAAATTGAACATGAGATTACTCCAAGAATTGATGGAAGAATTTGGGGATTTC
CAAAATAACAACAATACCAATGATAATCCGATTACCAAAATATCAATTATGACTTGAACCTTTCTTCAT
ACTATTGATGATATAGGACAAGATGTTATTTCTAAATTTATGCCAGGAGGTTACTCGTTTTATGGAGAC
AATAATGTGTGCGCAACTTCTTCAGCTAATGACTACAACCTCACCGAACAATATTGTTTCACCGAGCCAA
CAAAACAATCAATTTGCTCTTCACAACCAAGTCGTCAATCCTAGTGGTGTCTTACCACATTTAAACCAA
GCAATGATGAATAAAATGAGGTTGCATAACTATTCTAGCAACAATTTACTAATCATATAAGACAC
ATGATAAATAAGGCATTGGGTAAATACCCCATAAAGCGGCATAATGACACCTACTATACCCTCAAATGAG
AAACTAGAGTTTTATTTGAGTGTTCATTCAATCATTTTTTGGCACACCTCCCATTTATACATCCTTCT
AAATTGAATGAATATGAAATTATGGCCATGACTGGTAATGAAGATATAAACAATGAAAGTGCTAGAGTT
TGTTTGCCATTATTAAACAGCGACCATGGGGGCCTTGTTGGCCAATAACAAAAACGATGCTGAACATCTT
TATGAAGCCTCACGAAGAACAATACACATTTATCTAGAGAGTAGAAAAACAATTTCTACTAACGACAAG
AATTACAAGAATGGTAAGGATAAAAGCTCATCCGGTAATCCATTATGGTTACTTCAATCACTAATGTTG
TCTGTTCTTTACGGATTATTTTCAGATAATGAAAATAATGTTTATATTGTTATCCGTCAATTTGAACGCC
TTAAACTCATTAGTTAAGACATCCATAAAAAATAAAGGGCCAATTTTCTTTTCAACAATGGCGAAGAT
GAAGAATTTTATAATAAGTTAAATTTCTCATGATAATGGTACTTCTTATTTTCCAATAATTTGAATGAT
GAAATGCGATACAAAAATAATATAAACATGCAATCTCAAACGAGAATAGTATTTATCATTTATCGGTTG
ACGAATTTTGTGTTGATGATGTACAATGTACCGTTAACTTTCTCAATCAATGATATTAATCAATTTGGCA
GTCACTTCCAAGATGAAGAACTTTATGGAATTTAAAGATTATCAAGAGTTTCAAGAGTTTCTCAT
AAGAATAACAAGACTTTAGATGATTATTTGATAATAAAGAATGAGCCAATAATTTTCCGCGAATTATTG
TTGACAGTTATCAAATTTGGTATTTTCAGATAGTAACATTTACCAGAGATTGAAAAGAAAGTTACACAC
CAATTGCAGAATCTTTGTAAATATGGATTCAATTGTTTGGTGCATGGTATATATGAAATCAAACAATAT
CAAGAGATGAAAGAAGTAGATACATTCAAAGTGTTGGATTATTTAACCAAGTTTTATCCTACAAATGAT
GGATTGGGGTTCAATTGCTTTAGATTACCTGCCAATAAAGACTTGGAAAAGATTGATTATGCCTTATTA
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TATCAAGATTTAACTCAAAATTTATCATCGTCTTTTGGATGCTCACAGTACTGGGAATCCACTTAATTCA
ATTAATGATTATGATTATTTGAACTTGCTGATTGTTGTATTCTGGTACTCAAATTTGATATTATTTAAA
GTTGAGGATTCCAACAGTAATAGTAGAAATCGAAGCAAAAATGATCCAACAATGAAATCAATAACAAA
CTCAACAACAACAACAACAATAACAATGATATGAATAATAAACAAGTAATGGTGATCAATTAATTTCT
GCCTTTGATACTGATTTTGGATATTTGAATATGGATAATAATGGTTATGCCAAAAAAGAAGATTTTAA
CGATTACTGATGATGAGTTGCGATATGATAAAGAAAACGATGTCATATTTGATAAACATATTA
CTTGATATATTTGAAGAAGTTGAGAAATCAAGTAATTTGATACAAGCACAAATTTTCCATGCAATTT
TCCGTATTATCGATTTTTCGGTTTATGTTATGCGTAAAAATGATAATAATTCATCACCATTGCTAAT
ACTGATTTAATATTTGAATTGAATCATAGATATAGTATGGTCTTAGATTATTAGAAAGACTTGAACT
TTTTTGAAATTGAGATATCAAACATCAGCAGGAGGAGGGGAGGAGGTGTTAACAATAACAATAACAAC
GCCTTATCTATAAAATTAGAACAAGAATTCACAACTTGTATCTTTACAATGGGAATGTATTATCTTCA
GATCAATAACAAATACAAATACCACCAATACTATTACTACTACTACTACTACTACTACTACTACTACTAA
CAAAATCAGCATCATTCACAAGATTTTGGATTAGAAAAGACTTTATATATCTTAAAAATGGGAGAAAAT
GTTTTGAATTATATTTATGATTTAAATTTAAAGTTTGGGTATTTAAGAAATTTGGGTGATAGTTTATCA
GAAATTAGAAAATATTTAATTGATAATGAATCTACTTTGAATGGTTAA

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YDR216W_homolog 1418aa (SEQ ID NO 472)
MISPTHQSQYLYNFVNPVLMTESGDIIDSVTGTTTTTANMSNTTIDAPTPASTTKNYKHKKQNTNTGTSMSPSNSINSTNNNAAAAAATTTTSKSKSDIPELTAFGTTPSGKPRLFVCQVCTRAFARLEHLRRHERSHTEKEKPFSCGVCQRKFSRRDLLLRHAQKLHAGCTDAITRLRRKSIKKSQDGDGDDDDDDDDDEEMANSEENDHDESGNASTKNGKKDKDPPPEFNLNLFNSKQKPTKANTTKSKVAKLSTTTSRKNSTNPTRKNSSSLHKQVLDQRQKAAVNTKIVSSTKIVSGTNSGVSIPTPSRRGASFSAQSGANYAINIPEFNDIYPQSDNVEFSTPQFLPSSLDNEMTWLNNIPNIPGLSDSVSAANLMRQNSITNSADHVTPPVNVSQHGSFSHQSTFSATDMGQTRSESVNSLNTPFDDGSYMMPTVTISNQEIQNGVAHHHHQOQQOQHQQHNOHQPNQSSSLGLSRNDMLSEDHYGYSFYDIPENILNFPMDISSTTSNAMSSGPIQNFKPLSPITQEIEHEITPRIDGRIGDFQNNNNNTNDNPIHQNINYDLNLFHTIDDIGQDVISKFMPPGGYSFYGDNNVSATSSANDYNSPNNIVSPSQNNQFALHNQSSHPGASPHLNQAMNMKMLHNYSSNKLFTNHIRHMINKALGKYPISGIMTPTIPTSNEKLEFYLSVFIQSFLAHLPIHPSKLNVEYIMAMTGNEDINNESARVCLPLLTATMGALLANNKNDAEHLYEASRRTIHIYLESRTNSTNDKNYKNGKDKSSSGNPLWLLQSLMLSVLYGLFSDNENNVYIVIRQLNALNSLVKTSIKNGKPIFFSNNGEDEELYNKLNHDNGTSLFSNNLNDEMRYKNNINMQSQTRIVFIIYRLTNFLLMMYNVPLTFSSINDINQLAVTSKDEETLWNFKNYQEFQEFSHKNNKTLDDYLNNKNEPIIFRELLTIVIKFGISDSNISPEIEKKVTHQLQNLCKYGFNCLVHGIYEIKQYQEMKEVDTFKVLDTLTKFYPTNDGLGFNCFRLPANKDLEKIDYALLVDFTKISSIIDLKLKEQSWLKNYQDLTQNYHRLLDHSTGNPLNSINDYDYLKLADCCISVLKILFKVEDSNSNSRNRKNDPTNEINNKLNNNNNNNNNDMNNNSNGDQLISAFDPTDFGYLNDNNGYAKKEEFLRFTDDELRYDKENTMSYFDKHIKLDIFEEVEKSSNLIQAQMLFHAFSVLSIFSVYMRKNDNNSSPFANTDLIFELNHRYSMLRLLERLETFLKLRYSQTSAGGGGGGVNNNNNNALSILKEQEFNTLYLYNGNVLSDDHNTNTNTNTNTITTTTTTNDNGTKQNQHHSQDFGLEKTLYLKMGENVLNYIYDLNLKVCVFVKKLGDLSLSEIRKYLIDNESTLNG

YDR224C_homolog 393bp public: 1..393 (SEQ ID NO 473)
ATGGCCCCAAAAGCAGAAAAGAAACCAGCTTCCAAAGCTCCAGCTGAAAAGAAACCAGCTGCTAAGAAAACCGCTTCCACCGATGGTGCTAAAAAGAGAACCAGCTAGAAAAGAACTTATTCCTCATATATATATAAGTTTTTGAAACAAACACATCCAGACACTGGTATCTCCCAAAGGCCATGTCAATTATGAATTCGTTTGTTAACGATATTTTCGAAAGAATTGCCACCGAAGCCTCCAAATTAGCTGCTTACAATAAAAAATCCACAATTTCGGCTAGAGAAATCCAAACTGCTGTTAGATTAAATTTTGCCAGGTGAATTGGCCAAACATGCCGTTCCGAAGGTACCAGAGCCGTCACAAAATACTCATCTGCTTCTAGTTAG

YDR224C_homolog 130aa (SEQ ID NO 474)
MAPKAEKKPASKAPAEKKPAAKKTASTDGAKKRTKARKETYSSYIYKVLKQTHPDTGISQKAMSIMNSFVNDIFERIEATEASKLAAYNKKSTISAREIQTAIVRLILPGELAKHAVSEGTRAVTKYSSASS

YDR342C_homolog 1653bp public: 1..1653 (SEQ ID NO 475)
ATGTCATTAGATAATTCAACAGAAAACCGTGATTTGGAAGAAAAGGAAGAAATTCCAAAGAACGAACATAACGAACAAGGCGAACAACGAGAACAAATGAGCATATACCTACTTTGGAAGATAAACCATTTGAAGGAATATATTGGTATTAGTATTTTGTGTTTCCTTATTTGCCCTTTGGTGGTTTCGTTTTCGGTTTCGATACTGGTACCATTCTCGGTTTCATTAAACATGACTGACTTTTTAGAAAGATTTGGTGGTACTAAAGCTGACGGTACTCTTTACTTTTCCAACGTTAGAACTGGTATTATGATTGGTTTGTTCATGTGGGTTGTGCCATTGGTGCAATTATCTTTGTCTAAAGTCGGTGATATGTATGGTAGAAGATTGGTATCATGACTGATGATCATTTATATTGTTGGTATTATTTGTTCAAAATGCTTCTCAACATGCTTGGTATCAAATCATGATTGGTAGAATTATCCTGGTCTTTGCTGTTGGTATGTTATCAGTTTTGTGTCCATTATTTATCTCAGAGGTTTCTCCCAAACATTTAAGAGGTACATTAGTTTATTGTTTCCAATTGATGATTACCTTGGGTATTTCTTGGGTTACTGTACCAGTTACGGTACTAAGAAATATTCTGACTCCAGACAATGGAGAATTCATTGGGTTTATGCTTTGCTTGGCCCTTGTTGTTTGGTGGTATGGTAAGAAATGCCAGAATCTCCACGTTACCTTGTCCGTTAAAGATAGATTGACGATGCTAAGATTTCACTTGGCAAACATAACAGGTTTCTCCAGAGGACCCGTGATTATACCGTGAACCTCAATTAATCCAAGCTGGTGTGAAAGAGAAAGATTGGCCGGTAAGGCATCTTGGGGTGCTTTATCACTGGTAAACCAAGAATCCTTGAAAGAGTTATTGTTGGAGGTATGTTGCAATCATTGCAACAATTGACTGGTGATAACTATTTCTTCTACTACAGTACCACATTTTCAAGTCTGTCCGTTTTAAATGATTCTCTCGAAACATCTATTATCCTTGGTGTCACTCACTTTGCTTCCACTTTTGTGGTATTTATGCCATTGAAAGATTGGGTAGAAGACTCTGTTTATTAACCTGGTCCGTTGCCATGTCCATTGTTTCTTAATTTACTCATTGTTGGTACTCAACATCTTTACATTGATCAACAGGTTGGTCCAAACCAGAAAACAGATGGTAACGCTATGATTTTCATTACTGCACCTTTATGTTTCTTCTTCTCGCTTCTACATGGGCTGGTGGTGTCTACTCCATTGTTTCTGAACTTTATCCATTAAAAGTCAGAAGTAAGGCTATGGGTTTTGCTAATGCATGTAAGTGGTGTGGGGTTCTTGATTTCTTCTTCACTTCACTTATGATGCTATCCACTTCTATTATGGTTTTGTGTTATGGGCTGTTTAGTGTTTTCCATTTTCTTGTGTTACTTTATGATTTACGAAACTAAAGGTCTTACTTTAGAGAAATTGATGAATTATACTCTACCAAGGTTGTTCCATGGAATCAGCCGGTTGGGTTCCACCTTCTGACGAAGAAATGGTTCTGTCGAAAAGGCTATATCGGTGATATCCACGCAGATGAAGAGCAAGTTTAA

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YDR342C_homolog 550aa (SEQ ID NO 476)
MSLDNSTENRDLEEKEEIPKNEHNEQGEQNNNEHIPTLEDKPLKEYIGISILCFLIAFGGFVFGFDTG
TISGFINMTDFLERFGGTKADGTLYFSNVRTGLLIGLFNVGCAIGALFLSKVGDYMGRRVGIMTAMIIY
IVGIIIVQIASQHWYQIMIGRIITGLAVGMLSVCPLFI SEVSPKHLRGTLVYCFQLMITLGI FLGYCT
SYGTTKKYSDSRQWRIPGLGCFAWALCLLGGMVMPESPRLVVGKDRIDDAKISLAKTNKVSPEDPALYR
ELQLIQAGVERERLAGKASWGALITGKPRILERVIVGMLQSLQQLTGDNYFFYYSTTIFKSVGLNDSF
ETSIILGVINFASTFVGIYAIERLGRRLCLLTGVSAMSI CFLIYSLIGTQHLIYIDQPGGPTRKPDGNAM
IFITALYVFFFASTWAGGVYSIVSELYPLKVRSKAMGFANACNWLWGFLISFFTSFITDAIHFFYYGFVF
MGCLVFSIFFVYFMIYETKGLTLEEIDELYSTKVV PWKSAGWVPPSDEEMVRAGYTGDIHADEEQV

YDR343C_homolog 1641bp public: 1..1641 (SEQ ID NO 477)
ATGTCTCAAGACAACGTCTCATCAACATCTACAGCTGAGGCTGTAAATAATGAAATCAAAGTCAAAGAT
GAATTTTCGACAAGAACAAGCTCATACTAGTTTGAAGATAAACCTGTGAGTGCATACATTGGTATC
ATCATTATGTGTTTCCCTTATTGCCTTTGGTGGTTTCGTTTTTGGTTCGATACGGTACTATTTCCGGT
TTCATTAATATGTCTGACTTTTTAGAAAGATTCGGTGGTACTAAAGCTGACGGTACTCTTTACTTTTCC
AATGTCAGAACTGGTTTAATGATTGGTTTGTTCACGCTGGTTGTGCCATTGGTGCATTATTCTTGTCT
AAAGTCGGTGATATGTATGGTAGAAGAGTTGGTATCATGACTGCTATGATTGTCTATATTGTTGGTATT
ATTGTTCAAATTGCTTCTCAACATGCTTGGTATCAAGTCATGATTGGTAGAATTATCACTGGTCTTGCC
GTTGGTATGTTATCAGTTTTATGTCTTTGTTTCATTTCCGAGGTTTCTCCAAAACATTTGAGAGGTACT
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AAGAGTTACTCAGACTCTAGACAATGGAGAATTCCATTAGGTTTATGTTTTGCTTGGGCTTTATGTTTG
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AAAATGTCACCTTGCTAAAACTAACAAAGTTTCCCCAGAGGACCCAGCCTTATACCGTGAACCTCAATTA
ATTCAAGCTGGTGTGAAAGAGAAAGATTAGCCGTAAGGCATCTTGGGGTACTTTATTCAATGGTAAAC
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TATTTCTTCTACTACAGTACCCTATTTTCAAGTCCGTTGGTATGAATGATTTCTTTCAAACCTTCTATC
ATTATTGGTGTATTAACTTTGCGTCCACTTTTGTGGTATTTATGCTATTGAAAGAATGGGTAGAAGA
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CATCTTTATATTGACAAACCAGGTGGTGTCTAGTAGAAAACCAGATGGTGATGCCATGATCTTTATGACT
TCACTTTATATGTTCTTCTTTGCTTCTACATGGGCTGGTGGTGTCTTACTCCATTATTTCTGAACCTTAT
CCATTGAAAGTTAGAAGTAAGGCTATGGGTTTAGTCTTAATGCTTCCAATTGGACCTGGGGTTTCTTAATT
TCTTTCTTTACTTCAATTTATTTACTGATGCTATCCACTTCTACTACGGTTTCGTCCTTTATGGGATGTTTA
GTTTTCTCCATTTTCTTTGTCTACTTTATGGTTTACGAACTAAAGGCTTACCTTGAAGAAGAAATTGAT
GAATTGTACTCCACCAAGTCTTCCATGGAATCAGCTGGTTGGGTGCCACCTTCCGAAGAAGAAATG
GCAACCTCTACGGGATATGCTGGTGTATGCCAAACCAGAAGAGGAACACGTTTAA

YDR343C_homolog 546aa (SEQ ID NO 478)
MSQDNVSSTSTAEAVNNEIKVKDEFQRQEEQAHTSLEDKPVSAIYIGIIMCFLIAFGGFVFGFDTGTISG
FINMSDFLERFGGTKADGTLYFSNVRTGLMIGLFNAGCAIGALFLSKVGDYMGRRVGIMTAMIVYIVGI
IVQIASQHWYQVMIGRIITGLAVGMLSVCPLFI SEVSPKHLRGTLVCCFQLMITLGI FLGYCTTYGT
KYSYDSRQWRIPGLGCFAWALCLVAGMVMPESPRLVVGKDRIEDAKMSLAKTNKVSPEDPALYRELQL
IQAGVERERLAGKASWGTLFNGKPRIFERVVGVMLQALQQLTGDNYFFYYSTTIFKSVGMNDSFQTSI
IIGVINFASTFVGIYAIERMGRRLCLLTGVSAMSVCFIYSLVGTQHLIYIDKPGGASRKPDGDAMIFMT
SLYVFFFASTWAGGVYSIISELYPLKVRSKAMGLANASNWTWGFLISFFTSFITDAIHFFYYGFVFMGCL
VFSIFFVYFMVYETKGLTLEEIDELYSTKVL PWKSAGWVPPSEEMATSTGYAGDAKPEEEHV

YDR544C_homolog 1700bp (SEQ ID NO 479)
CTAAAGTCCAAAGTTGGTTCAATTTTGGCAGAAAAAAGAAGGAAAAATTCACCTGGA
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AGGAATTTCATCGGTGTTGTCTCGCAGTAACCTAAGATCTTTTATTGACCGCTTC
CATAGAGATGAGTCTAGCACTGGCATTAGCAGACAACATGAGCAGCACCAGCAGCCTTTG
AGTGATCCTTTGCCCTCACGCAGAGAAGCCTCAACCGGAAATTCCCCAATCACCAGAAGCT
CCACAGGCCAAATCACTAGAGCCTGTATCAGAAGTACTAAAAGAAGCTGTTCCACCTATG
CAAAACGGGTCCGAAAGGAAAGGTGAAAATCAGCAGTCGAGAGTTGATGTATCCTCTCAA
ACCTTGTACACAGTTACTCTACTCAGATGGATTTGGTGGTTCTGTAAACCATTACCA
GAACCTGTTGATTCTCCAAATGTGATTAAATACAATGACTCGGACGACTCTTCTACAGAA
GAACGTAGAGGCTCGTTACTTGAAAAACACAATTTAGAAGTACAACCTGTATCTTCCCCA
TTCACCTACTCAACCGCCAGCACCCTGTGCCACAAGAATCCAGATCTAGACAAAGCAGTGAT
GGCATTCTACTCGTTTGAAGCGGGTGTATGATTCCAACCCAATCTCGGCTACTCCAAGATCC
GAGCAAAATGTGTTTGGACAGATGCCAGACCCAATTTGTCTCTGAAAAGACTCTTGCT
CCACCACCACCACCTTCGAGAAAAGTTTGCACCATGAAGAACCAACTGTAAGGGAATCA

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GCTCTTTTCCACAATTTACCTGCTGCCTCCCATTCTGGAAGAGATTCCGGTAATGGCTCCA
TTAGCAAGTCAAGACAGGGGTCAATTCGTTGTTGAAAAATGATTTCAAACACGAAAACTTG
GCATCCACCCTCGGATTGAGCTCTTCTATTGCTGAAGTCATCAATGCCAGCTTTAAGGAT
GGACAGTTGATTAAATCACAAGTAGTTGGTGAAGTGGCCTTCAATTATAATGGTAATGCT
TCCGATCCACTTGTGGTCACTATTCTTAATAGTTTCGATAAAAGTACTCGTGAACAAGACT
TTTATTGAGGATTTAGGTCAAAGCAAGTATAAAGTGAACCCAACTTCAATTACGTCTAAA
ACTCTTGGTGGGTTGAAATATCTTTTGAAACCAACACAGGTACCAGTGATAATTCAACAA
ATATGGAAATTTGAACCTCATCAGTCAAGTTTGATGGTTAGCATTCGTTCAACTACACCT
TTGGTATTGGAAAATTTTGTGTCTCTGTAGCTTTGAATCAAGACATTGAAGCAACATCT
GCTTCCTCAAAGCCTCAAGGTGCGTTTAATAAAGAGAAAAACAGAATAACATGGAGATAT
CCACAGTCCCTCGCATTGAATGGTGTAGAGCGTTTGATAGCTAGATTTATGACTAATGGA
TTGGGTTCCGAACATGAGTCTGGTGTGAGATTAAATTTCAAGTTAAGGATCCACAAGTC
AAGTACTGTAGTATTTACAGTGAGAATGGCGAAGAGATTCTACGTTTAGAAATTTGGTT
AGCGGTAGTTATAGTGGTCATCTTTAAGTTATCTGTTTGGAGATTAGTCTCTTGTGTAAT
TGAAAAAATAAAAAACGTGA

YDR544C_homolog 548aa (SEQ ID NO 480)

LKSKVGSIFGRKKKKEKFTGADSLAEDESLSVSLPPTTRNSSLRSNSSTRRSFIDRF
HRDESSTGISRQHEQHQQPLSDPLPHAEPQPEIQSPEAPQAKSLEPVSEVLKELFPPM
QNGSERKGENQQSRVDVSSQTLSPVTPTHDGFSGSVKPLPEPVDSPNVIKYNDSDDSSTE
ERRGSLLEKHNLEVPVSSPFTTQPPAPVPQESRSRQSSDGIYSFEAGDDSNPISATPRS
EQNVFGQMPDPNLSPEKTLAPPPPSRKVLHHEEPTVRDSALFHNLPAAHSGRDSVMAP
LASQDRGHSLLNDFKHENLASTLGLSSSIAEVINASFKDGLIKSQVVGEVAFNYNGNA
SDPLVVTIPNSFDKVLVNKTFIEDLGQSKYKVNPTITSKTLGGLKYLLKPTQVPVLIQQ
IWKFEHPHQSSLMVSIRSTTPLVLENFVVSVALNQDIEATSASSKPQGAFNKEKNRITWRY
PQSLALNGVERLIARFMTNGLGSEHESGVQIKFQVKDPQVKYCSIYSENGEEIPTFRNLV
SGSYSGHL

YEL071W_homolog 1584bp public: 1..1584 (SEQ ID NO 481)

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CAAAAAGTCCAACGTGATGCAAAATTCAGCAACTTGAATCTCAAGACATCGAATACTTTAAAAGTGTA
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TATAGAGGTCAATCACAATTGGTTTTGAAACCGAAAACACCGAACAAGTCGCTTCTATCTTAAAGTAT
TGTAATGATAACAAGCTAGCTGTTGTACCACAGGGTGGGAATACTGGGTTGGTAGGTGGATCTAATCCA
ATTTTTGATGAAATCATCATTTCTTGTGCGCCATGAATAAAATCAGATCGTTTGATCCTGTCAGCGGT
ATATTGAAAGTCGACGCTGGTGTATTTTGAAACAGCTGATCAGTATTTGGCTGAGCAGGGCTACATT
TTCCCGCTCGACTTGGGAGCTAAAGGGTCTGTCATGTTGGTGGCAATGTTGCAATGCTGCTGGTGGT
TTGCGTTTGTACGATACGGTTCTTTCATGTTTCTGTTTATAGGTTTGAAGCTGTCTTGCCCCGCGGT
ACAGTTTATAACTCTATGCATTCATTGCGTAAAGATAATACTGGTTATGATTTGAAGCAGTTGTTTATT
GGATCTGAAGGTACTTTGGGTATTATAACTGGTGTTCGATTCTATGTCCATCAAGACCACAAGCGCAA
AATGTGGCATTTTTAGCTGTATCGAGTTATGAGGCCGTTCAAAGGTTTTTGTCCAGGCTAGAAAGGAG
TTGCAAGAAATTTATCGGCTTTTGAATTCATGGACAACACCTCACAAAAGTTGACTGCTAAGCATTTA
GGTTTGGAGCACCTTATTGAAAGCGGTGACTTCCCATTCTATGTGTTAATTGAAACCTCTGGCTCCAAC
AAAGAGCACGACGACGAAAAATTGGAACATTCTTGGGGAATGCAATGGAAGAAGGTTTAGTCGACGAT
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ACCACTATTGGAGGCGGTGTTTACAAGTATGACGTTTCTATTCCATTGGCAGATCTTTACGGGTTAGTT
GAGGACATCAATACCAGGTTAAATGATGCTGGAATCGCCAGCTTGGACGATGAATCGAAACTTGTGCTT
GCTGCATTGGGTTATGGTCACATTGGAGATGGGAATTTACACTTGAACGTTTCTGTGAGAAAGTATTCT
CCTGAAATTTGAAACTATCTTGGAGCCATTGTCTATGGAATGGATCGCAAAAAAATGGATCCATTTCG
GCTGAACATGGGTTGGGATTCCAAAAGAAAACTACATTGGGTATTCCAAGAATGAGATTGAGGTTCAAA
TTAATCAAAGAAATCAAACAACATTACGATCCAAATGGAATCATGAACCCATATAAATACGTGTAA

YEL071W_homolog 527aa (SEQ ID NO 482)

MQRRLVQTASYLIRRNNAVCRFSRYNGLPVASYSTKTVPFTADTYSQKVQRDAKFKQLESQDIEYFKSV
LPENSIITDEDDLLFFNEDWMRKYRGSQVLVKPKTTEQVASILKYCNDNKLAVVPQGGNTGLVGGSNP
IFDEIIISLSAMNKIRSFPVSGILKVDAGVILETADQYLAEQGYIFPLDLGAKGSCHVGGNVACNAGG
LRLRLRYGSLHGSVLGLEAVLPDGTVYNSMHSRLRKDNTGYDLKQLFIGSEGLGIITGVSI LCPSPRQAQ

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NVAFLAVSSYEAVQKVFVQARKELQEILSAFEFMDNTSQKLTAKHLGLEHPIESGDFPFYVLIETSGSN
KEHDDEKLETFLGNAMEEGLVDDGIIAQDEAQISLWSWRESIPEATTIGGGVYKYDVSIPLADLYGLV
EDINTRLNDAGIASLDDDESKLVLAALGYGHIGDGNLHLNVSVRKYSPEIETILEPFVYEWIAKNGSIS
AEHGLGFQKKNYIGYSKNEIEVKLIKEIKQHYDPNGIMNPYKYV

YER177W_homolog 795bp public: 1..795 (SEQ ID NO 483)

ATGCCAGCCTCCCGTGAAGATTCGGTTTACCTTGCTAAATTAGCCGAACAAGCAGAACGTTATGAAGAA
ATGGTTGAAAACATGAAAGCCGTTGCTTCCTCTGGCCAAGAATTGCTCTGTTGAAGAACGTAATTTATTA
TCTGTTGCTTACAAGAATGTCATTGGTGCTCGTCGTGCTTCTTGGAGAATTGTTTCATCAATTGAACAA
AAAGAAGAAGCCAAAGGAAATGAGAGCCAAGTTGCTTTGATCAGAGATTACCGTGCCAAGATTGAAGCT
GAATTGTCTAAAATTTGTGAAGATATTCTCTCTGTGTTGAGCGACCATTTAATTACATCTGCCCAAAC
GGTGAATCAAAAGTATTTTACTACAAGATGAAAGGTGATTACCACAGATACTTGGCTGAATTTGCTTATC
GCTGAAAAACGTAAGGAAGCTGCTGATTTATCATTAGAGGCTTATAAAGCTGCTTCTGACGTTGCTGTG
ACCGAGTTGCCACCAACCCATCCAATCAGATTAGGTTTAGCATTTGAACCTTCTCTGTTTTCTACTATGAA
ATTTTGAATCCCCAGATAGAGCTTTGTCATTTAGCTAAACAAGCTTTCGATGATGCTGTTGCTGATTTA
GAAACCTTATCTGAAGATTCATACAAGGATTCAACTTTGATTATGCAATTATTGAGAGATAACTTGACT
TTATGGACCGATTATCTGAAGCCCCAGCTGCCACTGAAGAACAACAACAATCCAGTCAAGCTCCAGCT
GCTCAACCAACAGAAGGTAAGGCTGATCAAGAATAG

YER177W_homolog 264aa (SEQ ID NO 484)

MPASREDSVYLAKLAEQAERYEEMVENMKAVASSGQELSVEERNLLSVAYKNVIGARRASWRIVSSIEQ
KEEAKGNESQVALIRDYRAKIEAELSKICEDILSVLSDHLITSAQTGESKVFYKMKGDYHRYLAEFAL
AEKRKEAADLSLEAYKAASDVAVTELPPTHPIRLGLALNFSVFYIEILNSPDRACHLAKQAFDDAVADL
ETLSEDSYKDISTLMQLLRDNLTLWTDLSEAPAATEEQQSSQAPAAQPTGKADQE

YGR192C_homolog 1008bp public: 1..1008 (SEQ ID NO 485)

ATGGCTATTAAAAATTGGTATTAACGGTTTCGGTAGAATCGGTAGATTAGTCTTAAGAGTTGCTTTGGGC
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AAATACGATTCTACTACGGTAGATACAAGGGTGAAGTCACTGCTTCTGGTGACGACTTGGTCATTGAT
GGTCACAAGATTAAAAGTTTCCAAAGAAAGAGACCCAGCTAACATTCCATGGGGTAAATCTGGTGTTGAC
TACGTTATTGAATCCACCGGTGTTTTACCAAACTCGAAGGTGCTCAAAAACACATTGATGCTGGTGCC
AAAAAAGTTATCATCACTGCTCCATCTGCTGATGCCCCAATGTTTGTGTCGGTGTTAACGAAGACAAA
TACACTCCAGACTTGAAGATTATCTCCAATGCTTCTTGTACCACCAACTGTTTGGCTCCATTAGCTAAA
GTCGTCAACGATACTTTTCGGTATTGAAGAAGGTTTGATGACCACTGTCCACTCCATCACTGCTACCCAA
AAGACCGTTGACCGTCCATCCCACAAGGACTGGAGAGGTGGTAGAACTGCTTCTGGTAACATTATCCCA
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TCTTTGAGAGTCCCAACCACCGATGTTTCCGTTGTTGACTTGACTGTCAGATTGAAGAAAGCTGCTTCT
TACGAAGAAATTGCTCAAGCTATCAAGAAAGCTTCTGAAGGTCCATTGAAAGGTGTTTTGGGCTACACT
GAAGATGCTGTTGCTCCACCGATTCTTGGGTCAAGCTACTCATCTATCTTTGATGAAAAAGCCGGT
ATCTTGTTGTCCCCAACTTTTCGTCAAATTGATTTCCTGGTACGATAACGAATACGGTTACTCCACCAGA
GTTGTTGACTTGTGTTGAACACGTTGCTAAAGCTTCTGCTTGA

YGR192C_homolog 335 aa (SEQ ID NO 486)

MAIKIGINGFGRIGRLVLRVALGRKDIEVVAVNDPFIAPDYAAYMFKYDSTHGRYKGEVTASGDDLVID
GHKIKVFQERDPANIPWGKSGVDYVIESTGVFTKLEGAQKHIDAGAKKVIITAPSADAPMFVVGVNEDK
YTPDLKIIISNASTTNCLAPLAKVNDTFGIEEGLMTTVHSITATQKTVDGPPSHKDWRRGRTASGNIIP
SSTGAAKAVGKVIPELNGKLTGMSLRVPTTDVSVVDLTVRLKKAASYEEIAQAIIKASEGPLKGVLGYT
EDAVVSTDFLGSSYSIFDEKAGILLSPTFVKLISWYDNEYGYSTRVVDLLEHVAKASA

YGR243W_homolog 399bp public: 1..399 (SEQ ID NO 487)

ATGGCTTCAACAGTTCAACACGCATCCAAATTTCAACGTTTTTTAAATTCAGAGACCGGTCCTAGAACC
GTGCATTTTTTGGGCTCCAGTGTTCAAATGGGCCTTAGTTGCTGCTGGACTTAATGACATACAACGTCCT
GTTGAAAAATTGAGCGGAACCAACAGATAGCATTTGTTGCCACTGGTGCCATATGGACTAGATGGGCC
GGGTTTGTATATAAAACCAAGGAACATGCTTTTGGCATCAGTGAATTTCTTTTGGGTGGAGTTGCTGGT
TACCAATTGTTAAGAATTGTCAACTACAGAAGAGATTTGGGTGATTCCCCAATGCAAGTATTTAATTAT
ATCTTGAACGGTGATGCAGCTGCTGTAAAAGAACCAGAACCAGCCAAGAATTAA

YGR243W_homolog 132aa (SEQ ID NO 488)

MASTVQHASKFQRFLNSETGPRTVHFWAPVFKWALVAAAGLNDIQRPVEKLSGTQQIALFATGAIWTRWA
GFVIKPRNMLLASVNFLLGGVAGYQLLRIVNYRRDLGDSPMQVFNYILNGDAAVKEPEPAKN

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YHL021C_homolog 1224bp public: 1..1224 (SEQ ID NO 489)
ATGTTAAGACAACCATTACGCCAAATCCGTTTCCACTCGAAATTGGCACTTGAGGATACAAACAGCAAA
GAAGTGACAGTCACCATCAACGGCAGAACCTGTACATTCAACAACGTGTTTTTGAGAGACGCATGCCAA
AGCCCAGACTCGGTAGACCCCATTTCTAGCCAAAACTATTCACTACAGCAGATGCAGCAACCGGCTTG
CAAATTAACGCACCCCCAGTGGTAGAGGATTCTCTATTGAAAATCCAATGGAGCAACAATGGCAAACTC
ACCAACTCAGTCTACCCCGTGTCTATTCTTAGAAAATACTCCACCAACAAACGACTCGGCAAAATCTTT
GACAAAGATAGAAAAGTTATGGGACAAACAAGAACTCGAAAACAACCTTGCCTCCCTCAACATGGACTAC
GACGACATTCTACCAACGACAACCTCTTTCTTCCAGACGTTGTACAACCTGAATAGGTACGGGTAAACA
TTTGTCAACAACATCCCCACCCACAAATTTCTGACATGACAGAGGACAACGCCACGCAATGGCCAGTG
TACAAGATCGCCGAAAAGTTTGGCTACATCAAGAAAACATTCTACGGGACATTATTTCGACGTCAAGAAC
AAGAAGGAAAAAGCAACCAACATTGCCTACACCAACACGTTTTTGGCATTGCACATGGACTTGCTCTAC
TACGAGTCACCCCGGGATTACAGTTGCTACACGCTATCCAGAATCTACGTTGGGCGGCGAAAACATC
TTCTGTGACTCGTACCTTGCTGCTGAGCATGTCCGAAAACCGACCCAGGGCATAACGGCACTACC
CAGACCCCAATCACCTTCCACTACGACAACAACAACGAGTACTACTACTACAAGCGGCCGTTAATCGTT
GAAGACCCCGAGGTTGGCGACGGGTTCCTCGAAAATCGCGTCCATCAACTATGCCCCGCCATTCCAGGGC
CCATTTCGAGGTTGACCCCCACCCAGACTTTATCCGCGGAATGCAGTTATTTCGAAACCTTCATCAACGAC
CCGGCAAACCACTTTGAAATCAAAATGCCAGAAGGCACTTGTGTCAATTTTCGAAAACAGAAGAGCCCTT
CACTCGAGAAACGCATTCTCCGACCTGAACAACGGCGACAGATGGTTAATGGGCACTTATGTTGACGGC
GACAGTTTTAGATCAAAATTACGTATAGGCTATAGAAAAGTACATACCTAA

YHL021C_homolog 407aa (SEQ ID NO 490)
MLRQPLRQIRFHSKLALAGYNSKEVTVTINGRTCTFNNVFLRDACQSPDSVDPDISSQKLFTTADAATGL
QINAPPVVEDSSLKIQWSNNGKLTNSVYPVSFLENYSTNKRGLGKFFDKDRKLWDKQLENNFASLNMDY
DDILTNDNSFFQTLNLRNRYGLTFVNNIPTQISDMTEDNATQWPVYKIAEKFGYIKKTFYGLFDVKN
KKEKATNIAYTNTFLPLHMDLLYYESPGLQLLHAIQNSTLGGENIFCDSYLAAEHVRKTDPRAYTALT
QTPITFHYDNNNEYYYYKRPLIVEDPEVGDGFPKIASINYAPPFQGPFEVDPHPDFIRGMQLFETFIND
PANHFEEKMPEGTCVIFENRRALHSRNASDSNNGDRWLMGTYVDGDSFRSKLRIGYRKVHT

YHR162W_homolog 354bp public: 1..354 (SEQ ID NO 491)
ATGTCATCATTTTAAAAAATTCAGTATTTTATTTTCAAAACAATCCCTTAGATATGTCTGTACAAC
CATTTTTGGGGTCCAGTATCAAATTTGGGATTCTATAGCTGCTATTTTAGATTGAAAAAAGATCCT
GATTTAATTAGTGGACCAATGACTGGTTCATTAATACTTTATTCTTTAGTGTATGAGGTATTCAATG
GCAGTTACTCCTCAAATTTATTATTGGGTGTCATTTTGTAAATGAATTGGCACAATTGAGTCAA
GGATTTAGATGGGTAAACATCACTATGATACTTCTTCAAATGATGGTGAAGATACAAAAAGATAACT
CAAAATTGA

YHR162W_homolog 117aa (SEQ ID NO 492)
MSSFKKFTDFLSKQSLRYVCTTHFWGPVSNFGIPIAAILDLKKDPDLISGPMTGSLILYSLVFMRYSM
AVTPQNYLLFGCHFVNELAQLSQGFWRVVKHGYDTSSNDGEDTKKITQN

YLR109W_homolog 531bp public: 1..531 (SEQ ID NO 493)
ATGACTGACGGTAAATTCCCACTAACATTGAACCAAAATACATTCTTATTCTAAAGATCATGCAAGT
TTAAGTCTTGTGCTAATCCAATACCATTGGATTTAAAATCTTTATTTCCAAATAATACTGTTGTTGTC
ACTGCTGTGCCTGGTGCTTTTACCCCAACTTGACTGAACAACATATCCCTGATTATTTGAAACATTTG
AAAGATTTCAAAGACAAGGGCGTCAAAAAAATCATTTGTTTTATCTGCCAATGATCCATTTGTAATGGCA
GCTTGGGCTAAAGCTTTGGGTATAGTGAAGAAAATTATGTTATTTTGTCTACTGATCCTAATGCT
TCTATTTCTAAAGAATTGGGTGATGGATTTGTTGCTGATTGACTCTGGCAGGTATGGGATTAAGATTA
CAAAGATATGCTAGTATTGTTGTTAATGGAGAAATCACTTATTTGGAAACTGAAGATAGTTTGGGATTC
CTGGAAATTTCTAGTGCTGAAACCATTTTAAAGAGAATCCACAATTAA

YLR109W_homolog 176aa (SEQ ID NO 494)
MTDGKFPTNIEPKYIPYSKDHASLTACANPIPLDLKSLFPNNTVVVTAVPGAFTPTCTEQHIPDYLKHL
KDFKDKGVKKIIVLSANDPFVMAAWAKALGYTDEENYVIFATDPNASISKELGDGFVADLTSAGMGLRL
QRYASIVNGEITYLETEDSLGFSEISSAETILKRIHN

YLR206W_homolog 879bp public: 1..879 (SEQ ID NO 495)
ATGAGAAAACAAAATAACAATTTATTGGATTGTAATGATGAAACACCACCACAACAACCTCAATATTAT
TTAGCAACCGGATTCTATCAACAACAACCAATTTTATGCCAGCAACCTCAATCGCAACAATCTCAA
CAATATGATATGTTTGGGAACCCAATACAGAAATCCAATGGACACAGGATTATATAATCAACAGGCCAT
TATCAACAACCACAACAGCAGCAACAACAGTTTCAACCAACACAGTTTACTGGTTTTAACTATGGACAA
CCACAACAACCACAAGCGCAACCAGAACCTTTACAACCATTGAAAACAGGATCCAATAATCCATTTGCC
ATGCTCTTCTGGGTGAGACAATACCAACAAGCCACCAACTCAATCCTTAAACAGTTTAGCTGAACAGCAA

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CAACAGCAACAGCAGCAGCAACCACAATTTTTTACTCAGCCAACTACTGCTCCACTCAAACAACAAAAC
ACATCATCATCAAGGTTTAAATGAACTCATGAGTTGAATGATTTATTAAGTCAAGGAACTGGATTAGAT
ACATTCGGTAACACTGGAGATACTAGAATCCCACATCAACATACAAAGACACAAAATTTTATAAATTCA
AGTGGAACTGGATATAAAACAACTGGTAATGAACCAATTAGATTAAAGTTCTAATGCTACAGGTAATCCA
TTTCTTAATACTGGTATTGGATATCAAGGTGCTACACAACAGCAAGTGCCACAACAGCAAGTGCCACAA
ATCAATCCTGCTTATACTGGGTATGGATTGGTTACGCTCAACCTCAACAACACCAGCAATACCAACAA
CAACAACAATCAGTAATGGTAATGATGGCCCAAGTTTAAATAGATATTTAA

YLR206W_homolog 292aa (SEQ ID NO 496)

MRKQNNNLLDLNDETPPQQPQYYLATGFYQQQPQFYAQPPQSQQFQQYDMFGNPIQNPMDTGLYNQQAY
YQQPQQQQQQFQPNQFTGFNYGQPQQPQAQPEPLQLKTSNNPFAMSSGSDNTNKPPTQSLNSLAEQQ
QQQQQQQPQFFTPPTAPLKQONTSSSRFNETHELNDLLTQGTGLDTFGNTGDTRIHQHTKTQNFINS
SGTGYKQTGNEPIRLSSNATGNPFLNTGIGYQGATQQQVPPQQVPPQINPAYTGYGFGNAQPPQHQQQYQQ
QQQSRNGNDGPSLIDI

YMR043W_homolog 789bp public: 1..789 (SEQ ID NO 497)

ATGGCTATTAAAGAAGAAACAAATGAATTTAGTCAAGGTAATGAGGGGAATTCCTTCAACCAATAAC
AACAATAACAGCAACAACAGCAACAACAATGCTGATGTTCTGCACAGTAGATGATGACGAT
GATGACGATGGTACTTCTCAAGGTAAAACCTCAAAAGGAAAGAAAATTGAGATCAAATTCATTCAA
GAAAATCAAGACGTCATATTACTTTTCGAAAAGAAAAGCTGGGATTATGAAGAAAGCTTATGAATTA
TCAGTATTGACAGGTACTCAAGTGTTATTATTAGTTGTTTCAGAACTGGTTTGGTTTATACTTTTACC
ACTCCTAAATTACAACCTTTGGTCACTAAATCTGAAGGGAAGAATTTGATTCAAGCATGTTTGAATGCT
CCTGAAGAAGGATTGGGTGATGATCAAGAGAATCAAAGTGATGGAAATACAGGAGATTACCTGATCAA
AGCCCTGCTCCAGCAACCAATCCAAATGTCTGGGTGCTGCAGGTCATGCTCATCATTCACAACAA
CAACAGCAACAACAAGCTCAACAGCAAGCTCAGCTAGCAACAATGGCACCAATGCCTTCTCATGGTTTA
CCTACACATTATTCCAATCCTCAAGGAGCTGGTAATCCTGGTGTACCTCCTCAACAACAAGGTCAACAT
CAACCTGGTATTCCATTACAAGGTGGTTATAGTGATCAATACCTGTATTTTGGTAATATTCAAATAAC
AACATACCTAATCAACAGCAATATCAATGA

YMR043W_homolog 262aa (SEQ ID NO 498)

MAIKEETNEFSQGNENSHSTNNNNNSMNSNNNADVSAVDDDDDDGTSQGKTQKERRKIEIKFIQ
EKSRRHITFSKRKAGIMKKAYELSVLTGTQVLLLVVSETGLVYTFTPKLQPLVTKSEGKNIQACLNA
PEEGLGDDQENQSDGNTGDSPDQSPAPATNPVMGAAGHAHHIQQQQQQQQQAQQQAQQQMAPMP SHGL
PTHYSNPQGAGNPGVPPQQQQQHQPPIPLQGGYSYDQYSYFGNIQNNNIPNQQQYQ

YMR256C_homolog 330bp public: 1..330 (SEQ ID NO 499)

ATGAGAATGAAACAACCAGACGACCAAAAGTCTGAGAGAGAGAGAGAGAAAATATCGGCTCATTATT
TTCAATTCACCTTTTAACTCCTAGTTAATACTATTTACTTTCTTTCTTCTAATCCATCCACCATCCT
ATCTATTCAATTATGAATCCACAAAGATTATTGAATTACAAAACATTATCAAAATACTCCTAAACCA
TTATGGTTAAGAGGTAGACAATCGGCATTTTATGTTTATCCATTTTATGCTTTATTTGCTGTTAGTACT
GCCATCCCATTATATTATAGTGTTAGAGCTGTTGCTGGTATAAAAGATGAATAA

YMR256C_homolog 109aa (SEQ ID NO 500)

MRMKQPDQKSEREREKKYRLIIFNSLLILVNTIYFLSSNYP SHHPIYSIMNPQRIIE LQKHYQNTPKP
LWLRGRQSAFLVYPFYALFAVSTAIPLYYSVRVAGIKDE

YOR267C_homolog 2091bp public: 1..2091 (SEQ ID NO 501)

ATGCCAGATAAACATAAACTCAAACCTATTTGGAAAAATAAACACGACAAAGATGACGAATTGTCTTGT
TCAACGTCAAACCATTTCTCACGGAAGTACACGGAAGTTTTTAGGATTTTCATATTGGAAGACATGAATCG
GGCGACTCGTTGACTTCTCCAGTTATGAGCAATTCATCCGAAAGTCATCATCACAGCCATCACCTTCAT
CAAGCCAATTCAAGTGCAAACCATCGTAACCTTCTCCAGTTCATTCCAATACTGGTACTGCCACTACC
ATTCCATCAATACAATCACCACAACCTCAAGCATCTGGATTACACCGCGGGGACTCCGATAAAAAATCA
TCTGGCTCAGTTGTTGATTTGAAAAAATCTTCAAAACAAAGAAAATCTCAAATCCAAGAAAGGAAGGA
CATAGTATTTTGGGACAATATAGCAATCAGTCCATTACCACCACCAATGGCGCAGGTTTCATTGCGCT
GGTGCAGGGTCGGGGAACGGCAGTGCCTTGCAATCACGTGAACAATCATCTACGTCATTAGCCACTTTA
ATCAATCAAACATCTTCTCAACTTTTGTACAATGCTTCACATTCTGTCAATAGCAATCGAGATCCCTTC
ACGGACGACAACCTCTCCATTGGTGAAGAAGTATGGTAAGATCGGGAAAGAGTTGGGCAGTGGAGCCGGT
GGGTCCGTCAAATTAATCACCAGGCCAGTGACTCCAAGACGTTTGCTGTTAAAGAATTTAGAGCGAAA
AGATCTACTGAATCATTGAAGGATTACACTAGGAAATGTACTGCTGAGTATTGTATTGGTTCTACTTTG
AGGCACCAACATCATTTAAACCATCGATATTATCCATGAAAACAATCGTTATTTTGAATTATGGAA
TATGCACCTATAGATTTCTTTGCTGTTGTTATGAGTGGAGAGATGTCTCGAACGGAAATCAATTGTTGT
TTAAAGCAAATTATTGAAGGTGTGGCATATTTACACAAATTAGGGTTGGCCCATCGTGATTTGAAATTG
GATAATTGTGTTATAACGAATGAAGGGATTTTGAAGATTATCGATTTTGGTAGTGCTGTCATTTTCAAG

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TATCCCTACGAACAGTTTGGTAACAACAATTCTATTACGCCGTGTCATGGTATTGTTGGATCTGATCCT
TACTTGGCCCCCGAGGTTTGAATCTCCTAATAGCTACAACCCACAACCTGTGGATTATGGTCTATT
GCCATAATTTACTGTTGTATGACTTTGAAGAGATTTCCTTGGAAAATACCTAGTCAAGAAAAGGATAAC
AGTTTCCGACTTTATTGCATGTATGATGATAATTTCCATGATTATTATTTAGTAACGAATGTCATAAA
CTTTTGTGCAACAGCGTAAACTAAAGAATACAATTGTTAGACTGAACAAAAGGAAAAAGCAGCTAGAA
GAGGAAAAGGGCGACAAGCCTGAAGAAGACGAAGAAATGAAAGATGCCGATAGTGCACCACAGCAACAT
CATCATTTCTCATGATGTAGAGCTGGGAAAAAACTGGTGGATCTACGGTTGGCAAAGACAAGTCAAATGAA
GCTGTTACCGTTTTAACAGATGAGCAAGCAGAAGAGATTATGGCACAATTAAATGAGATTGATAGAAAA
CTACAAGAGTTTGAAGATAAAAAGAATCAACTTAAAGAGAAATATGAGGCTTTGCGAGATGCTGATCCT
AGATATCAAAAACAGTTGGCACAATTCACGAAGAGGAAGAAAAGCAAAGACTAAAAGATGCCGAGCAC
GGTGGCGATGAGAAAAAGAAATCACATCATAAACAGATTTCATGGTCCGTATAGATTGATGAGATTGTTG
CCACATGCTGCTAGACCAGTCATATCAAGATTATTGGAGGTTGATCCAAAGAAAAGAGCAACTATGGAA
GAAATCTAGAAGATGAATGGATTAAAGAAATCAATGCTGTACAGTTAAGCCAGTTTCAAATCAACA
GATGCAACATTAGATTTTATTGAGGATGAGGACGAAGTATTGGTGAAAGGAGTACCTCCACACGAGCAT
ACAATTGTGAAAGAAGGTTGA

YOR267C_homolog 696aa (SEQ ID NO 502)

MPDKHKLKLFKGNKHKDDLSLSTSNHSHGSTRKFLGFHGRHESGDSLTSFVMSNSSESHHHSHHPH
QANSSANHRNPSPVHSNTGTATTIPSISQSPQASGLHRGSDSKSSGSVVDLKKFFKTKKTSNPRKEG
HSILGQYSNQLHSPPPMAQVHSPGAGSGNGSALQSRQSSTSLATLINQTSSQLLYNASHSVNSNRDPF
TDDNSPLVKYKIGKELGSGAGGSVKLITRPSDKTFAVKEFRKRSTESLKDVTYRKCTAEYCIGSTL
RHPNIIKTIDIHENNRIFYEIMEYAPIDFFAVVMSEMSRTEINCCCLKQIIEGVAYLHKLGLAHRDLKL
DNCVITNEGILKIIDFGSAVIFKYPYEQFNNSIQPCHGIVGSDPYLAPEVLKSPNSYNPQPVDLWSI
AIIYCCMTLKRFPWKIPSQEKDNSFRLYCMYDDNFHDYLSNECHKLLQLQRLKNTIVRSNKRKKQLE
EEKGDKPEEDEEMKDADSAPQQHHSHDVESGKTGGSTVGKDKSNEAVTVLTDEQAEIIMAQLNEIDRK
LQEFEDKKNQLKEKYEALRDADPRYQQLAQIHEEEKQRLKDAEHGADEKKKSHHKQIHGPYRLMRL
PHAARPVISRLLEVDPKKRATMEEILEDWIKIQCCTVKPVSKSTDATLDFIEDDEVLVKGVPPEH
TIVKEG

YOR374W_homolog 1500bp public: 1..1500 (SEQ ID NO 503)

ATGTTTAAAAAGGCCTTACCATTAGTCAGCAAGCTCACAACACCAAAAGGTATCACTTATAACCAACCC
CTTGGGTTATTTCATCAATAACGAATATGTTTACCCAAAAGCAACAAAAGACATTGAAAGTTTCTCCA
TCCACTGAAGAAAAAATAACTGATGTTTACGAAGCTTTAGAAGAAGATATTGATACTGCTGTGAAGCC
GCACAAGCCGCATACCACAATGGTTGGGCTCAAGGGCCACCAGAACAAAGATCAAAAGTTTTGTTCAAA
TTAGCCGACTTGATTGAAGAAAATGCCGAATTATTAGCTCAAATTGAAACTTGGGACAACGGTAAATCC
TTACAAAATGCCAGAGGTGATGTTGCCTTGACAGCTGCTTACTTCAGATCCTGTGGTGGTTGGGCCGAC
AAAATTTTGGGTTCCCAAATCAATACTGGTAACACTCATTTCAACTACACTCAAAGAGTCCCATTAGTC
TGTGGTCAAATTATTCTTGAATTTCCCATTATTGATGGCTTCTTGGAAATTGGGACCAGTTCTTGCT
ACTGGTTCTACCAGTGTGTTGAAGACTGCTGAATCCACCCATTATCTGCTTTTATATCTTTCCAAATG
TTAGTCGAAGCCGGTATGCCAAAAGGTGTTATCAACATTGTTTCTGGTTTTGGTGCTACTGCTGGTGCT
GCCATTGCTAAACATCCAAAGATTGAAAAAGTTGCTTTCACTGGTTCTACTGCCACCGGTAAAATTATC
ATGAAATTGGCTGCTGAATCAAACCTGAAAAAGTTAACTTTGGAATTGGGTGGTAAATCTCCAAACATT
GTTTTCAACGATGCTGATTGGACAAGACTATTCAAACTTGATTGTTTCTATCTTCTACAATTCTGGT
GAAGTCTGTTGTGCTGGTTCTCGTCTTTGATTCAATCCGGTGTACGACCAAGTTGTTGAAAAATTC
AAAGAAGCTGCTGAAAGTGCAAGGTTGGTAACCCATTTCGACGAAGACACTTTTATGGGTGCCCAAGTT
TCTGACGTCCAATTGTCCAAAATTTGAAATACGTTGAATCTGGTAAATCTCAAGGTGCTACTGTTGTT
ACCGGTGGTGCTAGAGCTGATGGTAAAGGTTACTTTGTCAAACCAACTATTTTCGCTGATGTCAAGAAA
GATATGGATATTGTGAGAGAAGAGATCTTTGGTCCAGTTGTCACTTTGATCAAATTTGATACTGTTGAC
GAAGCCGTTGAATTGGCCAATGATTCCGATTATGGTTTGGCTGCTGGTATTCACTCTGCTGACGTTAAC
AAATGTATTGATGTGGCCAACAGAGTTAAAGCCGGTACTGTTTGGGTCAACACTTATAACGATTTCAC
CCAATGGTTCCATTCCGAGGATTCAGTGCTTCAGGTATCGGTAGAGAAATGGGTGAAGAAGTTTGCAT
GAATACACTCAAGTCAGAGCTGTGAGAATGAAAATCAACCCACCAAACTAA

YOR374W_homolog 499aa (SEQ ID NO 504)

MFKKALPLVSKLTPKGIYTNQPLGLFINNEYVHPKQKQTFEVIISPSTEEKITDVVEALEEDIDTAVEA
AQAAHYHNGWAQGPPEQRSKVLFLADLIEENAELLAQIETWDNGKSLQNARGDVALTAAYFRSCGGWAD
KILGSQINTGNTHFNVTQRVPLVCGQIIPWNFPLLMASWKLGPVLATGSTTVLKTAESTPLSALYLSQL
LVEAGMPKGVINIVSGFGATAGAAIAKHPKIEKVAFTGSTATGKIIMKLAESNLKKVTLELGKSPNI
VFNDADLDKTIQNLIVSIFYNSGEVCCAGSRLLIQSGVYDQVVEKFKEAAESVKVGNPFDEDTFMGAQV
SDVQLSKILKYVESGKSQGATVVTGGARADGKYFVKPTIFADVKKDMDIVREEIFGPVVTLIKFDTV
EAVELANDSDYGLAAGIHSADVNCIDVANRVKATGATVWVNTYNDFFHMPVPFGGFSASGIGREMGEVLH
EYTVQVRAVRMKNIPPN

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YPL089C_homolog 1836bp public: 1..1836(SEQ ID NO 505)

ATGGGTAGAAGAAAGATTGAAATAGAACCATTGACAGACGATAGAAATCGTACAGTGACTTTTGTGAAG
CGTAAGGCAGGGTTATTTAAAAAGCTCATGAATTAGCTGTGCTCTGTCAAGTGGATTTAACGGTTATT
ATCGTTGGCAATAATAATAAAGTATATGAATATTCTACTGTTGAGGCAATGAGATTTTAAATGCCTAT
AATAAAACCATTAAGTCAGAAAACAAGTACATGAATCGAAGTCTCCAGAATATTATTCGAAATTTAGA
AAGAAACGACATTTAAATGAACCACTTATGAATAAATCAGGGTCTGTAGTTGGCACTAATACACATTTG
AACGATGAAGACTATGATCATAATGTTTCATGAAGCGGGCGATGAGGATTCGGAATATGAAAGCGATGAT
AATTCCTCCACAACCTAAACGGCACAAAAGATCAGAGTCGGTTAAAAAGAGCAAAACCCCAAGTGTTT
AATAGTACCCAACCTCCACCACCGCTCCACCACCTCATATATCTTTAAATAATGTTCCAACATTTACC
AACCCCAAAATTACAAAAACAGATTGATGAGACAAATAACACTTCGGCACCGCCCGCTACTGGGACA
AAAAATGAACCAACGATGCAACGACCAGTATTGAGGGTACAAATACCGAATGATGCCAAGAGCAATACG
AATAATTCCCATAGTGGTGTAAATAATAGTGATGGCAAGGACACGGCGAGAACAGTGACGGCAGTCGAC
AATAGTGCACCAACCAAAACACTCAATCGAGCAATACAACATCAGGTACAGGGACTGCTGATACCAAT
TCATCGCAACTAAATTCAAATGGTAATAGTAATTTAGTGCCCGGGAATGTTCCAAATACCAGATTTTCG
GGATATTCATCGTTTCGATCACCAGACTCACGAAAACCAACATTACCGTTACCTTTGCAAACCAATCA
CAAACGTCATCTCCAGCTAGTGTGTAGCACCAGGTTTACCATTGACAGGAGGAAGCAATGCATATTTT
GCAGGAATGCAACAATCACCCGTGGGTGGTTTCGTATGTCAATTATCCAGCCCAAGTATATCAGCAGTAT
CAACAGTTCCAAAATCAACTACAACATAAGAACAACAACAGCAACAGCAACAGCAACAGCAAAAAACAA
CAATCTCAGCCCGCAGCCATCATCGCAACTGGTTGGAAATCAAATGCACAATTGGAATCAGCAGCACGA
TTCCGTTCTGGTTTACCGACAGGGACACAATTTAATAATGGTGAACAAACACCAATTTTCAGGATTGCCA
TCACGATACGTTAATGATATGTTCCCTTCCCATCTCCATCAAACCTTTCTTGACCTCAAGATTGGCCA
TCAGGTATAACACCAACTACTCATCTACCACAGTATTTTGTGAATATGCCATTGAGTGGAATTGGACTG
CAACAACCTGCAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACA
CAACA
CAACAGCAACTGCAAGTACCTGTTATCCCAATACAAACACAACATCACAACAATGGCTTCAACTACC
AATCACAATCAGCTAATCTAATACCAGGGTTTTTACAAAACCCAAACACAAGCCACTGGAAATTCGGCA
AATGCTTCCAAGCTGAGTGATGCTGGTGATGGTACTAATCCAACCACAGCAGGAAGTTCAAGTTCAGCA
GATGTCAATAACACCAACAATGGACCTAATAAAAATACATAA

YPL089C_homolog 611aa(SEQ ID NO 506)

MGRRKIEIEPLTDDRNRVTTFVVKRAGLFKKAHELAVLCQVDLTVIIIVGNNNKVYEYSTVEANEIFNAY
NKTIKVRKQVHESKSPEYYSKFRKKRHLNEPLMNKSGSVVGTNTHLNDEYDHNVEAGDEDSEYESDD
NSPQPKRHKRSESVKKEQNPVFNSTQPPPPPPPHISLNNVPTFTNPQNYKKQIDETNNTSAPPATGT
KNEPTMQRPVLRVQIPNDAKSNTNNSHSGVNSDGDRTARTVAVDNSATNQNTQSSNTTSGTGADTN
SSQLNSNGNSNLVPGNVPTNTRFSGYSSFRSPDSRKPTLPLPLQTKSQTSSPASAVAPGLPLTGGSNAYF
AGMQLPTGQSVYVNPQAVYQQYQQFQNLQLLEPQQQQQQQQQQSQPQPSQSVGNQNAQLESAAAR
FRSGLPTGTQFNNGEQTPISGLPSRYVNDMFFQSSQNFLAPQDWPSGITPTTHLPQYFVNMPLSIGIS
QQSQQQNAQQQSQVPVPIPIQTQTSQQMASTT
NHKSANLIPGFLQNPTQATGNSANASKSSDAGDGTNPPTTAGSSSSADVNTNNGPNKNT

YAL003W_homolog 693bp public: 1..693(SEQ ID NO 507)

ATGAGTGACAAAGAAGATTTAAATCTTATATCTGACAATAATAGAGTTATTTCAATGAGACAATTGATT
TTACAATTACTGACTACAGGAATAAACAATAAATAAACGATATACTAACATGTTTGATAGTACTACT
GCCACTCAAGCTGATGTCACTGTCTACAAAGCTTTCCAAAAGGAATTCCACAAATTCACCAGATGGTTC
AACCACATTGCTTCATTCAGTGAAGAATTCGAAGACTTGCCAGCCGGTAAAGCCCCAGCCGCTTCTGGT
TCTGCTGCTGCCGCTGCTGAAGAAGAAGATGACGAAGATGTGCACTTGTTCGGTTCTGATGATGAAGTT
GATGAAGAAGCTGAAAAATTGAAGCAACAAGATTAGCTGAATACGCTGCTAAGAAGGCTGCTAAAGGT
CCAAAACAGCTGCCAAATCTATTGTCACTTGGATGNTCAAACCATGGGATGATGAAACTGATTGGAT
GAATTATTGACCAACGTCAAAGCTATCGAAATGGAAGGTTTGAAGTTGGGGTGCTACCAATGGATTCCA
GTTGGTTTTCGGTATTAAAAAATTACAAATTAACCTGGTTGTTGAAGATGCTTTAGTCTCATTGGATGAC
TTACAAGCTGCTGTTGAAGAAGATGAAGACCACGTCCAATCTACTGATATTGCTGCTATGCAAAAATTG
TAA

YAL003W_homolog 230aa(SEQ ID NO 508)

MSDKEDLNLISDNNRVISMRLILQLSTTGINKKYKRYTNMFDSTTATQADVTVYKAFQKEFPQFTRWF
NHIASTFEEDLPAGKAPAAASGSAAAAAEEEDDEDVDFGSDDEVDEEAELKQORLAEYAAKKAAGK
PKPAAKSIVTLDVKPWDDTDLDELLTNVKAIEMEGLTWGAHQWIPVGFGIKKLQINLVVEDALVSLDD
LQAAVEEDEDHVQSTDIAAMQKL

YAL060W_homolog 1185bp public: 1..1185(SEQ ID NO 509)

ATGAAGGCAATTGTATACCACGATAGAGGAGATATTAGATACGACCCCAATTTCCCTGATCCACAAATC
ATTTCGACTGGATGATGTCAAATCAAAGTTCATTATTGTGGGATTTGCGGTACTGATTTAAAAGAATAT
AGTGATGGGCCGATTTTTTTCCACCAGAAAGGTGAATTGAATGAAATTTCTCAAATGGAATCAATTCAA

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GTCATGGGTCATGAAATTAGTGGTGAAGTAATTGCTATTGGGGATGATGTAACCAATGTTAAAGTGGGT
GATAAAGTTGTTGTTGAAGTGACAGGAACCTGTTTATAGATAGACATCGTTACCAAGATCCTAAAAATGGC
GATCTGCCTAAACCAAATTGTCCAAGTTGTGTTTCGGGTAACTATAATGCGTGTGATTATCTTGTCTTTA
ATTGGTTGTGGATTTGCTAATGGTGGATGTGCAGAATATTTAGTTGTTGCTAGTCTGAAAGTTATTGCA
TTCGATCAGAATAAAATCCCTATGGATATTGCCGCATTAATTCACCAATAGCTGTTAGTTGGCATGCT
GTTAAAGTATCAAATTTTAAACCCGGTTCATATGCATTAATTTTAGGTGGTGGCCCCATTGGATTAAACA
ACAATTTTTGCTTTGAAAGGTAATCAAGTCTCCCAAATTGTTTTAAGTGAACCAGCATTAGCAAGACGT
CAATTGGCAGAGAAATTAGGAGTTATTACTTATGACCCCTACGGGTAAATCAATCGAACAATGTGTTGAA
GACTTAAAAAATTATCCCCGGGAGGTTATGGTTATGAATATTCATATGATTGTTCTGGAGTTAAGGCA
ACTTTTGAAACTGGATTGAAAACCTTGAAAATTCGTGGATGTGCAACAAATGTTGCCATTTGGGCTCAT
AAATCAATTCCATTATATCCTATGGAAATTACCCTTTCAGAAAAAATGTTAACTGGATCAATTTGTTTT
GTTAAAAAGATTTTGAAGAATCAATTAAAGCAATTGAAAAATGTTTAAATATCGATTGATGAATTGAAA
ATGTTGATTACTCTGAAAAATTCATTTACAAGATGGAATTGAAAAAGGGTTTTTGGAAATTAATTAATCAC
AAGGAAAAACATATTAAAAATTTGTTTTCTCCGAAAAGTGAATATTTACTATGCAATGGAGTAAATGAT
TCCAATAATAA

YAL060W_homolog 394aa (SEQ ID NO 510)

MKAIVYHDRGDIRYDPNFPDPQIIRSDDVKIKVHYCGICGTDLKEYSDGPIFFPPKGELNEISQMESIQ
VMGHEISGEVIAIGDDVTNVKVGDKVVVEVTGTCLDRHRYQDPKNGDSPKPNPCSCVSGNYNACDYLAL
IGCGFANGGCAEYLVVASSKVIAFDQNKIPMDIAIQPIAVSWHAVKVSNFKPGSNALILGGGPIGLT
TIFALKGNQVSQIVLSEPALARRQLAEKLGVTITYDPTGKSIEQCVEDLKKLSPGGYGYEYSYDCSGVKA
TFETGLKTLKIRGCATNVAIWAHKSIPLYPMEITLSEKMLTGSICFVKKDFEESIKAIENGLISIDELK
MLITSKIHLQDGIKGFLELINHKEKHILFSPKSEYLLCNGVNSNK

YBL058W_homolog 1116bp public: 1..1116 (SEQ ID NO 511)

ATGTCTGAAATACTCCAGATTCCCAATTGATTGCTGAATTTGTATCTATAACAAATTTCTTCTACATAC
CTTGCTGAACAGTATTTACTGAGAAACAGCAATGATTTAGTGGAAGCAGTTGAGGATTTCTATGCCAAC
AATGAACCATCTCAAAAATCAGAAACCAAAAATCTTCTTCTTCTAATGCTAAAGGCTCTGGTGTAA
ACATTTAGAGACTTGAACGATGAAGATGATGATGAAGAGGATGACAAGACCAATACCAATTTCTTTACT
GGAGGAGAGAAATCAGGATTGCAAGTTGAAGATCCCAATAAAGATAAGGATAATGACAGATCAATAATT
GATCAAAATTTTCCAAAAGCCAGAGAACAATGCAACAACCAGATGATAGACCAAGTGCTTCTCAAGAT
GATCAACCATCACCAATTAATTTTCAGGCAAGGGTTCAAATTTGGGTGACGGGAATGAACCAAGTCAA
GTAGTGGAGGATCCTAATGCCAGTGCTAAAAAATTCAGACCTAGTAAAGTGACTAGAGAAATTACATTT
TGGAACAAGGTTTTCACAGTAGGTGATGGACCTTTGCATAGATACGATGATCCAAAGAACGCCAGTGTT
TTGCAAGAATTGAACCAAGGAAGAGTTCCAATGTCAATTTTAGATGTTGAATTTGGCCAAGATGTTGAT
GTTTCTGTATACAAGAAAACCGACGAAGATTGGACACCTCCGAAAAGAAAATTTGGTGGTTATCACGGT
GCAGGTCTAGACTAGGCTCACCAGTACCTGGGGAAGTACTTGTAAATAATGAAGCATCATCTCAACCT
GATATCAAAACCGAACTGAAATTTCTAAACCAAAAGACGAAGGCGAAGGTGACTCCACAGTTCAAATA
AGATTTGCCAATGGTAAAAGAACATCACACAAATTCATTCCTCGGATTCTATTCTCAAGGTTTATGAA
TTTGTTAAAAATCATGAATATAATTCTGAACCTACTAGACCATTCACTTTAAGTCATGCATTCCAGTC
AAACCAATAGAAGAAAGTAGTGACATTACAATTTCTGATGCTAAATGAAAAATGCAGTGATTGTTCAA
AGATGGAAATAG

YBL058W_homolog 371aa (SEQ ID NO 512)

MSENTPDSQLIAEFVSITNSSTYLAEQYLSRNSNDLVEAVEDFYANNEPSQKSETKKSSSSNAKSGSVK
TFRDLNDEDDDEDDKTNTNFFTGGEEKSLQVEDPNKDKDNDRSIIDQIFQKAREQMQQPDDRPSASQD
DQPSPIKFSKGKFLGDGNEPSQVVEDPNASAKKFRPSKVTREITFWKQGFVGDGPLHRYDDPRNASV
LQELNQGRVPMISILDVEFGQDQDVSVYKKTDEDWTPPKRKIGGYHGAGHRLGSPVPGEVLVNNEASSQP
DIKTETEISKPKDEGEDSTVQIRFANGKRTSHKFNSSDSILKVYEFVKNHEYNSEPTRPFTLSHAFPV
KPIEESDITISDAKLKNAVIVQRWK

YBR039W_homolog 804bp public: 1..804 (SEQ ID NO 513)

ATGCGTCTTAAATCCATTAAAAACATTGAAAAAATCACCAATACCATGAAGATTGTTGCCTCTACTAGA
TTGAGTAAAGCTCAAAAAGCCATGGCTTCATCTCGTGTGTTTCAATGAAACTGATAAAGAATCTTGTCT
AATGCTGAACCAAAACCAATTGAAGAAGAAGCTTCTAAATCTGATGACAAAACCTTTATTGATTGTTGTT
TCTTCCGATAAAGGTTTATGTGGTTCTATTCACTTCTCAAGTTTCCAAAGCTGCCAGAAAGAGAACTGAA
GAATTAATGGTAATGTGATATTGTTTGTATTGGTGATAAAGTCAAAGCACAAAATTTTGAGAACTTAT
GCTGACAAAGTTAAATTGGCATTCAATGGTGTGGTAAAGAAGAACCAATTTCACTGAAGTTGCCTTA
ATTGCTGATGAAATTGCTAAATTAGGTAACATGAAAATGTTGAAATTTCTTTACAACAAATTTGTTTCT
GGTGTTCATTGTAACCATCTAAATTTTCCATTTATGCTGCTGATGCCATTGCTAACTCTCCAGGTTTA
AGCAATATGAATTGGAATAATGAAGAATCACTTCTGATGTTGCTCAATTCCTTTAGCTAACAACCTTG
TTGACTGCTATGGCTGAAGGTTATGCATCTGAAGTTTCTGCTAGAAGAAATGCTATGGACAATGCCTCC

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AAGAATGCTGGTGATATGATCAACAGTTACTCTATTTTGTATAACAGAACTAGACAAGCCGTCATTACC
AACGAATTGGTTGATATCATTACTGGTGCTTCCTCATTGGACTAG

YBR039W_homolog 267aa (SEQ ID NO 514)

MRLKSIKNIEKITNTMKIVASTRLSKAQKAMASSRVFNETDKEFLSNAEPKPIEEEASKSDDKTLILIV
SSDKGLCGSIHSQVSKAARKRTEELNGNVDIVCIGDKVKAQILRTYADKVKLAFNGVVGKEPNFTEVAL
IADEIAKLGNYENVEILYNKFVSGVSEFSPKFSIYAADAIAANSPLSKYELENEEITSQVQFSLANNL
LTAMAEGYASEVSARRNAMDNASKNAGDMSINSYSILYNRTRQAVITNELVDIITGASSLD

YBR062C_homolog 450bp public: 1..450 (SEQ ID NO 515)

ATGTTATCTGCATCTAACGAAGAAGCCATAGCATCAGCATTGCGACAATTGAGTGAATCAGAAGGATCA
ACACTTGCTCAATCACTCATGGATCTGCTTGGTGAACAAAAGACATCGAAGGGGGTCACTGACGAATAC
TTGGATACCTTTGGAACGTATTCCAGTAAACAAAATTACTGTATAAGACGCATCTTGTCCAATTTGTACA
AATCGATTCAAAGATGATAAGCATCCATTGATTGTGAGATTGCCTTGTGGTCATGGAGTCAATCATATT
TTTGATTTGGAATGTGTTGGGCCGTGGTTGCAAATGAATTCCACTTGTCCAATGTGTGCAACCAATATC
TTAGAGGTAGAAGCTAATAGAAGGAAAATAATAGATGAAGAAATAAAAAAGGCCCAAGAAGAAGATTCC
GAGGAAGAAGAAGAAGGTTGGGATATATATGGATAA

YBR062C_homolog 149aa (SEQ ID NO 516)

MLSASNEEAIASALRQLSESEGSTLAQSLMSLGEQKTSKGVTDYLDTLERIPVKQITDKDASCPIC
NRFKDDKHPLIVRLPCGHGVNHIFDLECVGPWLQMNSTCPMCRNTNILEVEANRRKIIDEIEIKKAQEEDS
EEEEEGWDIYG

YBR101C_homolog 855bp public: 1..855 (SEQ ID NO 517)

ATGGAAAAATTATTACATTGGACAATTGCACAACAATCAGGGGATAAAGCAGCTCTTGAAAAGATTGGA
GAACCCGATCAAAAGGCACCTTAATCAATTATTTGGTGGTCCCGATGAAGCCACTTTAATGAAGGAAAGT
ATAAAAGTTGTTGAATCAACCGATGTTTCATTAGAAGATAAAGAGATCGCCTTGAAAATTTGAAATG
TTGATTGAAAATTTAGATAATGCAAATAATATTGGTAATTTGAAATTATGGAATCCATTGATTGACATT
TTAGCCAAAGAAGATACCCCTGTTGAATTGAAAGTACTTATTTGTGGAATAATTGGAACCGCTGTACAA
AACAACCCCAAATCTCAAGAAGATTTCAATGAACTGAAGGATTGAGTGAATTGATAGAATTAGCACAA
GATGACAAAAAATTTGAATTACAACCTGAAGGCATTGTTTGCTATTTCTTCATTATCAGAAAATTTTCAA
CCTGGATATGCAAAGTTTGAGAAATTGCAAGGTTTGAACTCATTAATTTTGATAACAAGAACAACAAG
TATCAATTGAGAATTTTATCATTAATATCATCCATTTTGAGTAATGGGTTAGACGATAGCTTGAAAGCA
CAATTCAAAGAAGCAAAATTACCTCACTATTTAGCCTCGGTATTGAATGAGGATTCAAACACTAGTTTG
GTGGACAAATCTTTAAACATTGTTTCTCAATTGAATCAATTAACTATGAGTTTAGCTTAGAAGAAAAA
TATGAAATAAATAGAGGAATCCAAGTGGTTGAAGGGTTGAGTGAGAACTTAATATTGATGATCTCAAT
AATGCCAAACAGGCCACATCCTCTTAG

YBR101C_homolog 284aa (SEQ ID NO 518)

MEKLLHWTIAQQSGDKAALEKIGEPDQKALNQLFGGPDEATLMKESIKVVESTDVSLLEDKEIALENFEM
LIENLDNANNIGNLKLWNPLIDILAKEDTPVELKVLICIGIIGTAVQNNPKSQEDFNETEGLSELIELAQ
DDKKFELQSKALFAISSFIRNFQPGYAKFEKQLKLINFLDNKNKYQLRILSLISSILSNGLDDSLKA
QFKEAKLPHYLASVLNEDSNTSLVDKSLNIVSQLNQLNYEFSLEEKYEINRGIQVVEGLSEKLNIDDLN
NAKQATSS

YBR139W_homolog 1653bp public: 1..1653 (SEQ ID NO 519)

ATGCAATTATCTACATTAGTCACTTGGTTGGCTGCTTTAACTGTCGGTGCACAGGCAGTATCATTCGGC
AACAATTTAAAAGATCAGATTATATTGGATTCTGAGGAAAGCTCCCAGATTTATATTGGAGTCAGTG
TTCAAAGACTTGGGTTCAATTGCCAGTTGATTGTGATTACTGCTTGGGCAGAAATGCAATCTGAATTATCA
CCTGAACAAATTGCCAAATTAATCAATCAATATGAGTCTAAAAATGAAAAACCAAGAAAAATAAGTTT
AATCCAATGTCGACATTTTCTTCACCAAGTTCCAAGTTTGAAAAGCTTTCCAATGATAAATTTGCTGGT
TATTCATGCGTGTAAGAGAGATTTCCAGAAATTTGGGCTCTTGATACAGTGAAACAATACACTGGG
TATTTAGATATTGACTCATTAGATAAACATCTTTCTATTGGTTTTTTGAAAGTAGAAATGATCCAAAG
AATGATCCTATTATTTTATGGCTCAATGGTGGTCCAGGTTGCAGCTCTTCAACGGGATTATTTTGGAA
TTAGGACCATCCTCGATCAACAAAACCTTTACACCCAGTTTACAACCCATATTCTTGGAATTCCAATTGCG
TCGGTTATTTTCTTAGATCAACCCGTTGGAGTTGGATATTCTGTATACAGGAGGAGATGAAGTTAAGAAT
ACTCTCACTGCTGCTAAAGACGTTTATGTGTTTTTGGAAATTGTTTTTCCAAAAATTTCCACAATTTTGT
ACTAATAAGTTTCACATTGCCGGTGAATCTTACGCCGGTCAATTATATACCAGCATTTGCTTCAGAAATC
ATTAACAATGCCGATAGGTCATTGAGTTGGCATCTGTGTTGATTGGTAACGGTATCACCGGATCCATTG
ATTCAAGATGGTTCTTATAAACCAATGGGCTGTGGTGAAGGTGGTTACAACACTGTTTTGACAACCTGAA
CAGTGTGATCAAATGGAAAGGGATTATCCTAGATGTGCTAAATTGACTAAATTATGTTACAGTTTCCAA
TCTGCCTTGACTTGTGTTCCAGCTCAATACTACTGTGATTCCCGTTTATTTCAACCTTATGCTCAAACA
GGATTAAATCCTTATGATATCAGAAAGGATTGTGCCGAGCAAGGTGGTAATTGTTACGTAGAAATGGAT

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TACTTGGATGAATACTTGAATCTCGATTATGTGAAAGAAGCTGTTGGTGCTTCTAATATTGACATTTTT
ACTTCATGTGATGACACCGTGTTTAGAACTTTATTTTAGATGGTGATGAAATGAAACCTTTCCAACAA
TATGTTGCTGAGTTATTGGACAATAATGTACCTGTATTGATTTATGCTGGTGACAAAGATTATATTTGT
AATTGGTTGGGTAACCTGGCATGGGTAACGAATTGGAATATTCAGATAGTGAACATTTTGCACCAAAA
CCATTACAATTATGGAACAAGATGGCAAGAAAGCTGCTGGAGAAGTCAAGAATCACAAACATTTTACA
TTCCTTGAGAAATTTATGACGCTGGTCACATGGTTCCCTTTTGATCAACCAGAAAATGCTCTTAGTATGGTT
AATACTTGGGTACAGGGAGATTATCTTTTGGTTTAGAGGGTAATAAATTATCTGAAGCTGATTAA

YBR139W_homolog 550aa (SEQ ID NO 520)

MQLSTLVTLAALTVGAQAVSFGNNLKDQIILDSESSPDLYLESVFKDLGSLPVDLITAWAEMQSELS
PEQIAKLINQYESKNEKPKKNKFNPMSTFSSPSKFEKLSNDKFAGYSMRVKESFPEILGLDTPVKQYTG
YLDIDSLDKHLFYWFFESRNDPKNDPIILWLNNGPGCSSSTGLFFELGPSSINKTLHPVYNPYSWNSNA
SVIFLDQPVGVGYSYTGDEVKNTLTAADKDVYVLELFFQKFPQFLTNKFHIGESYAGHYIPAFASEI
INNADRSEFELASVLIGNGITDPLIQDGSYKPMGCGEGGYKPVLTTEQCDQMERDYPKAKLTKLCYSFQ
SALTCVPAQYYCDSRLFPYAQTGLNPFYDIRKDCAEQGGNCYVEMDYLD EYLNLDYVKEAVGASNIDIF
TSCDDTVFRNFILDGDEMPPFQYVAELLDNNVPLIYAGDKDYICNWLGNLAWNELEYSDSEHFAPK
PLQLWKQDGKKAAGEVKNHKHFTFLRIYDAGHMPFDQPENALSMVNTWVQGDYSFGLEGKNLSEAD

YCL052C_homolog 1446bp public: 1..1446 (SEQ ID NO 521)

ATGAGACAAAGAACAACCATTTATAATCCTTATTCTAGTCATGATGGAATCATAACTAATCTTAATCGA
ACAAATTTCCAATTATCAAGCATACCTAATCATTTATTCACAATTGAGAATAAATATACCATCACCACC
ACCACCACACAACCTAACAAATCATCATTTATATCTGGCAATTAAAGAATTAAAGAATTCAAACGAAATTC
AATAAATGAATCAGGTATACCAATTTTTCTCATTTTATTATGAACCAGGACTTAATATTTATGCTGTA
CCACAATCTAATGTCGACAAATTAGAATTTTGGCAACAAGTTGAACAATTGATAATGGAATTTATAGGG
ATTAAATTTATCTTCACAACAATGGATTGCTAATGTTAATTTCTTTTATTATCATGATATTCAACCTCAA
CCATTATTGAATTTGAAAGAAGGATGGAATTCATTTTACATCCTAAATCCAATTATGATTATATATAT
AATCAAGATAAAATTTATTTCCGGGAATTGTTAACAATGTGTCAGAAATAGAATTTAATCTTGAAGT
GGTATTTATAAAGAAATTTGGTTTGT'TTTAATTTGATGAAAAATCTCAACTAATGATGATTTGAATTTA
AGTGGTATTAGAGTGATATTAGATGAAGATAGTAATCAATAACAAGAAGAACCGATACATAAGACA
ATGTTTTCATATAAAACCAAGACATAGGAGTTTGTAGTATTCTACCACCATCACCACCACCAAGATCAT
CCACAAGGATTACATCCTATTTTGTAGTACTGAAC'TTAACACAACAACATATTTGTTATTCCAAGTATTT
GATGTTGAAGAATGTAAATTTTATTATTATTGAAATTTAAATAAATCATTAATATTTGATCAATTTCAA
AACATTTCCAATAGGATCGCAATTAATTTAATAATGGGAATAAAAAATTTAGAATTACCAGAATATAAA
ATTAATCAATGGGGTAATGAAC'TTTATTTGAATTTGAATTTGATAATGATAATGATATCCCTCATCAT
ATAAATTTAACAGTTTCAATTCAGATATCAATTTACCTCAAAATAATCATTTCCCATTTCCCAATTAGTAAT
GTTTTAAATTCGTTACCAAAATTTTTTATAGTTGTAATGTCAAAGAAGGAAATTTATTAGATAAATCA
CCTTTTGATACTAAAAGAGATGTTAAATTTGGTGGTAATTTATGAAATTTATTTTACTGAAGATACAGTT
TTTTATCATTTACAGAATTCGACAATTCGGCAATTCGGGTAGTTCAACATTATTAGAAATTAATATT
CCTCATGGGAAAAC'TACATTTGATAGAGTCAATAATATAACTTCAC'TTGGTTTATTAATTTGGTGTATTG
ATGATTTTATATGCCATTTCAATAAGAGTTTTCATGAGTACCAC'TCAAAGACGAAAAGGGATTA

YCL052C_homolog 481aa (SEQ ID NO 522)

MRQRTTIYNPYSSHDIITNLNRTNFQLSSIPNHLFTIENKYITTTTTQPNKSSLYSAIKELRIQTKF
NNNESGIPIFSFHYEPGLNIYAVPQSNVDKLEFWQQVEQLIMELLGIKLSSQQWIANVNSFYHDIQPP
PLNLNKEGWKFNHLPKSNYDIYNQDKIIIRELLTNVSEIEFNLESIGIYKEIGLFLIDEKISTNDDLNL
SGIRVILDEDSNTNNKEESIHKTMFHIPRHSFDDSTTTTKIIPQGLHPILSTELNTTTIIVPTDF
DVEECKFYYYLNLNLSLIFDQFQNIPIGSQLIINNGKNLELPEYKINQWGNELLFEFEFDNDNDIPH
INLTVHSRYQLPQNNHSHSQISNVLNSLPNIFIGCNVKEGNLLDKSPFDTKRDVKIKGNYEIFYTETD
FYHLQNSDNSGNSGSSTLLEINIPHGKTTTFRVNNITSLGLLIGVLMILYASIRVFMSTTSKTKRD

YCR009C_homolog 882bp public: 1..882 (SEQ ID NO 523)

ATGTGGAAAAAGAAAAAGAGGAATTTTTTTTTTGTTCATTTTTTTTTTTCTTTTATCTCGCACAT
TTCCTTCTTCAACTAGACATGCTTGGGGGAGGATTTAAGAAAGCAATCAATCGAGCTGGCGCATCTGTT
ATTGTCAAGGATGTTGACAAGACTATGGATAAGGACTTTGATGTGGAGGAGAGAAGGTACAAGACCTTA
AAGACTGCAGGGACGAATTTACAGAAAGCTGCCAAGGGGTATTTGGACAACATCAGAGCAATCACGAAT
TCCCAAGTCACAAATGCCGAGATTATTTATAACTTGTACGAGGAGTCGAAGCAGGACAAATCGCTCTAC
TCGAATGTTGGGACTTATTTACATGCAGAGTGTCAAGGAGTTTGTATGAGGAGACTGTGAAACAGATTGAT
GGCCCGTATAGGGAGACTGTTTTGGATCCAATTTGGAAGTTTCCAACTACTTTTAGTGAGATTGACGAA
GCAATCAAAAAGAGAGCACACAAGAAGATTGACTATGAGCAGTGCAGGAGGAAAGTTAGACGGTTAGTC
GATAAACCTGCCAAAGATGCGGCCAAGTTGCCACGCGCCGAGAAAGGAAATTTGTCGATGGCCAAAGAGATT
TACGACGAGTTGAATGACCAGCTCAAGGCCGAGTTGCCGAGTTGATTGCATGAGGGTGCCTTTCTAC
GATCCGTCGTTTGAGGCGTTGGTCAAGATCCAGTTGAGGTTCTGTACTGAGGGGTACTCGAGATTGGCA

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CAGATCCAACAGTACTTGGACCCAGCGTCCAGAGACGAGTATGCCAATGGGTTGTTGGACGGCAAGATT
GATGATATGTTGGCACAAATGCAAGGTTTGGAGTATACTTCTTTAGGAAAGTAG

YCR009C_homolog 293aa (SEQ ID NO 524)

MWKKKKREFFFFCHSFFFFFYLAHFFLQLDMSWGGFKKAINRAGASVIVKDVKMDKDFDVEERRYKTL
KTAGTNLQKAAGYLDNIRAITNSQVTIAEIIYNLYEESKQGQSLYSNVGTYYMQSVKEFDEETVKQID
GPYRETVLDPIGKFSNYFSEIDEAIKKRAHKKIDYEQCKAKVRRLVDKPAKDAAKLPRAEKELSMKEI
YDELNDQLKAELPQLIALRVFPYDPSFEALVKIQLRFCTEGYSRLAQIQYLDPASRDEYANGLLDGKI
DDMLAQMQGLSITSLGK

YCR010C_homolog 858bp public: 1..858 (SEQ ID NO 525)

ATGTCAGCTGATTTAGAAAATCAACAACCACAAGATCATCATCTTATTATTGAAAACAAGGGTGATAAC
AGTAGCAACCACCACCACCACAACAACAATTCAACATCACCTTATGATCCTCATCATCCAATTACTAAA
ATTGAAACTGATGGAGATTATGTTACTTTTGGTAATGAAAGATATTTACGTTCTGATTTAGTTGAAGCA
TTTGGTGGTACTTTAAATCCAGGGTTAGCTCCACCACCTAAAAATGATTTTGCTAATCCTGCTCCATTG
GGATTATCGGCATTTGCTTTAACAACATTTGTTTTAAGTTTAATTAATTGTGAAGCTAGAGGGGTTACT
ATTCTAATATTGTTGTTGGATTGGCATTCTTCTATGGTGGTGGTGGTCAATTAGTTGCTGGTATGTTT
GAATTGGCCGTTGGTAATACTTTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT
GCTGCTATTCAAGTTGATTCAATTTGGTATTAAAGCTGCTTATGCTAATAATACTGAAGAATTACATTAT
GCTGTGGGGATATTTTAATTGGTTGGTTTATTTTTCACATTTTCTTGGATGCTTTTAACCGTTAAATCT
ACTGTGGCATTCTTTTAAATATTTTCTTTTAAAGTATTACATTTTATTATTGGCAATTTCTGATTTT
ACTGGTAAAGTGGCAATTAAAAAGCCGGTGGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT
AATGCTTATGCTGGTATTGCTAATCCTCAAAATAGTTATATTACTGTTAAAGCTATTCCATTACCAGAT
TTACAAGATCCAACAAGAAAAATAAATAA

YCR010C_homolog 285aa (SEQ ID NO 526)

MSADLENQQPDHHLIIENKGDNSNHHHHNNNSTSPYDPHPITKIDTDGDYVTFGNERYLRSDLVEA
FGGTLNPLGLAPPPKNDNFANPAPLGLSAFALTTFVLSLINCEARGVTIPNIVVGLAFFYGGAAQLVAGMF
ELAVGNTFGGVALSSYGGFWGAWAAIQVDSFGIKAAYANNTTEELHYAVGIFLIGWFIFTFFLMLLTVKS
TVAFFLIFFFLSITFLLLAISDFTGKVAIKKAGGVFGLITAFVAWYNAYAGIANPQNSYITVKAIPLPD
LQDPTRKNK

YCR021C_homolog 1029bp public: 1..1029 (SEQ ID NO 527)

ATGTCGCGCTGCTGTTTCAACTTTATCCGATATCATCAAACGTAATGATGCTGTAAACGTGAACCCACCA
AACCCAATTATTGATTTACATATCACTGAACATGGTAGTGATTGGCTTTGGGCTGTTTTCAGTTTTT
GCATTATTTGCAATTGTGCATGGATTCAATTTACAGTTTTACTGACGTTAGAAAATCTGGTTTGAAGAGA
GCTTTATTGACTATCCCATTATTTAATAGTGTGCTTTTGGCCTTTGCTTACTATCTTATGCTTCTAAC
TTGGGCTATCTTGGATTTTGACAGAATTCAACCATGCTGGTACTGGTTTTAGACAAATCTTTTATGCA
AAATTTGTTGCTTGGTTCTTGGGTTGGCCATTAGTGTGGCTATTTTCCAAATTATCACCATAACCAGC
TTTACTACTACTGAAGATGAGTCTGATTGCTTAAGAAATTCATTTCTTTGTTTGAAGCTTTGTTTACT
AGAGTTTTGGCAATTGAAGTTTTCGTCTTGGGTTTATTGATTGGTGGTGTAAATTGAATCTACTTACAAA
TGGGGTTATTTCATTTTGTCTGTTGTGTTCCAATTGTTTGTCTATTTATTAGTCATTAATGATGTGGTT
GTTTCATTTGGTTTCATCTTCTCATTCACTTTTGGCAATGCTCTTATCCTTGGTTTGTATTGTTGG
ATTTTGTACCCAGTTGCTTGGGTTTGGAGTGAAGGTGGTAATGTTATTCAACCAGATTGAGAAGCAGTG
TTCTATGGTATTTTGGATTTGATCACTTTTGGTGTATTCCAATTATCTTGACTTGGATTGCCATTAAT
AACGTTGATGAAGAATTCTTCAACAAAATATGGCATTTCATTTGAAACCAGAAAATGAACATGCTCCA
ACTGCTACTGAAGATGTTGAAAAAGCAGTTGGTGAACCCCAAGACATTCTGGTGATACTGCTGTTGCT
CCATCAGGTGTTCCAGACACTGGTGTGCTCAAGCACAAGCCGAAGCTGAAGAACGTATTTAA

YCR021C_homolog 342aa (SEQ ID NO 528)

MSAAVSTLSDIKRNDVNVNPPNPIIDLHITEHGSDWLWAVFSVFALFAIVHGFYISFTDVRKSLKR
ALLTIPLFNSAVFAFAYTYASNLYGTWILTEFNHAGTGFRQIFYAKFVAVFLGWPLVLAIQIITNTS
FTTTEDESDLLKKFISLFEALFTRVLAIEVFVLGLLIGALIESTYKMGYFTFAVVFQLFAIYLVINDVV
VSFGSSSHSVFGNALILAFVIVWILYPVAVGLSEGGNVIQPDSEAVFYGILDITFGVPIILTWININ
NVDEEFFTKIWHFHLKPENEHAPTATEDVEKAVGETPRHSGDTAVAPSGVPDTGVAQAQAEAEERI

YDR178W_homolog 510bp public: 1..510 (SEQ ID NO 529)

ATGATTTCAACTTATTCACGTATTGGTTTAAACCACTTAACTAAATCATCATCATCATCATTAACCT
ACTACTGTTAGACCATTATTATTGGCCAATTTTACTAGAGGAATTAACCTATTCTCAACCACCAGGT
TATATTGTTGGTACAGTTAATGATGCTTATGTACCACCACCACACATAAATAGAAGGTTTACATTACAT
TGGACTAGTGAAAGGATTGTTGCTATTGGTATTGTACCATTAGTTTACACCACTTATTAATGTTGGT
GGTGGCTTCGACTTTAATTGATTCCACCATTGTCAGCATTATTATTATTTCATTGTCATACTGGTTTCCAA
AGTTGTATTATAGATGATATTCCTAAAAGAGTTTATGGATCTTATCATAATTATGCCATGTATTTATTG

ACTTTTGGTACTGGTATTGCTGGTTATGGTATTATCAAATTGAACTAAAGAAGGTGGTGTTC CAAT
ATTATTTTCAAAACTTTGGAAAGCTTAA

YDR202C_homolog 387bp CDS: 1..>387 public: 1..387 (SEQ ID NO 531)
ATGACAGCAAATATCTTGAATAATAAAACATTCATAGATACTGTATTATCAATACAATCAACTCAAAAT
GATAAGAATTACATTGGTATATTATAAAATATAATTTTACCCGATTACCTCAAATCATAGAGACTTTA
CAGATTTGTTCAAATTTGTGTGATGTACAATTCACCACAAGAACCTGATTCCAACAATGTATTGAAAAA
GGTCCATCTATCAAGCTACCTTTGTCTTTAACCAATCAACAAGATTCTGTCAATGGGATAATAACCCGA
GATGGACCATAATACAGATCTTAATTTGACGGTTAAGAATCATTAATTTCAACAAGCATTTCCATAAG
TTGGCGCTTAATAAAGCCAAATGGTTTATTAGAACCACTGTGTTAAT

YDR256C_homolog 1458bp public: 1..1458(SEQ ID NO 533)
ATGGCTCCAACATTTACGAATTTCTAACGGTCAACCAATTTCCAGAACCATTTGCCACTCAAAGAGTTGGT
CAACACGGTCCAATTGTTGTTTACAAGATTTTCACTTGATTGATTCAATTGCCCCATTTGATAGAGAAAGA
ATCCCAGAAAAGAGTTGTCTCACGCTAAAGGTTCCGGTGCTTATGGTGTTTTTTGAAGTCACTGACGATATC
ACTGATATTTGTGCTGCCAAATTTCTGGACACTGTGTAGTAAGAAAACATAAGATCTTCCAGGATTTCTCT
ACTGTTGGTGTGTAATTTAGGTTTCTGCTGATACTGCTGAGATGATCCAAAGAGTTTGTCTACCAAATTTTAC
ACTGAAGAAGGTAACTTGGATTTGGTTTACAACAACACTCCAGTGTTTTTTCATTAGAGACCCATCTAAA
TTCCCACATTTTCATCCACACCCAAAAGAGAAAACCCAGAAACTCACTTGAAGGATGCTAACATGTTTTGG
GATTACTTGACTAGCAATGAAGAATCCATTTCATCAAGTTATGGTTTTATTCTCCGACAGAGGTACTCCA
GCTTCTTACAGAGAAATGAATGGTTACTCTGGTCACACTTATAAATGGTCCAACAAAAAAGGTGAATGG
TTTTACGTTCAAGTTTCATTTATCATGCTGACCAAGGATTTAAGACTTTGACCAACGAGAAGCTGGTGCT
TTAGCTGGATCTAACCAGATTTACGCCCCAAGAAGATTTGTTTCAAGAACAATTTGCTGCTGGTAACTACCCA
TCATGGACTGCTTACATTTCAAACCATGACTGAAGCCGAAGCTAAAGAAGCTGAATTTTTCTGTGTTTGAT
TTGACCAAAAGTTTGGCCACACAAGAAATACCCATTGAGAAGATTTGGTAAGTTCACTTTGAATGAAAAC
CCAAAGAACTACTTTTGCTGAAGTTGAACAAGCTGCTTTCTCTCCAGCCACACTGTTCCTTACATGGAA
CCATCTGCTGATCCAGTCTTGCAATCAAGATTTGTTCTCCTATGCTGATACTCACAGACACAGATTTGGGT
ACCAACTATACTCAAATCCCAAGTGAACTGCTCTCACCAGTGCTGTTTTCAACCCACATATGAGAGAT
GGTGCTATGACTGTTAATGGTAACTTGGGTAGCCATCCAAACTACTTTGGCCAGTGATAAGCCAGTTGAA
TTCAAACAATTTTCTCTTCAAGAAGACCAAGAAGTTTGAATGGTGCTGCCACTCCATTCCACTGGAA
GCCACCCACAGCTGATTTCAAACAAGCTCAAGAAATTGTGGAAGTGTTGAAGAGATATCCAACCAACAA
GAACATTTGGCCACAAACATTTGCTGTACATGCTGCTGGTGCTGATGCTGCTATCCAAGACAGAGTGTTT
GCATACTTTTGGTAAAGTCTCTCAAGACTTGGCTGATGCTATCAAAAAGGAAGTTTGGAAATTATCTCCA
AGAAAAATAA

YER103W_homolog 1971bp public: 1..1971(SEQ ID NO 535)
 ATGTCTAAAGCTGTTGGTATTGATTTAGGTACAACCTATTCTTGTGTTGCTCATTTTGCCAATGATAGA
 GTTGAAATTATTGCTAATGATCAAGGTAATAGAACTACCCCTTCATTTGTTGCCCTTCACTGATACTGAA
 AGATTGATTGGTGATGCTGCCAAGAATCAAGCTGCTATGAACCCAGCAAACTGTTTTCGATGCTAAA
 CGTTTAATTTGGGAGAAAAATTGATGATCCAGAAGTTATAAATGATGCTAAACATTTCCCATTTTAAAGTC
 ATTGATAAAGCAGGTAACACAGTGATTTCAAGTTGAATATAAAGGTGAAACTAAAACATTTTCACCAGAA
 GAAATTTCTTCAATGGTTTTTAAACAAAAATGAAAGAAATTTGCTGAAGGTTATTTGGGTTCTACTGTTAAA
 GATGCCCGTTGTTACCGTTCCAGCTTATTTCAATGATTCCTCAAGACCAAGTCCACCAAGATGCTGGTACT

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ATTGCTGGTTTGAATGTTTTAAGAATTATTAATGAACCTACTGCTGCTGCCATTGCTTATGGTTTATAGAT
AAAAAAGGTTCCAGAGGTGAACATAATGTTTTAATTTTCGATTGGGTGGTGGTACTTTTGTATGTTTCA
TTATTAGCCATTGATGAAGGTATTTTCGAAGTTAAAGCCACTGCTGGTGATACTCATTTGGGTGGTGAA
GATTTTGATAACAGATTAGTCAACTTCTTTATTCAAGAATTCAAGAGAAAGAACAAGAAAGATATTTCC
ACCAACCAAAGAGCTTTAAGAAGATTAAGAAGCTGCTTGTGAAAGAGCCAAGAGAAGCTTTGTCTTCTTCT
GCTCAAACCTCAATTGAAATTGATTCCCTATATGAAGGTATTGACTTCTACACTTCAATCACCAGAGCC
AGATTTGAAGAATTGTGTGCTGACTTGTTCAGATCCACTTTAGATCCAGTTGGTAAAGTTTTAGCTGAT
GCCAAGATTGATAAATCTCAAGTTGAAGAAATTGTCTTGGTTGGTGGGTCCACCAGAATTCCAAAGATT
CAAAAATTGGTTTCTGATTTCTTTAATGGTAAAGAATTGAATAAATCTATCAACCTGATGAAGCTGTT
GCTTATGGTGCTGCTGTTCAAGCTGCCATTTTAACTGGTGATACTTCTTCCAAGACTCAAGATATTTTG
TTATTGGATGTTGCTCCATTGTCTATTAGGTATTGAACTGCTGGTGGTATCATGACCAAAATTGATTCCA
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TTGATTTCAAGTGTTGAAGGTGAAAGAGCTAAAACCTAAAGATAACAACCTTTGGTGGTAAATTTGAATTA
TCTGGTATTCCACCAGCTCCAAGAGGCGTCCCTCAAATTGAAGTTACTTTTCGATATTGATGCTAATGGT
ATCTTGAATGTTTCTGCTTTAGAAAAAGGTACTGGTAAACTCAAAGATTACTATCACCAACGATAAA
GGTAGATTATCCAAAGAAGAAATTGATAAATGGTTAGTGAAGCTGAAAAATTCAAAGAAGAAGATGAA
AAGGAAGCTGCTAGAGTCCAAGCCAAGAATCAATTGGAATCTTATGCTTATTCAATTGAAAAACACAATC
AATGATGGTGAAATGAAAGATAAGATTGGTGCGATGATAAAGAAAAATTAATAAGCCATTGATGAA
ACTATTCTTGGTTAGATGCATCTCAAGCTGCTTCTACTGAAGAATACGAAGATAAACCTAAAGCAATTA
GAATCAGTTGCTAATCCAATCATTAGTGGTGCTTATGGTGCTGCCGGTGGCGCTCCAGGTGAGCAGGC
GGATTCCCAGGTGCTGGTGGCTTCCAGGTGGTGCCCCAGGTGCCGGTGGTCCAGGTGGTGCTACTGGT
GGTGAATCAAGTGGACCAACTGTTGAAGAAGTTGATTAA

YER103W_homolog 656aa (SEQ ID NO 536)

MSKAVGIDLGTTPYSCVAHFANDRVELIANDQGNRTTPSFVAFDTERLIGDAAKNQAAMNPANTVFDK
RLIGRKFPDDPEVINDAKHFPFKVIDKAGKPVIVQVEYKGETKTFSPPEISSMVLTKMKEIAEYLGSTVK
DAVVTVPAYFNDSSQRQATKDAGTIAGLNLVRIINEPTAAAIAVGLDKKGSRGEHNLVIFDLGGGTDFDVS
LLAIDEGIFEVKATAGDTHLGGEDFDNRLVNFIIQEFKRKNKKDIISTNQALRRLRTACERAKRTLSSS
AQTSIEIDSLYEGIDFYTSITRARFEELCADLFRSTLDPVGKVLADAKIDKSQVEEIVLVGGSTRIPKI
QKLVSDFENGKELNKSINPDEAVAYGAAVQAAILTGDTSSKTQDILLLDVAPLSLGIETAGGIMTKLIP
RNSTIPTKKTSETFTSYADNQPGVLIQVFEGERAKTKDNLLGKFELSGIPPAPRGVPQIEVTFDIDANG
ILNVSALEKGTGKTQKITITNDKGRLSKEEIDKMVSEAEKFKEEDEKEAARVQAKNQLESYAYSLKNTI
NDGEMKDKIGADDKEKLTKAIDETISWLDASQAASTEYEDKRKELESVANPIISGAYGAAGGAPGGAG
GFPAGGFPFGAPGAGGPGATGGESSGPTVEEVD

YGR086C_homolog 954bp public: 1..954 (SEQ ID NO 537)

ATGCATAGAAGCTTATTCTTTAAGATCCACTAGAGCTCCAAGCTGCATCTCAATTACAAGCTCCACCTCCA
CCACCATCATCTACCAAATCCAAATTTTTTGGTAAAGGTTTCGATTAGTCATACTTTCCGTAAACAAGCT
GCTGGTGCTTTAGGTCCAGAATTGTGAGAAAATTTGGCCATTTTAATTAATAATGGAAGAAATTTAATG
AGATCAATTGAAATCACTTCTCGTGAAAGAAAAGATGTTGCTAAACAATTATCTTTATGGGGTGAAGCT
AATGAAGATGATATTAGTGATATCACTGATAAATTTGGGGTTTTAATCTATGAAGTTGGTGAATTGGAA
GATCAATTGATTGATAGATATGATCAATATAGAATCACTTTGAAATCTATTAGAGATATTGAAGGTTCA
GTTCAACCAAGTAGAGAAAGAAAAAATACTGATCAAAATTGCTTATTGAAATATAAAGATCCCT
CAATCACCAAAAATTAATGTTTTAGAACAGAATTGGTTAGAGCTGAAGCTGAATCTTTAGTTGCTGAA
GCTCAATTGAGTAATATTACTAGAGAAAAATGAAAAGCTGCTTTAATTATCAATTTGATTCTATTAGA
GAACACGCTGAAAAAATGCTTTAATTGCTGGTTATGGTAAAGCTTTATTAGAAATTATTAGATGAAAGT
CCAGTCACTCCAGGTGAACTAGACCAGCTTATGACGGTTATGAAGCTTCTAAACAAATATTATTATGAT
GCTGAAAACGCTTTAGCTTCTTGACTTTTGATTCTGCCGTTGTTTCGTCCAACCTTATCATTTAGCTGCT
CATGATGAAGAAAGCAGAAGAAGATTTAGAAGGTGCTTATGAAGATGATGAATTGGCTAATGAAGCTGAA
AATTTAAGAATTGCTGAAAAAGATTTTGATGAAGTTGAAGCTAAAATTGCTGCTTAA

YGR086C_homolog 317aa (SEQ ID NO 538)

MHRTYSLRSTRAPTASQLQAPPPPSSTKSFFGKGSISHTFRKQAAGALGPELSRKLAAILIKMEKNLM
RSIEITSRERKDVAKQLSLWGEANEDDISDITDKLGVLIYEVGELEDQFIDRYDQYRITLKSIRDIEGS
VQPSRERKQKITDQIAYLKYKDPQSPKINVLEQELVRAEAESLVAEAQLSNITREKLKTAFFNYQFDSIR
EHAEKIALIAGYGKALLELLDESPVTPGETRPAYDGYEASKQIIDAENALASWTFDSAVVRPTLSLAA
HDEEAEEDLEGAYEDELANEENLRIAEKDFDEVEAKIAA

YGR197C_homolog 1536bp public: 1..1536 (SEQ ID NO 539)

ATGTCTCATGATGATCAAAATCTGAATTCAAACCCAGCTCAAATCCAACCTCCAATCCTGTGTCAAAG
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CCACTCGAACCACAAGGCGATGAAGAGGATATGGAATGGGTGAGCCAATATCACGACAATCAACCTTT
CTTGAGAGAGTACAATCTCGATATTCATTTTCCACGAGAATTTGCGAGCTCAAAGAAAGGAATTGTC

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ATGAAATATCTTAAATTTATCTAGTCATGGCCATTGGTTGCTTAGGAGTGTTCCTATATATTGGGGT
TCAATGTATCAAAGAGAAACCCGAATTAACAACTTGAAATGTTGGTAGTTTTAGAGATGAAGAAATT
AATGGCATCCCTCCACTTTTTGGCAATCAGCTTCGTGATTTATTGGCCACCCCAACGGCTAGAACACTC
GGCGATTGGAAAATATATAACACTAGCGAATTTGAACTATTGCATCAAAACACAACAACAATAAAT
GAAGAGGTCATTCGTCAAATTCATCATCAAAATTATTGGGCCCTCGATATATGTCAAGCAAAATTCATCT
TATAACATATACAATGCATTAGCCAATGGTAATCAGTACAATGTCAGTGACTCTGTGTATTGTTACTAT
GAAACAGGAAGACACCTAAGTAGTGTGGCCCATATGTGGTGGCATCTATAGATGCCATTCAAACATATG
TGGTTGGATCAAACCTGGTGATGAGGGACATTGTGAGAATTGGTAATATAACTCTTGACAATGCAAAAC
TCGGTTGCTGTGCGCCACTACCGCTTGGCATTCCAAATAATTGATATGAGACCATCTACTAGTGGAGTT
TTAGTTGCAGCTTTACAAATTGGTCTTCTTTATCTTGTCAATTGTTAGTTTTTTCAGTTTCAATTTTTTT
GTCGATATACACCGATCAGTGGCATTAAATGGTGAAGCAAAGAACTTTTTACTTTTATCGAGTTTTTGCA
TCAATCATATCGTATTTTTGTTATCAGTTTAAATGTTTGGTTTGGTTACTTTAGCGTTTCAAGTTGATTTT
GCTGTTACATTTGGTAAATCTGGCTTCTTAGTTTACTGGATGGTAACATTTTAAACAATGTGGAGTGT
GGATTGGCTAACGAATTGGCCGCTATGCTCATACTTACTATCTATCCACCAATGGTTGGGTTTTGGTTG
ATCTTCTGGGTAATTATAAATATCACACCCACATTACACCAATTGCTTTGTTACCTGAATTTTATCGG
TATGGTTACGCCATGCCATTGCATAATGCTTTTGAATTTTATCTGTTATTTTTTCAACACGTATAAG
GGATTAATAGGAAGAAGCATTTGGAATCATAATTGCATGGGTGGTATTTTAAACATTAATGGCACCATA
GTGGTGGTTTACTTTGGTAGCATTAGAGTAAAAAGCTGCTGCTCCCGCTGCTGCTGCAAAAAAGGAA
AAGGAAAAGTCAAAGTAA

YGR197C_homolog 511aa (SEQ ID NO 540)

MSHDDSNNSNPSSNPSTSNPVSKPSDMGRSSNDGSEPSIQHFTLAPLEPQGDEEDMEMGEPISRQSTF
LERVQSRYSFFHENLRAQRKELSMKYLKIYLVMAIGCLGVFSIYWGSYQRETRIKNLKMLVLEDEEI
NGIPPLFGNQLRDLATPTARTLGDWKIYNTSEFETIASKHNNTINEEVIRQIHQNYWASIVYKQNSS
YNIYNALANGNQYNVSDSVYCYETGRHLTSVGPYVVASIDAIQTMWLDQNSVMRDIVRIGNITLDNAN
SVAVATTALAFQIIDMRPSTSGVLVAALQIGLLYLIVVSFFSFNFVDIHRVALMVKQRNFFLLYRVFA
SIISYFVISLMLFGLVTLAFQVDFAVTFGKSGFLVYWMVTFMTMWSVGLANELAAMLILTIYPPMVGFWL
IFWVIINITPTFTPIALLPEFYRYGYAMPLHNAFEIYSVIFNTYKGLIGRSIGIIIAWVVFLLTMAPI
VVVYFGSTMSKKAAPAAAAKKEKEKSK

YGR250C_homolog 1890bp public: 1..1890 (SEQ ID NO 541)

ATGTCCTGCTGCTGAACTAATCAACTTCAAGAATCTATGGAAAAGTTGAACATTGGTTCAACTACTGAA
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GTTGCCGAGAAATCTGCCTCCTTGTACGTTGGTGAATTGAACCCATCTGTTAATGAAGCTACCTTGTTT
GAAATCTTTTCTCCAATCGGTCAAGTTTCTCTATCAGAGTTTGTCTGATGCTGTCTCTAAAAAATCT
TTAGTTTATGCTTACGTCAACTACCACAAGTACGAAGATGGTGAAGAGGCTATTGAAGAATTGAAGTAC
AACCCGATCGAAGGTCGTCATGCTGATCATGTGCTCTCAAAGAGACCCATCTGCTAGAAGATGCTGCT
GATGGTAATATTTTCATCAAGAATTTGCATCCAGCCATCGATAACAAAGCTTTGCATGACACCTTTTCT
GCTTTTGGTAAAAATTTTGTCTTGTAAAGTTGCCACCGATGAATTTGGTCAATCAAAGTGTTTTGGTTTT
GTCCACTATGAACTGCTGAAGCTGCTGAAGCTGCCATTGAAAATGTCAATGGTATGTTATTGAACGAT
CGTGAAGTTTTCGTTGGTAAGCACATTTCTAAAAAAGACCGTGAATCTAAGTTTGAAGAAATGAAAGCC
AAGTTCACTAACATTTATGTTAAAAACATTGACTTGAACATTTCAGAAGAAAGCTTTGAAAAATTTGTTT
TCTCCATTCGGTAAGATTACTTCCATTTACTTGGAAAAAGACCAAGATGGGAAATCTAAAGGTTTTGGT
TTTGTAAATTTTGAAGATCATGAATCTGCTGTTAAGGCTGTTGAAGAATTGAACGATAAAGAAATCAAC
GGTCAAAAGATCTACGTTGGTAGAGCACAAAAGAAAAGAGAAAGATTGGAAGAATTGAAGAAACAATAC
GAAGCTGTTAGATTAGAAAAATTTGGCCAAATACCAAGGTGTCAACTTGTGTTTGAAGAATTTGGATGAC
ACTATTGATTCTGAAAAATTAGAAGAAGAAATCAACCAATTTGGTACCATTACATCTGCCAAGGTTATG
GTTGATGAAGCTGGTAAATCAAAAGGTTTTGGTTTCGTTTGGCTTCACAACCCCAAGAAGAAGCACCAG
GCTATCACTGAAATGAACACCAGAATGATTAACGGCAAGCCATTGTATGTTGCTTTGGCTCAACGTAAG
GATGTTAGACGCTCTCAATTAGAACAACAAATTCAGCCAGAAACCAATGAGAATGCAAAATGCTGCT
GCTGGTGGTTTACCTGGTCAATTCATTCCACCAATGTTCTACGGTCAACAAGGCTTTTTCCACCAAAT
GGCAGAGGTAACGCTCCATACCCAGGTCCTAATCCACAAATGATGATGAGAGGTAGAGGTCAACCATTC
CCAGAACAATGGCCAAGACCAGGTCCAAATGGCCAACCAAGTTCCTGTCTACGGTATTCCACCTCAATTT
CAACAAGACTTTTAAACGGTCAAAAATGAGACCTCAGCAACAACAACAACAACAAGAGGTGGATAC
TATCCAAACCGTAACCAAAACCAGCAAGAGAGACTTGGCTGCTATCATTTCTAGTTTCCACAAGATCAA
CAAAAGAGAATTTTGGGTGAAGAATTGTATCCAAAGATTGTTGCTACCGGTAAGGCTCAAGAACCAGAA
GCTGCTGGTAAAAATCACTGGTATGATGTTAGGTTTAGAAAACCAAGAAATTTTGGATTTGTTAGATGAT
GATGAATTTGTTCAATAACCATTTTCAAGATGCTTTTGAAGAGTACAAGAAGTCTGAAGCT
GCCGTAATGCTGAAGAGCAAGCTTAA

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YGR250C_homolog 629aa (SEQ ID NO 542)
MSAAETNQLQESMEKLNIGSTTEEQSAAAATTTADQSAEEQGESSGVAENSASLYVGELNPSVNEATLF
EIFSPIQVQSSIRVCRDAVSKKSLGYAYVNYHKYEDGEKAIEELNYPNPIEGRPCRIMWSQRDPSARRSG
DGNIFIKNLHPAIDNKAHDTFSAFGKILSCKVATDEFGQSKCFGVHYETAEEAAEAAIENVNGMLLND
REV FVGKHISKDRESKFEEMKANFTNIYVKNIDLNYSEESFEKLFSPFGKITSIYLEKDQDGKSKGFG
FVNFEDHESAVKAVEELNDKEINGQKIYVGRAQKKRERLEELKKQYEA VRLEKLAKYQGVNLFVKNLDD
TIDSEKLEEEFKPFGTITSKVMVDEAGKSKGFGFVCFITPEEATKAITEMNTRMINGKPLYVALAQRK
DVRRSQLEQQIQARNQMRMNAAGGLPGQFIIPMFYGOQGFPPNGRGNAPYPGPNPQMMMRGRGQPF
PEQWPRPGPNGQVPVYGI PPQFQDFNGQNM RPQQQQQQQPRGGYYPNRNQT SKRDLAAI ISSVPQDQ
QKRILGEELYPKIVATGKAQEPEAAGKITGMMLGLENQEILDLLDDDEL FNNHFEDALTA FE EYK KSEA
AGNAEEQA

YKL117W_homolog 666bp public: 1..666 (SEQ ID NO 543)
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AAAAATATCATTTATTTAACCATTCAAATATCTGATCCAATTGATTTAAAAATAGATTTAAAAAGTGAT
CATTTAATTATTGATTCTAAATCTAATGATTCAAGTTTATTCATCAATTGATTATCATTTACAAATGAT
TTTTTCAAAGAAATAGATCCTGATCAATCAAAAATTAATACTGAAAATGGTTACATATTTTTATGATT
CTTCGTAAAAAAGATCAACAAGAAGAAATATTGGCCACGTTTAACTAAAGAAAAAATGAAATATCATTAT
ATTAAAACTGATTTTGATAAATGGGTGGATGAGGATGAACAAGATGAAGTTAAAGATGATCCAAATGAT
TTTGGTGGACCTGGTGGACCTGGTGGAGCTATGGATTTCTCACAATGTTGAGCGGCATGGGCGGTTTA
GGTGGCACTGGTGGAGTGGCGGTCTGGTGGCGTCGATCTTAGTGCATTGGCTTCTCAATTGGGTCAA
GCTGGTGGTGGTGGTGGTGGTGCAGGTCTTGATGGTGAAGAAGGCGAAGAAGGCGATGAAGAAGCTAAA
AAAGCGCAAGAAGAAATCAAATGCCACTGCTACTGAAAAAGAATAA

YKL117W_homolog 221aa (SEQ ID NO 544)
MSSTTTQTPTVLWAQRSEDDAAKNIIYLTIQISDPIDLKIDLSKSDHLIIDS KSNDSVYSSIDYHLQID
FFKEIDPDQSKINTENGSHIFMILRKDQEEYWPRLTKEKLKYHYIKTDFDKWVDEDEQDEVKDDPND
FGGPGGPGGAMDFSQMLSGMGLGGTGGSGGPGGVLDLSALASQLGQAGGAGGAAGLDGEEGEEGDEEAK
KAQEE SNATATEKE

YKR075C_homolog 3042bp public: 1..3042 (SEQ ID NO 545)
ATGTCGTTATCAGGAGAAGTGTTCAGGAGGAGCAACCACTTCTCAACATATCGAGGCACAAGATGAT
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CCTGATAAACTAAAAGAACAAGATGGTAATAATTCAGAAGCAAATTCATCAACAACAGCTGCATCAACA
ACCAGCTCAAGAACTTGGCAGCTATGGCAGCTATAGCATCACAAACAATTCGTCATATGTTAACGAA
ACTCCAAGCAGTCAACATCATGAACTATAGAATCCATATCTAATAACTCCGATGGCGATGAACCCAT
TCATCAGATGTAGCGCCATCATCTACATCACCTGTCAATTCACCTTCACCAACTTCCTCACCAGCATTA
GATTTAAAATCTCCAGAATTGTTGCCTCATGATGATACAGATTTAGCTGTTGAACCTTCACGTCATGTT
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AAAGATGTTGCTAATGCTGCAAGATTGGAATGCTTCATGGAGAAGCTTGGGCTCAAAGACGCTCTAAT
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CCTACTCATAACACTAGTGTGGCCAAATTACAAAGCTTGGTTGAAAACCTCCCAATTTCTCATCTTCTGCT
AGTTTGAAAGATTTGATGAAAGATGAAGCCGTTGTTGTGCCTTCTTCAGAACAAATCAGTCACGATCAA
AACCAAGAAGATGGTAATGTTTCTGGGACGTTGAATCCAAAGGTGAAAGACACATACATTTTAATGAC
GAAGTGATGCAATGTATTGCCATTGATGTGTATTTCAGATGATGAGCAACGATATAATTCTGATGAAGAA
GATTATGATTCTGATGATGACGATGATGATTATTATGATCAATATGAACCATCTAATGACAGTCTAGCT
CAAAGTCACCTATATGAAGGAGACGATGAATCCATTGAGGAAGCGGATGAAGAGGTAGAGGATGATGAA
GATGGATCTGAAGATGAAGAAGACGATGAAGGGGATCTTTTTAAATGTGAAATCCAATTCCAATGCC
CCAATAATTTGGGCCAGCATTCAGTGCATCAACTTCTACTCCAGTGGCACCATCTTTAAGTCGTCAC
ACAGATATTACTGATGATACAGCATCAATATCTACCACCAACAGTAAATCTTATAAAACAATTCAATTA
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CTTTCTCATAATGTCAATAATGATATTAGTAGAGGTTATGATTATTATTATGATTACAACACTGTATAC
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CTTGATATGGGATCCAATTTTGATTATGAATTTATTGAAAATAACGATAGTATCCCTGTAGATACACA
ACATTTGAGAATAATAGTACCATTAAATAATATGCCAATTCTGTATAGTCTGCCGTCATCACCTTTATCA
GTTGCTATTTCCGGTGGAGGTAAAAATCTGGTGTCACTGTTAATCCCCAAATTTCCCATAGTTAAT
GTCAACTCTAACCACAACAACAACAATCACAAGCAAAACCAAGCCAAAGACAAGGCATCTCTCT

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TTCCAATTGAGTGATTCAGAAGATGATTCAAATAGTGATTCCGGATGATGATGGTATTTTCAGGATTATCA
ATAGGTACAAGAAGATCTAGTCAAGCTTTAGCTGAACTGGTATTTCAATCATCATTGACAAGTTCTACA
CAAGAAACAGCACCAACATTTCCCCGATGCTAAAGAGATTGAACCGGTTGCTGAACATGTTTCGAGT
ATTAACCCACGATATTCTTCGACTTCGATTTCTAAGCAACCTACAAGTTCAAGTTCACTTTTCACAACTG
TTTTTCGGAGGTGCTGGTGGGTTAAGTAGTACTGATAAAGAGTTGTGCGAACTGTTTTTAGGAGGATCA
ACGTCAGCATCAACATCAACATCGCATGATGAGAAGACTACTACTATTGATTCTTCAAGTACTGGGTTT
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ACATCCAAGAAATCTTCACCATTACCACCACAAACAACCTTCAGAGAATGCATTCAGAGGTGATGGACAA
CAATCACAATCACAATCACAATCACAATCACAGTTGCCACTGCAACAACAACCTGCAACCACGACGGGGA
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CCAAGTCCACAATTGGTAAATGCTAGTGCACATCTTCAAGATCAAGATCAAGGTCATGAAAATGAACAT
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GGATAA

YKR075C_homolog 1013aa (SEQ ID NO 546)

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DLKSPPELLPHDDTDLAVEPSRHVDYLSHQWVDVSDIWKSWRYVISKRKDVANAARLENASWRTWAQRRSN
LKTISPVVNWSKSDSVTWLYGPILKDDHVNENHDSDAIETTATSSVAGDISIAKKCSSKNGPKPIL
KKRTMEQSMISHSNLLKLQLATQIHQKKREQKLKQEELEKQHLNHPDEYFDPEALSNKLNQSYKNTA
PTHNTSVAKLQSLKTPNSSSSASLKDLMKDEAVVPSSEQISHDQNOEDGNVSGDVESKGERHIHFND
EVMQCIADIVYSDDEQRYNSDEEDYSDDDDDDDYDQYEPSNDSLQSHLYEGDDSEIEADEEVEDEDE
DGESEEDDEGGFFLNVKSNSNAPIILGQHSSASTSTPVAPSLSRHTDITDDTASISTTNSKSYKTIQL
LPSTSINYGSDESSDEANPYTSSLSHNVNDISRGYDYDYDYNTVYTCNPNNSVYASYQSPDVPEN
LDMGSNFDYEFIEENDSIPVVDTTFENNSTINMPIISYSSPSSPLSVAISGGGKNSGVTVNSPNFPIVN
VNSNPQQQQSQAKPKPKTKASFFQLSDSEDDNSDSDDDGISGLSIGTRRSSQALAESVFQSSLTSSST
QETAPQHFPDAKEIEPVAEHVSSINPRYSSTSISKQPTSSSSLSQSFFGGAGGLSSSTDKELSKSFLGGS
TSASTSTSHDEKTTTIDSSSTGFFQVFNRYDTPSPDNNTLTRLNNTSKKSSPLPPQTTSENAFRGDGQ
QSQSQSQSQSLPSQQSQPRRGLLFDEEDSEDSDEGMVIGGKREEKKLHGQGYNALSQVAGRNGIHS
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YLR216C_homolog 1221bp public: 1..1221 (SEQ ID NO 547)

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ATTTTCATGCAACGGCAAACCCAAAGGGCCGTGTTGTTTCAAACCTCTACGATGATGTGTTCCTAAAAACA
GCAGCTAATTTCCGTTCTTATGTACTGGTGACAAAGGTATATCACCAAAATCTGGTAAACCACTTTCC
TATAAAGACTCAATTTTCCACAGAGTGATCAAAGACTTTATGTGCCAAGGTGGTGACTTTACCGCTCCT
TCCGACCATTTTGGGAACCTGGTGGTGAGTCCATTTACGGAGAAAAGTTTGAAGATGAAAACCTTTAAGTTG
AACCATAACAAACCATTTTTGTGTCAATGGCTAACTCTGGACCAAAACACCAATGGCTCTCAATTTTTT
ATCACAACAGTTTCCAACACCACACTTGGACGGTAACACGTTGTGTTTGGAGAAGTCATTGAAGGGAAA
TCAATTGTACGTCAATTAGAGAGAAGCGAAAAGGGTGCCAAATGACAGACCAGTAGAAGATTGGAAAAT
GCTGATTGTGGTGAGCTTCCAGCCAACTATGAGCCGGTTGCACTGGGTGCCGATGATGGAACCTGGTGT
ACGTACGAAGAGATTTTAACCGACAACGACACTATCGACATCAACAACCCGCAATCTGTTTTCGCGGCT
GTCAGCAAAATCAAGGATATTGGTACCAAACTTTTGAAAGAAGGGAAATTAGAAAAATCATACGAAAAG
TATACCAAGGCCAATAGCTACTTGAATGATTACTTTCCCGAAGGTTTGTCTCCAGAAGACTTATCAACA
TTGCATGGCCTCAAATTATCGTGTTACTTGAACGCTGCGTTAGTGGCATTGAAATTGAAACACGGCAAA
GATGCAATTGCTGCTGCAACAATGCATTAGAAGTAGAGCAAAATCGACGACAAATCCAAAACCAAGCA
TTATACAGAAAAGGTATGGGCTATATCCTAGTCAAAGACGAAGAACAGGCTCAAAAAGATTCTTGAAGAA
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TTGCGTCTGTGACAAACAAAAGAAGGCAATGGCCAAGTTCTTCTCATAA

YLR216C_homolog 406aa (SEQ ID NO 548)

MCKVVSFENIPPVFFPNLYKNEIKFSFSVFFFFHQLMTATPVYFDISCNGKPKGRVVFVKLYDDVVPKT
AANFRSLCTGDKGISPKSGKPLSYKDSIFHRVIKDFMCQGGDFTAPSDHLGTGGESIYGEKFEDENFKL
NHNKPFLLSMANSGPNTNGSQFFITTVPTPHLDGKHVVFGIEGKSIVRQLERSEKGANRFPVEDWKI
ADCGELPANYEPVAGSADDGTGDTYEEILTDNDTIDINNPQSVFAAVSKIKDIGTKLLKEGKLEKSYEK
YTKANSYLNDFPEGLSPEDLSTLHGLKLSCYLNAALVALKLKHGKDAIAANNALEVEQIDDKSKTKA
LYRKMGYIILVKDEEQAQKILEEALELEPNDAIQKGLQEAKHNIKLRDKQKKAMAKFFS

YMR009W_homolog 537bp public: 1..537 (SEQ ID NO 549)

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GAACCAGTTAGTTTTGATCAACTAGCTGAAATTGGTGTATTTACAAGTACATTACTACCCAGGAAGAA

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TTAGACGCATTGGCTACTGAAAGAGAATACAAGAATAGAGATGTTGTTACTTTTAACTTACCAGCCTTC
AATAATGATATTGATGCTTATAATGCCAAAATGCAACAGTTTACAAAGAACATTATCATGAAGATGAG
GAAATTAGATATATTGCTGAAGGTGAAGGTTATTTTGATGTTAGAGATAAACAAGATCGTTGGATTAGA
GCTAAATTATCACCCTTACGATTTGTTGATTTTACCAGCAGGAATTTATCATCGTTTACATTGACTAAT
GCTGCAAAACACGTCAAGGCAGTTAGATTATTTAAAGATGAACCTAAATGGGAAGCTATCAATAGAGAC
ACAGGAAAAAATACCGAAGCTCGTGAACCTATGCTAAGACTATTGCAGTATAG

YMR009W_homolog 178aa (SEQ ID NO 550)

MVEFYFHDNKDTLENFTEDHNSGEPVSFDQLAEIGVIYKYITTTQEELDALATEREYKNRDVVTNLNPAF
NNDIDAYNAKMQQFYKEHYHEDEEIRYIAEGEGYFDVRDKQDRWIRAKLSPYDLLILPAGIYHRFTLTN
AAKHVKAVRLFKDEPKWEAINRDTGKNTEARELYAKTIAV

YMR011W_homolog 1641bp public: 1..1641 (SEQ ID NO 551)

ATGTCCTCAAGACAACGTCATCAACATCTACAGCTGAGGCTGTAAATAATGAAATCAAAGTCAAAGAT
GAATTTTCGACAAGAAGAACAAGCTCATACTAGTTTGAAGATAAACCTGTGAGTGCATACATTGGTATC
ATCATTATGTGTTTCCCTTATTGCCCTTTGGTGGTTTCGTTTTCGGTTTCGATACCTGGTACTATTTCCGGT
TTCATTAATATGTCTGACTTTTTTAGAAAGATTCCGGTGGTACTAAAGCTGACGGTACTCTTTACTTTTCC
AATGTCAGAACTGGTTTAATGATTGGTTTGTTCACGCTGGTTGTGCCATTGGTGCATTATTCTTGTCT
AAAGTCGGTGATATGTATGGTAGAAGAGTTGGTATCATGACTGCTATGATTGTCTATATTGTTGGTATT
ATTGTTCAAATTGCTTCTCAACATGCTTGGTATCAAGTCATGATTGGTAGAATTATCAGTGGTCTTGGC
GTTGGTATGTTATCAGTTTATGTCTTTTGTTCATTTCAGAGTTTCTCCAAAACATTTGAGAGGTACT
TTGGTGTGCTGTTTCCAAATTGATGATTACCTTGGGTATCTTCTTGGGTATTGTTACTACCTATGGTACT
AAGAGTTACTCAGACTCTAGACAATGGAGAATTCCATTAGGTTTATGTTTGTCTTGGGCTTTATGTTTGT
GTTGCTGGTATGGTTAGAATGCCAGAATCTCCACGTTACCTTGTCCGTAAGACAGAATTGAAGATGCT
AAAATGTCACCTTGTCTAAAACCTAACAAAGTTTCCCCAGAGGACCCAGCCTTATACCGTGAACCTCAATTA
ATTCAAGCTGGTGTGAAAGAGAAAGATTAGCCGGTAAGGCATCTTGGGGTACTTTTATTCAATGGTAAA
CCAAGAACTCTTTGAAAGGGTTGTTGTTGGTGTCTGTTACAAGCCTTACAACAATTGACTGGTGATAAC
TATTTCTTCTACTACAGTACCCTATTTTCAAGTCCGTTGGTATGAATGATTCTTTCCAAACTTCTATC
ATTATTGGTGTATTAACTTTGCGTCCACTTTTGTGGTATTTATGCTATTGAAAGAATGGGTAGAAGA
CTCTGTTTGTAACTGGTTCCGTTGCCATGCTCTGTCTGTTTCTTAATCTATTCTTGGTTGGTACTCAA
CATCTTTATATTGACAAACCAGGTGGTGTCTAGTAGAAAACAGATGGTGATGCCATGATCTTTATGACT
TCACCTTATGTGTTCTTCTTTGCTTCTACATGGGCTGGTGGTGTCTTACTCCATTATTCTGAACTTTAT
CCATTGAAAGTTAGAAGTAAGGCTATGGGTTTAGCTAATGCTTCCAATTGGACCTGGGGTTTCTTAATT
TCTTTCTTTACTTCAATTATTACTGATGCTATCCACTTCTACTACGGTTTCGTCTTTATGGGATGTTTA
GTTTCTCCATTTTCTTTGTCTACTTTATGGTTTACGAACTAAAGGCTTACCTTGGGAAGAAATTGAT
GAATTGTACTCCACCAAGTCTTCCATGGAATCAGCTGGTTGGGTGCCACCTTCCGAAGAAGAAATG
GCAACCTCTACGGGATATGCTGGTGTATGCCAAACAGAGAGGAACACGTTTAA

YMR011W_homolog 546aa (SEQ ID NO 552)

MSQDNVSSTSTAEAVNNEIKVKDEFQRQEEQAHTSLEDKPVSAIYIGIIMCFLIAFGGFVFGFDTGTISG
FINMSDFLERFGGTKADGTLTYFSNVRTGLMIGLFNAGCAIGALFLSKVGDYGRVRVIMTAMIVYIVGI
IVQIASQHWYQVMIGRIITGLAVGMLSVLCLPLFISEVSPKHLRGLTVCCFQLMITLIGFLGYCTTYGT
KSYSDSRQWRIPGLCLFAWALCLVAGMVRMPESPRYLVGKDRIEDAKMSLAKTNKVSPEDPALYRELQL
IQAGVERERLAGKASWGTLFNGKPRIFERVVVGVMQLQALQQLTGDNYFFYYSTTIFKSVGMNDSFQTSI
IIGVINFASTFVGIYAIERMGRRLCLLTGSVMSVCFILYSLVGTQHLIDKPGGASRKPDGDAMIFMT
SLYVFFFFASTWAGGVYSIISELYPLKVRSKAMGLANASNWTWGFLISFFTSFITDAIHFYGYFVFMGCL
VFSIFVYFMVYETKGLTLEEIDELYSTKVLPWKSAGWVPPSEEMATSTGYAGDAKPEEHV

YMR110C_homolog 1986bp public: 1..1986 (SEQ ID NO 553)

ATGAGTAAACCATCTTCCATCAAAAAGTCTAAGGCATCTGCTATTAAACCCCTCGGCTAATTCAAATCA
AAAACCCCAAAAATTGAGACCCCAAAATTGCAACAGTTGAAACACGATTAGAAGGCGAAGTTCCAACA
ACTAAAGTTTCAATTAAAGAAACAGTATTACTACTGAATCTGTAAAGGCTTCAGAAGATAAGTCTACT
CCACAAAGCTACTAACACCCCTGCTGCTGCTGTAGCAAAGTCTAATCCAAATACCAATGCAGAGCCAGCT
AAAATTCCAAACGAAAACTGTAAAAACAGAAATCAGCACTGAGTCAAAAACAAAACGGTGCAACAACA
ACAAAGGAAAAATCTGATGTTCTGTTGGAGACAAAATCGACGTCATCAACTACTGTCTAGCAACAATAAC
TCGGTCTTACAATATACCGAGTTGTCCGAGATCCCTATTGGTGTGAAAGAATTACTAAGGCCTTCCAT
AGTGGCAAAACACACTCTTTACAGTTTAGATTGAAACAAATACGAACTTGTACTTTACAATGAAAGAC
AACCAGGAAGCTTTGTGTGACGCTTTGCAAAAGGACTTTACCCGCTCTTCCCTTCCGAAACAAGAACTAT
GAATTTGCCACTGGATTGAATGAGCTAGTGTATTATTATGTCACAGCTCCACAAATGGAGCAAAACCACAA
CCTGTTGACAGAGTTGCCATTGAATTTGTCTTTTGAATCCAGTTTACATTGAGAGAATTCCCTTTGGGAACA
ATTTTAGTCATTGCTGCTTTCAATTATCCGTTTTTTGTCTCGATCTCACCATAAGTTGGTGCAATAGCA
AGTGGCAACACAGTTGCACTCAAGCCTTCTGAGTTAACACCCCGTTTTTCCAAGCTTTTTACTGACTTG
TTGTCAAAAGCATTTGACCCAGAGATATTTTTTGTGTTCAATGGGGCCATTCTTGAACAACATGCTTG

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TTGGAACAAAAATTTGACAAAATTGTTTATACTGGTAGCGGTTTGGTAGGTACAATAATTGCGAAAAAG
GCTGCGGAAACCTTGACACCAGTTATTTTGGAGTTGGGAGGAAAGTCACCTGCTTTTGTGTTTGGATGAC
ATTTCTGACAAGGACTTGGAACCTGTTGCTCGAAGAATTGCTTGGGGTAGATTTGTAAATGCTGGTCAA
ACATGTATCGGTGTTGACTATGTATTGGTGGCAAAGTCCAAGCACGACAAATTTATCCTGGCCTTGCAA
GAGGTAATTGAAAAAGAGTTTTTTCAAGACGTTGACAAGACGAGAACTTTACCCATATGATCCATGAC
CGGGCATTGAGAAAATGGAGAGTATACTCAACACTACTTCTGGTAATGTGATAATTGGAGGCAAGCTT
GATCATGGCACAAAGATATGTGGGACCTACCGTGATTGATAACGTAACCTGGACAGATTCCCTCTATGAAA
GACGAGATTTTCGGTCCAATTTTACCAATTTTAACCTACACTGATCTTGAAAAATCCTGTCGTGAAATT
ATTGCTAACCACGATACTCCCTTGGCACAATATATCTTTACAAGTGGACCTACATCTAGACAGTATAAT
TCCCAAATTAACACTATTACCACTTTGGTTAGATCTGGGGGATTGGTTATCAATGACGTTTTGATGCAT
ATTGCTTTGCACAATGCTCCGTTTGGTGGTGTGGAACCTCGGGAACGGTGCCTATCATGGAGAGTTC
TCATACAGAGCTTTTACACATGAGAGGACCGTTCTCGAACAACATTTGTGGAATGATGGGTACTCAA
TCAAGATATCCCCCATATGCCAATAAAAAAGACAAATTGATCGCCAGCTCCCAACAAAAGTACGGTGCT
AGAGTTTGGTTCAATAGAGAAGGAATGTGAGAATTGGAGGTCCACCCCTCTTGTGTTTCTGCTTGGAAAC
AATGCTCTTGGGGTAGCTGAATTAGTACGTGATTTTATTGGAGCTGGTTTGTGA

YMR110C_homolog 661aa (SEQ ID NO 554)

MSKPSSIKKSKASAIKPSANSKSKTPKTIETPKLQOVETRLEGEVPTTKVSIKRNSTTESVKASEDKST
PQSTNTPAAAVAKSNPNTNAEPAKIPNEKSLKTESPSSQKQNGATTTKEKSDVSLETKSTSSSTTVSNNN
SVLQYTELSEIPIGVERITKAFHSGKTHSLQFRLKQLRNLTYFTMKDNQALCDALQKDFHRLPSETRNY
EFATGLNELVFIMSQHLKWSKPQPVDELPLNLSLNPVYIERIPLGTILVIAAFNYPFFVSIPIVGAIA
SGNTVALKPSLTPRFSKLFTDLLSKALDPEIFFVNGAIPETTCLEQKFDKIVYTGSGLVGTIIAKK
AAETLTPVILELGGKSPAFVLDDISDKDLATVARRIAWGRFVNAGQTCIGVDYVLVAKSKHDKFISALQ
EVIEKEFFQDVKTRNFTHMIHDFEKMESILNTTSGNVIIGGKLDHGRYVGPVTVIDNVTWTDSSMK
DEIFGPILPILTYTDLEKSCREIIANHDTPLAQYIFTSGPTSROQYNSQINTITTLVRSGLVINDVLMH
IALHNAPFGGVGTSGNGAYHGEFSYRAFTHERTVLEQHLWNDWVLKSRYPYANKKDKLIASSQQKYGG
RVWFNREGNVRIGGPPLLFSAWNNALGVAELVRDFIGAGL

YNL031C_homolog 411bp public: 1..411 (SEQ ID NO 555)

ATGGCTAGAACAAAACAAACAGCAAGAAATCTACTGGTGGTAAAGCCCCAAGAAAACAATTAGCTTCC
AAAGCTGCTAGAAAATCTGCTCCATCTACTGGTGGTGTCAAGAAACCACACAGATATAAGCCAGGTACT
GTTGCCTTGAGAGAAATTAGAAGATTCACAAAATCTACTGAATTATTGATTAGAAAATTACCATTCCAA
AGATTAGTCAGAGAAATTGCTCAAGATTTCAAACTGATTTAAGATTCCAATCTTCTGCTATTGGTGCT
TTACAAGAGCCGTTGAAGCTTACTTGGTTGGTTTATTTCGAAGATACTAAGTTGTGTGCTATCCATGCT
AAGAGAGTTACCATTCAAAAGAAAGATATGCAATTAGCTAGAAGATTGAGAGGTGAAAGATCTTAG

YNL031C_homolog 136aa (SEQ ID NO 556)

MARTKQTARKSTGGKAPRKQLASKAARKSAPSTGGVKKPHRYKPGTVALREIRRFQKSTELLIRKLFPQ
RLVREIAQDFKTDLRQSSAIGALQEAVEAYLVGLFEDTNLCAIHAKRVTIQKKDMQLARRLRGERS

YNL134C_homolog 1086bp public: 1..1086 (SEQ ID NO 557)

ATGAAAGCAGCTATCATTTCTGGATCTTTTCAACCTTATCAATTAGCGGAAATTAAAGATATTCTTCAA
CAAAAAATAAAAGAAAATGAAATATTAATCAAAGCAGTAGCTTTTGCAATAAACCCAACTGATTGGAAG
CACATTGTTTATCAATTGGGCAGCCCAGGTGATGTTGTTGGTTGCGATGTTAGTGGGATCATTGAAGAA
GTGGGTTCTCAAGTAACTGGGTTTGCAAAAGGTGACACTGTAAGTGCTTTTATACTGGTAATAGATCA
CCTCGCACTGGAGCTTTTGCAGAAATATGTAGCTGTTGATCCTGCTACTTCGATAAAGTACAATAAGAAT
TTTGAACATTTGACTAATTTACAAGTATCTGAAATCCACTCATTTGAAGGGGCAGCAAGTATTAATTTA
GGTTTGGTTACCGTTGGGCTTTTCATTTTCTCATTACTTACGAATTGACAACAAAAGCAACCTGGGGAT
AGTATTTTGATTGTTGGGGAGGAGCAACTGCAACTGGAGTTCTAGCCATTGAGGTTGCCAACTAGTGTAT
AATCTCAAAGTAATCACACAGCATACCCAAAAACCACACCTCTTGAAACAATTAGGGGCAGATTAT
GTTTTCGATTATGGAGACGCTGATGTTGTCAATAAAATTAAGAATATTGGCCAAATTAAATTTGCTCTT
GATACGATTGCAACACCAGAAAACGTTTCAAAAAGTTTACGACTCAACAGAGGGGTCTCAAGAAGTATTT
ATTGATTCTTTAGCAGGTTTAGACTATCGATCAATTGCTGCCAATGATGCCAGAGGAGATCAAGTACAT
TGGGGGCACACCATTGCTTGTGTTGGCATCTTTAAAGAGAAAAGTGTGTTTAAATGAAAATTATGTTCAA
ACACCTGAATTGTTAGATGATTTTACTCAGTGGTGGCAAAAGGTGGTCCCTCAAATAATTGATCGTATT
AAACATACAAATTTAAAGTTATTAATGAAGGATTAGACTCCGTAAGTGAAGGGTTAGAATTGTCTAGA
AATAATAAACTCTCTGCTGAAAAGGTTGTATTTAGAGTTCTGGATCTGTGA

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YNL134C_homolog 361aa (SEQ ID NO 558)

MKAAIISGSFEPYQLAEIKDIPQQKIKENEILIKAVAFAINPTDWKHIVYQLGSPGDVVGCDVSGIIEE
VGSQVTGFAKGDTVSAFITTGNRSPRTGAFAEYVAVDPATSIKYNKNFEHLTNLQVSEIHSFEGAASINL
GLVTVGLSF SHYLRIDNKKQPGDSILIWGGATATGVLAIQVAKLVYNLKVITTA SPKNHTLLKQLGADY
VFDYGDADVNNKIKNIGQIKFALDTIATPETFQKVYDSTEGSQEVFIDSLAGLDYRSIAANDARGDQVH
WGHTIACLASLKEKTVFNENYVQTPELLDDFTQWWQKVVPQIIDRIKHTNLKLNEGLDSVSEGLELSR
NNKLSAEKVVRVSDS

YNR002C_homolog 798bp public: 1..798 (SEQ ID NO 559)

ATGACGCTCTTCATCTTCTCAAAAATCTGTTGGATCTTCAATCATAGATGCAAACCAAGGACCAATAAAA
AAAGTTGAAATTGCTGGAGAGGGTGGTGAATTTGTTATTATCAATCGTCACAAGTACTACAGACATGAC
TTGATGGCTGCCCTTCGGGGGTACTTTAAACCCAGGTGCTTCTCCTTGCCCAAAGATCAATATCAACCCT
GCTCCCCCTCGGGTTATGTGGGTTTGCCATGACCACCTTTTGTCTTATCCCTTTTACAATGCCCAAGCTATG
GGTATCAAAGTTCCAAATGTGGTAGTTTCACCTTGCATGTTTCTACGGTGGTGCAGCTCAATTTTTTGTCT
GGATGTTTTTGTAGTTTGTGACTGGAAATACATTTGGTATGACTGCATTGACATCTTACGGTGCCTTCTGG
TTGAGTTATTTCAGCAATCTTGGTTGATAGTTTGGTATCGCTGCAGCCTACGAAGCTTCTGAAGAAACA
GCTTCACAGTTACCAAATGCCATTGGATTTTTCTTACTTGCCTTGGGGTATCTTTACATTTATGTTGTGG
TTGAACACTTTTAAAACTTACAGTTACTTTTCAAGTTCTTTGTTTCTTATTGTTTGTAAACATTCCTTTTG
TTAGCTGGTGGTGAATTTAGTGGAAAGAGTCGGTGTACTAGAGCTGGTGGTGTTTTTTGGTGTATTACACA
GCCATTGTTGCTTGGTGGAAATGCCCTTAGCCGGTACTGCTACTCCAACCAACTCTTACTTCCAACCTGTT
TCTATTCCATTGCCAGGTAACGTTGTTTTCAAGAAATAG

YNR002C_homolog 265aa (SEQ ID NO 560)

MTSSSSQKSVGSSIIDANQGPIKKVEIAGEGGEFVIINRHKYRHDLMMAAFGGTLNPGASPWPKININP
APLGLCGFAMTTFVLSLYNAQAMGIKVPNVVSLACFYGGAAQFFAGCFEFVTGNTFGMTALT SYGAFW
LSYSAILVDSFGIAAAEASEETASQLPNAIGFLLAWGIFTFMLWLNTLKSTVTFSSLFLLFVTFLL
LAGGEFSGRGVTRAGGVFGVITAIVAWWNLAGTATPTNSYFQPVSIPLGNVVFVK

YOL139C_homolog 630bp public: 1..630 (SEQ ID NO 561)

ATGTCTGAAGAATTAGCTCAAAAACTGAAGAATTGTCAATTAGATTCCAAGACTGTTTTTGTATTCCAAA
GAAGAATTTAATGCAAAGCATCCATTGAACAGTAGATGGACATTATGGGTACACTAAACCACAAACCAAC
AAGAGTGAAAACCTGGCATGATTTATTAAAGCCAGTTATAACTTTCTCATCTGTTGAAGAATTTTGGGGA
ATTTACAACTCGAATCCACCAGCAAATCAATTACCTTTGAAATCAGATTATCATTGTTTCAAAGAAGGA
ATTAGACCGGAATGGGAAGATGAGGCTAACTCAAAGGTGGTAAATGGCAATTCTCCTTCAACAAAAAA
CTGGAAGTCAATCCAATCATAAATGATTTGTGGTTAAGAGGTTTGTGTCAGTTATTTGGTGAAGACCAT
GAGGATGAAGAAAACGAAGTCAATGGGATTTGTGTTGAATATCAGAAAGCAAGCTTACAGAGTCGGTATT
TGGACCAAAGATTGTGATGAATCCAAATTTAAAGACTGTCCGGTGAGAGATTGAAGAAAGCTTTGCAATTA
AACGATGAACAAAAAGTTGAATTCATGTCGCATGATGCTTCCAATACTAGAGGCGCTGAACCTCAAAT
GTTTTGTAA

YOL139C_homolog 209aa (SEQ ID NO 562)

MSEELAQKTEELSLDSKTVFDSKEEFNAKHPLNSRWTLWYTKPQTNKSENWHDLLKPVITFSSVEEFWG
IYNSIPPANQLPLKSDYHLFKEGIRPEWEDEANSKGGKWQFSFNKKSEVNPIINDLWLRGLLAVIGETI
EDEENEVNGIVLNIRKQAYRVGIWTKDCDESKLKTVGERLKKVLQLNDEQKVEFM SHDASNTRGAEPQI
VL

YOR120W_homolog 888bp public: 1..888 (SEQ ID NO 563)

ATGCCAGCTCAATTGCAAGTTAACTGATTTATTTCACTTTTAAACAAATGGAAACAAAATCCCAGCTGTT
GGATTAGGTACTTGGCAAGCAACCAATGAAGACGAAGCTTACAGAGCCGCTCTTAGCAGCTCTTAAGAAC
GGATACAAGCACATTGATACCGCTGCAATTTATGGAATGAAGAACAAAGTCGGTAAAGCCATCAAGGAC
TCTGGAGTTCCAAGAGAAGAAATTGTTTGTACTACTAAATTTGTGGAAATGCTGACCATAAAAAATATTGAA
GAAGCCTTAGAGACTTCATTGAAAAAATTGGGCTTAACTATGTTGACTTGTACTTGTATCCATTGGCCA
GCTTCAATTGACAAGTCAACTAATAAACCATATAGACTGATTTTGTATTATGTTGATACCTTATAGAGGTTTA
CAAAAAGTTTATAAGAACAGCAAGAAAATCAGAGCAATTTGGTGTCTTCTAATTTTCAACCAAAAAGAAATG
GAAAGGTTATTGTCTTCGGAAGGTGTCGATGTTGTTCCCTGCTGCTCAACCAAATTTGAAGCTCACCCATTG
TTGACTCAGCTTGAAATGTATGATTTATTTGAAAGAAAAGGTATCGTTTGTGAAGCTTATTACCATTTG
GGTTCTACAAACTCTCCATTATTCAAGAACGAAACCATCGTTAAATTCGCTGAAAAGAAATGGTGTGAA
CCAGCTCAAGTTTGGTATCTTGGGCAATTCAAAGAAAGACTGTGGTTTTGCCATAATCCGTCACCGAA
TCAAGACTTATTTCTAACTTGAAAACATTACATTTTACCTTCAGAAGATTTCCGAAACATTGAACAAATG
TCTGAAAAAGATGGTGTGTCAGAACTTGTAAACCCAGCTTTCAACAACTTTGATGATTAA

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YOR120W_homolog 295aa(SEQ ID NO 564)

MPAQLQVNTDYFTLNNGNKI PAVGLGTWQATNEDEAYRAVLAALKNGYKHIDTAAIYGNEEQVGKAIKD
SGVPREELFVTTKLWNADHKNI EEALETSLKKLGLNYVDLYLIHWPASIDKSTNKPYPDYVDYRGL
QKVYKNSKKIRAI GVSNTFKKKLERLLSSEGV DVPVAVNQIEAHPLLTQPELYDYLKEKGIVLEAYSPL
GSTNSPLFKNETIVKIAEKN GVEPAQVLVSWAIQRKTVVLPKSVTESRVISNLKFTLPSDFETLNKL
SEKDGVVRTCNP AFNNFDD

YOR122C_homolog 381bp public: 1..381(SEQ ID NO 565)

ATGTCTTGGCAAGCCTACACTGATAACTTAATTGCTAACGGTAAAGTCGATAAAGCAGCCTTATATTCA
AGAGCCGGTGACGCATTATGGGCCCAATCGGGATCATTCGAATTACAACAACAGAAATCACTGAAATP
GCCAAAGGTTTCGATAGTGCTGAAGGTTTGCAAACCAGCGGTTTACACGTTCAAGGCCAAAAGTACTTT
TTGTTAAGAGCTGACGACAGATCAATTTATGGTAAACACGAAGCCGAGGGTGTTATTTGTGTTAGAACT
AAACAACTATTTTGATCGCCCATTTCCAAGTGGTGTTCAACCAGGTGAAGCTACCACTCTTGTGTGAA
AAATTAGCCGATTACTTGATCAATGTGCGTTATTAG

YOR122C_homolog 126aa(SEQ ID NO 566)

MSWQAYTDNLIANGKVDKAALYSRAGDALWAQSGSFELQQPEITEIAKGFDSAEGLOTSGLHVQGQKYF
LLRADDRSIYGKHEAEGVICVRTKQTILIAHYPSGVQPGEATTLVEKLADYLINVG

YOR261C_homolog 993bp public: 1..993(SEQ ID NO 567)

ATGTCAACAACCTGCAACTAGCACAAATGAATTGGCCCTTTTGGATAAGTCAGTAGTAGTTTCTCCGTTG
GTTTTACTATCTGTGGTGACCATTTATAATAGAGTTGCCAAAGATTCTAAGAAGAGAGTTGTTGGGGTA
ATATTAGGAGATAACTCTACTGACACAATCAAAGTTACAACTCGTACGCAATTCCTTTTGAAGAAGAC
GAGAAGAACCCTGGAGTATGGTTTTTGGACCACAATTTTATAGATTCAATGGGAGAAATGTTTAAAAAA
ATTAATGCCAAAGAGAAATTGATTGGCTGGTACCATTCAAGACCTAAATTGAAACCATCAGATTTGAAA
ATTAATGAGGTTTTGAGAAGATACACCGACAACCCATTGTTGTTAATTGTTGACGTTCAACCAAGAGAA
GTTGGTATTCCAACAGATGCATATTTGCCGTTGATGATATTAACCAACGATGGCTCTGCTGCTGAAAAG
ACATTTATTTCATGTCCCTTCCTTGATTGAAGCAGAAGAAGCTGAAGAAATTGGAGTTGAACATTTGTTA
AGAGACATCAGAGACCAAGCTGCTGGTAACTTGTCCTTAAGAGTTTCTGAAACACATCAATCATTATTG
GGTTTACATCAGAAGCTTGGAGAAATTGCAAATTATTTGGATAAGGTTTACCAAAAGAAATTACCTATG
AATCATACTATTTTGGGGAATTACAGAATGTTTTTAATTTGTTGCCAACTTGATGCAACAACCTGGGG
AGTGATCTCGATGGTGGTTCAGACTCGTCTCATGCATTAGCCACTGCATTTACTGTCAAGACAAATGAC
GAATTGATGATCATATACATTAGTACATTAGTTCGAGCTATTATTGCATTCCATGATTTGATCGAAAAC
AAGTTAGAAAATAAAAAGTTGAACGAAAATAAAGCACAAGCTTCCGTGGCTGAAGTGTCAATAAATAGC
GAAAAGAAAGATTCTATAGAAGATTAA

YOR261C_homolog 330aa(SEQ ID NO 568)

MSTTATSTNELALLDKSVVVSPLVLLSVVDHYNRVAKDSKKRVVGVILGDNSTDTIKVTNSYAIIPFEED
EKNPGVWFLDHNFIIDSMGEMFKKINAKEKLIGWYHSGPKLKPSDLKINEVFRRYTDNPLLLIVDVQPRE
VGIPTDAYFAVDDIKNDGSAAEKTFIHVP SLIEAEAEIEIGVEHLLRDIRDQAAGNLSLRVSETHQSL
GLHQKLGEIANYLDKVYQKKLPNMHTILGKLQNVFNLLPNLMQQSGSDLDGGSDDSHALATAFTVKTND
ELMIIYISTLVRAIIAFHDLIENKLENKAQASVAESSLNSEKDSIED

YPR035W_homolog 1122bp public: 1..1122(SEQ ID NO 569)

ATGACTACTTCCCTTACAGAACAACTGCTATTTTGGCCAAATATTTGGAATTGTCTCAAAATGGTAAA
ATCTTAGCTGAATACGTCTGGATTGATGCTGAAGGTAACACTAGATCCAAATGTAGAACTTTATCCAAA
AAACCAACTAGTGTGATGATTACCTGAATGGAATTATGATGGTTCATCTACTGGTCAAGCTCCAGGC
CATGATTCTGATGTGTATTTAAGACCAGTTGCTTTTTATCCTGATCCATTTAGAAAAGGTGACAATATC
ATTGTTTTAAATGAATGTTGGAACAATGATGGTACTCCAAACAATTTAATCATCGTCATGAATGTGCT
AAATTGATGAAGGCTCATGCTAGTGAAGAAGTTTGGTTTGGTTTAGAACAGAATATACTTTATTTGAT
CAATATGATTATCCTTATGGTTGGCCAAAAGGTGGATTCCAGCTCCTCAAGGTCCATTCTACTGTGGG
GTTGGTACTGGTAAAGTTGTTGCTAGAGATGCTATTGAAGCTCATTATCGTGCTTGCTTTTATGCTGGT
ATCAACATTTCTGGTATTAATGCCGAATTATGCCATCTCAATGGGAATTCGAAGTTGGTCCATGTGAA
GGTATTGAAATGGGTGATCAATTATGGATTGCTCGTTATTTATTACAAAGAGTTGCTGAAGAATTTGCC
GTCAAGATTTCTTCCATCCAAAACCTTTGAAAGGTGATTGGAATGGTGCTGGTTGTCATACTAATGTT
TCTACCAATCTATGAGAGTGCCTGGTGGTATGAAAGTTATTGAATCTGCTTTGAGTAAATTGGCCAAA
AGACACAAGGAACATATGTTATTGTATGGTGCCGATAATGATCAAAGATTAAGTGGTCGTCATGAACT
GGTCATATGGATACTTTTTCATCAGGTGTTGCTAACAGAGGTGCATCTATCAGAATTCCAAGACAAGTT
GCTAAAGAAGGATATGGTTATTTTCGAAGATAGAAGACCAGCTTCTAACATTGATCCATACTTGGTCACT
GGTATCATGGTGGAGACAATCTGTGGTTCTATTCCAGATGCTGATATGGCTAAAGAATTCCTTAGAGAA
AGCAGTGATGATAACTAA

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YPR035W_homolog 373aa (SEQ ID NO 570)

MTTSLTEQTAILAKYLELSQNGKILAEYVWIDAEGNTRSKCRTLSKKPTSVDLDPEWNYDGSSTGQAPG
HDSVYLRPVAFYPDPFRKGDNIIVLNECWNNDGTPNKFNRHECAKLMKAHASEEVWFGLEQEYTLFD
QYDYPYGWPKGGFPAPQGPFFYCGVGTGKVVARVDIEAHYRACLYAGINISGINAEVMPQSWEFQVGPCE
GIEMGDQLWIARYLLQ RVAEEFAVKISFHPKPLKGDWNGAGCHTNVSTKSMRVPGGMKVIESALSKLAK
RHKEHMLLYGADNDQRLTG RHETGHMDTFSSGVANRGASIRIPRQVAKEGYGYFEDRRPASNIDPYLVT
GIMVETICGSIPDADMAKEFLRESSDDN

YMR099C_homolog 900bp public: 1..900 (SEQ ID NO 571)

ATGCCAGTTGAAGAGCTTGAAGACCGTGTATTACTGATCCAAATGACTCAACTAACAGAGCCACC
ATTTTGAAATTTGGTGCTACTGTAGTTTCTTGGA AAAACAATAATCAAGAAAATTGTGGTTATCAGAA
GGTGCTCATTTAGATGGAAGTAAAGCCGTTAGAGGTGGTATCCCATTAGTTTTCCAGTTTTCCGGTAAA
CAAAAAGATTCAAATCATCCAACCTTTCAAATTACCTCAACATGGATTGTCTCGTAATTCAAATTGGGAA
TTCTTGGGACAAACTCAAGAAAGTCTATTACGGTTCAATTTGGATTAGGTCCAGAAAATGTTGATCCA
GAACTTTGAAATTATGGAATTATGATTTCACTTTGATTTTAAGTTAGTTTGAATAAGATAAAATTG
GTTACTTCAATTGACGTGGAAAACACTGGTAAAGAAGCATTGAATTTAATTGGTTGTTCCATACATAT
TATAGAATCCATGACATCACCGATACATTAGTTACCAATTTAATTGACCAACAATGTTACGATCAATTG
ATTGGTGAATCATATATCGAAAAGGCACCAGTTATCAGTTTCCATGAAGAATTTGATAGAATTTATTCA
AAAGTCAGTTTGGAAAAATCCATTCAAGTCGTTGATAAAGGTCAAGTTCTTTTCAATCTTCATAGAAAA
AACTTGCTGATTCCGTTGTATGGAATCCATGGACTAAGAAAGCTGAAGGTATGGCTGATTTCCAACCA
AAATCAGGGTTTCATCAAATGGTCTGTGTTGAGCCAGGTGATGTTAACTCAATGGTCTCTTTACCAGCT
GGTGGGAAATGGTCAGGTGGTCAAGAAATCACTATTGGCGGTGAGATTAAAGTTCAAGCTAATATTTAT
TAG

YMR099C_homolog 299aa (SEQ ID NO 572)

MPVEELEDRIITDPNDSTNRATILKFGATVVSWKNNNQEKWLSEGAHLDGSKAVRGGIPLVFPVFGK
QKDSNHPTFKLPQHGFARNSTWEFLGQTQESPITVQFGLGPENVDPETLKLWNYDFTLILTVSLTKDKL
VTSIDVENTGKEAFEFNWL FHTYYRIHDITDLVTNLIDQQCYDQLIGESYIEKAPVISFHEEFDRIS
KVSLEKSIQVVDKGQVLFNLHRKNLPDSVVWNPWTKKAEGMADFQPKSGFHMVCVEPHVNSMVS LPA
GGKWSGGQEITIGGEIKVQANIY

YBL085W_homolog 3519bp public: 1..3519 (SEQ ID NO 573)

ATGGATGGTGGCGATACTTATATATGTATAAAACAATTTAATGCCAGATTAGGCGATGAATTGAGTCTT
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AAGTTGGTGGAGAGAGAGGCTTATATCAAAAACATTTACTCAATTAATAACCAACAATGATAGT
AAAACACTTCTTAGATCGAGGTCAAGAAGAATGATGGCACCTAAAAGTTCCGACCAAGAAAACAACACCA
AAGGACACCACTACTCCCGTGGTGTGAGTAATCTCAATCCCAACACTCCTCCAAATTACCCTCCAACA
TTGTCTATCTTCAACAGAACCTTCCCATTTAGCTGAACCAATGTCTCAGTTAAATTTAAATAAAGATTCT
CAATCTTCTCAATATACTGGGTCTCATTTGAACAGCCAAATTGATAGAGCATTACAAGAATTCAAGGG
TCTAATGCCGACTTGACCAATTCTGGCAATAGTTTAAATGAGCACAGAAACCACCACTACAATAACAAC
ACTAATAATAATAATAATAATAATAATAATGCTGCTACTAGTAATAATTACAACAACACAGTAAATG
TCGAAGAAATCAAATGATAGTCTTTCTAGTCAATATCAATATCAATCACAATCCCAACAACCAAAACAT
TTGAGTGGAGATAAATCTCGACAATCCTTAAGTACGATTTGGACCCTTTGAAAGCAAATACTTGGACA
CCAAAGCAAGTTTCTTCTTATTTTGCCTTGGTGTAGGGTTTGATATGGATGTGGCTGGGAAATTTGCT
CAACACAAAATCACTGGAGAAATCTTGTGTTGAATTGGATTTAAATCTTTTGAAGAATTGGATATTGAT
TCATTTGGTACCAGATTCAAATTATATAAAGAAATGGGAAATTAAAGGAATTGAATACTGAAGGAGTT
AAAGATAAACAATTGAGAACAGATTCTCTGTGCTGACTGGATCAACTGGTAAAAATGACACTACGTCATCA
GCATTAAATTTCTCCACCAACTGCTTCCACAACCTTTACACGATGCCGTGCCTCATATCGATGATAATAAT
ATGTTAAATAATACTGGCAACAACAACAACAATAATGCCATCAGCCGTTTTGACCAACACTTCTGAC
TACAATAATAATAGTCAACAACAAGTGGTTCTCAACATCATCAGAGGAAAAGGTCACTGTGGTGGAT
GTTGCCCCACAACAATACTTGGCTTCTGATTCTACATTTATGTGCGCTAGAAGAGCTCCTCAACCACCA
TCTGGTGAGAGCCCAATTGATACAAGTTATAAATTTGGTGCTGGAAGCGAATACGATAGACCACTTCA
CACTATGGCATGTACATGACACGTACTAACGCTTCAAGTCATGCCTTGGGAAGTTTCACTACCAAGAAATC
AACTCAGCAGCAGCTTCAATTTATGATCTGTTTTCCAATCATAATAGAAATGGATCATCAACTTCA
AAACAACACCACAAGAGAAATTCATCAGTAACCAACAATAACAATAACAATAACGGTAACAGCAACCAC
AAGCATCATCACAGACGTCATTCTTCGGTATTCTCATACCTTTCTGCTGGTAATGATGATTGGGCAAAA
CCAACACCAAAATTTAGTAGTAAGTTCCAAAGTAACAATTTGTACAAGGGTGGTATGATGGTCAAT
GGAGATTTCACTTCTTCAAGCAATAACAACAACAGTAAGTTAGTGTGCGCCAGCCGATGATGATCAAG
AGAGAAACCACTAGTGGTCAATCGTCTCTTCATGAATCAGGATCCAAATCGAAAGGAAAATCACAATTT
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TCAGTTCCGACCAAGTCAATGGATGCAATTTGGTGGTAATGGAGACGATAGACGTGTTGCTAGTGATTCT
ACAGGATTGAGTCAATCAAAACCTAATAATTCATCAAGACTTAAAGGCATTCTGTCCACGTCAACTCAA

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AGTTTCCGAAGTTTAAACAGGGTCGAAGAACTGAAAAACATCAGCATTTCAGAAGGTATACGTGAGATT
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GCGTGGAGAACAAGATATTTACATTACACGGTACCAGATTATCATATTTCCAATCTTTGAAAGATAAA
AAGGAAAAAGGTTTGATTGATATTACTGCTCATAAAGTGATACCTATTGATAGTGCTAGTGATGATACT
GATAAAGCTGATAGATATGCTGCGATGTATGCCTCGACAACATTTGCTGGTAATTATTGTTTTAAATTG
GTTCCACCGGTCCAGGGTTTAAAAAGGGTTAACGTTTACGCAACCGAAAACTCATTATTTGCTGTT
GAAACAGAAGAAGAAATGAGAGCTTGGGTCAAAGCATTAAATGCAAGCCACTATTGATATTGATGATCT
GTTCTGTTGTGAGTAGTTGTTCTACCCCACTGTGCTGTTGAATAAAGCTCAAGAATTGTTAGCTAAA
GCCAGAGAAGAAACCAATTACGAGATGAACAATAAAAGCTAATGGCTACATTAGAAGCTTAGAAGAT
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ACTTCTCCAGTAGCAGCAACTTCAGCACCTAAATTGACTCTTGATACTAATTTTAATAGGAAAAAGTTCT
GGAACCTATGGGAACAACGGGGACAATAGGTACTCCAGGAACATCAGGTGGTACGGTACCAACAACACCA
CAAAATACCAGTATCAAGTCAAAGTGGTGGGTTTGCTTACCTTATTTATTAGCTTCTGGGTTATTA
TCACCCAAATCAGGAGGTGGTGCCGGTCCAGGAGGAATTGTATCATCGTCTTCTCCAATTAATGAAAAT
GGACCTTTAAGAAATTCAACTTCAAATTCAGAATATTTTGGTGATATTACTTATAAAAGTTTAAAAACA
CCATCTCGACAAAATTTCCAATATGCAAGTATCACTAGTGGTGGTGGCAGTATTGGGTTTGGATATGGT
TCCAACAATAGTGGCCTAGGTGGACCAGCAACAGCAATTGGAGGAGGAGGAGGAGGAGTATTATCATCA
TCCACTCCATATTCTACTGGTTCTGGATCAACAGCAAGTTCAATGAATTATAAATCATAACAACAAC
AACAACAACAACAATTCTGTTAATAGTCCGATTAATGAATTTAGATCTTCAAGGGATTGAAATCATCA
TCGTACCAACGACAACAACAGGTACATCTTCAACATCAGGGAAAAAACCCCAATCACGTAGAACATCA
GATAAAATGTTGGGATTTTCAAGTGATGCTTCAGGTAGTCATACTTTTGTATTAAACCGAAAAATAA

YBL085W_homolog 1172aa (SEQ ID NO 574)

MDGGDTYICIKQFNARLGDLSLKIGDKIQVLADDDREYNDGWYMGKNLLTGEAGLYPKTFTQLITNND
KTLRLSRSRMMAPKSSDQETTPKDTTPVVSNNLNPNTPPNYPPTLSSSTEPHSLAEPMSQLNLNKDS
QSSQYTGSHLNSQIDRALQELQGSNADLTNSGNSFNEHRNHYNNTNNNNNNNNNAATSNNYKQPQLM
SKKSNDLSQYQYQSQQPKHLSGDKSRQSLTDDLDPLKANTWTPKQVSSYFALVLGFDMDVAGKFA
QHKITGEILFELDLNLLKELDIDSFGTRFKLYKEIGKLKELNTEGVKDKQLRTDSSSTGSTGKNDTTSS
ALNSPPTASTTLHDAVPHIDNMLNNTGKQQTQLMPSAVLNTSDYNNSQSQSGSQHHQRKRSSSDV
VAPQYLASDSTFMSPRRAPQPPSGESPIDTSYKFGAGSEYDRPPSHYGMYTRTNASSHALGSSSPGI
NSRPASSIYDSFSNHNRRNGSSTSKQHHRNSSVTNNNNNNNGNSNHKHHHRRHSSVFSYLSGNDSDSAK
PTPKLLSSKFQSNLYKGGDDGHGDFTSNNNNNNNSKLVSPAQIKRETTSGQSSLHESGSKSKGKSQI
FDLSNPVDIDDAKFSPKKSNSVSVRTKSMDAIGNGDDRRVASDSTGLSQSKPMNSSRLKIRATSTQ
SFRSLTGSKSKTSFAQEGIREITPDEAIKTASHSGYMSKRSNNNLAWRTRYFTLHGTRLSTYFQSLKDK
KEKGLIDITAHKVIPIDSASDDTDKADRYAAMYASTTTFAGNYCFKLVPAPGFKGLTFTQPKTHYFAV
ETEEEMRAWVKALMQATIDIDSVPVVSSCSTPTVSLNKAQELLAKAREETKLRDEQLKANGYIRSLD
INDTSFSASLDYPMMSGDIGFGSTSPVAATSAPKLTLDTNFNKRKSSGTMGTTGTIGTPTGSGTVPPTP
QIPRSSSQSGGFASPYLLASGLLSPKSGGAGPGGIVSSSSPINENGPLRNSTSNSEYFGDITYKSLKP
PSRQNSQYASITSGGSGIFGYGSNNSGLGGPATAIGGGGGVLSSTPYSTGSGSTASSMNYNNHNNN
NNNNNSVNSPINEFRSSRDLKSSSSPTTTTGTSSSTSGKKPQSRRTSDKMLGFSSDASGSHTFVIKPKK

YBR019C_homolog 2028bp public: 1..2028 (SEQ ID NO 575)

ATGTCAAACGAATATATTCTTGTTACTGGTGGTGAGGTTACATTGGTTCTCATACAGTTATTGAATTA
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ATTGAATTCATTGTCAAACAACATGTTCCATTCTATGATGTTGATATCAGAAATTATGAGCAATTGAAT
AAAGTTTTCCAAGATTATAAGATCTCTGGAGTCATTCATTTTGCTGCTTTGAAAGCTGTTGGTGAATCA
ACAAAAATCCCTTAGCATATTATGATAATAATGTATCAGGTACTGTCAACTTATTGGAAGTATGTAAA
GCCAATGATGTGAAGACAATTGTTTTTCAGTTCTTCAGTACTGTCTATGGTGATGTGTTACTAGATTGGT
GATAATTCAATGATTCTCTATCCCTGAACATTGTCCAATGGATCCAACAAATCCATATGGAAGAACA
TTCATTATTGAGTCGATTTTAAAGATATTTATAATAGTGATGATGCTTGGAAAGTAGCAATTTTGAGA
TATTTCAACCCAATTGGTGCTCATCCATCTGGTTTATTAGGTGAAGATCCATTGGGGATCCCAAATAAC
TTATTACCTTATTTGGCTCAAGTTGCTATAGGTAGACGTGAAAAATTGTCTATTTTCGGAAATGATTAT
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GCATTGGCGTATTTGAAAAACTTGCAATCTAAAGGCTTGATCGTGAATGGAATTTAGGTACTGGTAAA
GGATCCACTGTTTTTGAAGTTTATCATGCATTTAGTAAAGTTGTTGGTAGAGAATTGCCCAATGAAGTT
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TGGAAACTGAACCTACCATTGATGATGCTTGTAAGATTTATGGAATGGACTACTGAGAACCCTTTT
GGATTCAACATTGAGAATTATTCTTGGAAAGAATTGTATGGGTTCAATAACCGTTTGCACAGTTTGT
CTGGTGACTTGAAGTTAACTTAGCGAATCGTGGTGCAATGATCCAAGCTATCACGTTGAAGGATTC
AATATGGTCAAAGCTTATAAATAGCTGAAGATTTTCAATCTGAAACTAACCCTTTTCGGTACCCT
GTTGGTAGATATGCCAATAGAATTTCCAATGGAGAATTTAAATTTGAATGGAAAAGGTGTACAAATTA
AAAAATGAAGGAGCAAACAACCTGCATGGTGGTGCAATGGATTTCGATAACAAGATTTCTTTGGTCCA
GTTGTGAAAAGTCGTGATGGTAAGTTTTCTGTTGATTCTTGTGGTTGATAAAGATGGTAATGATGGG

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TTCCCAGGTGAGCTTGAAGCTATCGTACATTACACAATTGATGACTCCTCAGTGGAAATTGAATATGAA
TGTCAATTATTATCTGGTGAAGCAACAATTGTCAATATGACTAACCATAGTTATTTCAATGTTTCCAAC
TCAGACACTATTGAAGGAACCGAGGTAAATTTGATTACTGATAAAATGTTAGAAGTGGATTACACAATTA
TTACCAACTGGTAAATTTATTGAAAATGAAAAAGCTGCTAGCCCAATTGTGTTAAATGAGAATGACGTA
TTTGACAATTGTTTTATTGTTGATGAAGAATGTGGTATAGATACTCGTGATAAACCTTTGAAACAAGTC
TTTGAAAGCACTAGTTTTGTGACAAACAACAATTTGAAGATATCCACCACTGAACCAGCTTTCCAATTT
TACACTGGTGACGGTGTAAATACTAAAGGTTTTGGGAAAAGATGTGGTTTTCTGCGTGGAACCAAGTAGA
TTTATTAATGCAATCAATCACAAGAATGGTCTAATCAAGTCATCTTGAAAAAGGTGATGTTTATGGA
AGTAAATTAATATGAATTTCAATAG

YBR019C_homolog 675aa (SEQ ID NO 576)

MSNEYILVTGGAGYIGSHTVIELISNGYKVVIVDNLSSSYDAVARIEFIVKQHVFPYDVIDIRNYEQLN
KVFQDYKISGVIHFAALKAVGESTKIPLAYYDNNVSGTVNLLLEVCKANDVKTIVFSSSATVYGDVTRFG
DNSMIPPEHCPMDPTNPYGRTKFIIIESILKDIYNSDDAWKVAILRYFNPIGAHPSGLLEDPLGIPNN
LLPYLAQVAIGRREKLSIFGNDYNSRDGTPIRDYIHVVDLAKGHIAALAYLKNLQSKGLYREWNLTGK
GSTVFEVYHAFSKVVGRELPHVVGRRAGDVLDTAKPDRANKELQWKTELTIDACKDLWKWTENPF
GFNIENYSWKEFDGFNNRLHSFVAGDLKVNLANRGALIQAITLKDSNMVKAYNNAEDFKSETNPFPGTT
VGRYANRISNGEFKLNKQVYKLTKNEGANNLHGGANGFDKQDFGFPVVKSRDGKFFVDFLLVDKDGNDG
FPGLEAIVHYTIDDSSVEIEYECQLLSGEATIVNMTNHSYFNVSNSDTIEGTEVKLITDKMLEVDSQL
LPTGKFIENEKAASPIVLNENDVFDNCFIVDEECGIDTRDKPLKQVFEATSFVTNNKLKISTTEPAFQF
YTGdGVNTKGFGRKCGFCVEPSRFINAINHKEWSNQVILKKGdVYGSKIKEYEQ

YCR005C_homolog 1194bp public: 1..1194 (SEQ ID NO 577)

ATGAGAGGTATCAAAGGTTTAGTTTGGGAAGGTTCTGTTTTGGACCCAATTGAAGGTATCCGTTTCAGA
GGAAGAACCATCCAGACATTCAAAAAGAATTGCCAAAAGCACCAGGTGGTGAAGAACCATTACCAGAA
GCTCTTTTCTGGTTGTTGTTGACTGGTGAAGTTCCAACGACGCCCAAACCTAAGGCTTTATCCGAAGAA
TTTGCTGCTAGATCAGCATTACCAAAGCACGTTGAAGAATTGATCGACAGATCTCCATCTCACTTGCAC
CCAATGGCTCAATTCTCCATTGCCGTTACTGCTTTGGAATCTGAATCCCAATTTGCCCAAGCTTATGCT
AAAGGTGCCAACAAATCCGAATACTGGAAATACACTTACGAAGATTCCATCGATTGTTTAGCTAAATTG
CCAACCATTGCTGCTAAGATTTACAGAAACGTTTTCCACGATGGTAAATTGCCAGCTGCCATTGACTCC
AAATTGGATTACGGTGCTAACTTGGCCAGTTTGTGTAGGTTTTGGTGACAACAAGGAATTTGTTGAATTA
ATGAGATTGTACCTTACCATCCACTCTGACCACGAAGGTGGTAACGTCTCTGCACACACCACCACTTG
GTTGGTTCCGCTTTATCTTCCCCATTCTTGTGATTAGCTGCTGGTTTGAATGGTTTAGCTGGTCCATTA
CACGGTAGAGCTAACCAAGAAGTTTTGGAATGGTTGTTCAAATTAAGAGAAGAATTAAACGGTGACTAC
TCCAAGGAAGCCATTGAAAAATACTTGTGGGAAACCTTGAACCTCCGGTAGAGTTGTCCCAGGTTACGGT
CACGCTGCTTTGAGAAAGACCGATCCAAGATACACTGCTCAAAGAGAATTTGCTCTTAAACATATGCCA
GACTACGAATTTGTTCAAATTTGGTTTCAAACATTTACGAAGTCGCTCCAGGTGTTTTGACCAAAACACGGT
AAGACCAAGAACCCATGGCCAAATGTGGACTCCCACTCTGGTGTCTTGTACAACTACGGTTTGACT
GAACAATCTTTTCACTGTCTTGTTCGGTGTTCAGAGCCTTTGGTGTCTTGCCACAATTGATCTTG
GACCGTGGTATCGGTATGCCAATTGAAAGACCAAAATCTTTCTCCACTGAAAAATACATTGAATTGGTC
AAAAACATCAACAAAGCTTAA

YCR005C_homolog 397aa (SEQ ID NO 578)

MRGIKGLVWEGSVLDPIEGIRFRGRTIPDIQKELPKAPGGEEPLPEALFWLLLTGEVPTDAQTKALSEE
FAARSALPKHVEELIDRSPSHLHPMAQFSIAVTALESSESQFAQAYAKGANKSEYWKYTYEDSIDLLAKL
PTIAAKIYRNVFHDGKLPAAIIDSKLDYGANLASLLGFGDNKEFVELMRLYLTIHSDHEGGNVSAHTHL
VGSALSSPFLSLAAGLNLGAGPLHGRANQEVLEWLFKLREELNGDYSKEAIEKYLWETLNSGRVVPYG
HAVLRKTDPRYTAQREFALKHMPDYELFKLVSNIEVAPGVLTKHGKTKNPWPNVDSHSGVLLQYYGLT
EQSFYTVLFGVSRAFGVLPQLILDRGIGMPIERPXSFKSTEKYIELVKNINKA

YDR345C_homolog 1653bp public: 1..1653 (SEQ ID NO 579)

ATGTCATTAGATAATTCAACAGAAAACCGTGATTTGGAAGAAAAGGAAGAAATTCCAAAGAACGAACAT
AACGAACAAGGCGAACAACGAGAACAAATGAGCATATACCTACTTTGGAAGATAAACCATTTGAAGGAA
TATATTGGTATTAGTATTTTGTGTTTCCTTATTGCTTTTGGTGGTTTCGTTTTTCGGTTTCGATACGTGGT
ACCATTTCTGGTTTCATTAAACATGACTGACTTTTTAGAAAGATTTGGTGGTACTAAAGCTGACCGTACT
CTTTACTTTTTCCAACGTTAGAACTGGTTTATTGATTGGTTTGTTCATGTGGGTTGTGCCATTGGTGCA
TTATTCTTGTCTAAAGTCGGTGATATGTATGGTAGAAGAGTTGGTATCATGACTGCTATGATCATTTAT
ATTGTTGGTATTATTGTTCAAATTTGCTTCTCAACATGCTTGGTATCAAATCATGATTGGTAGAATTATC
ACTGGTCTTGTCTGTTGGTATGTTATCAGTTTTGTGTCCATTATTTATCTCAGAGGTTTCTCCCAAACAT
TTAAGAGGTACATTAGTTTATTGTTTCCAATTTGATGATTACCTTGGGTATTTTCTTGGGTTACTGTACC
AGTTACGGTACTAAGAAATATTCTGACTCCAGACAATGGAGAATTCCATTGGGTTTATGCTTTGCTTGG
GCCTTGTGTTTGGTGGTATGGTAAGAATGCCAGAATCTCCACGTTACCTTGTGCGGTAAAGATAGA
ATTGACGATGCTAAGATTTCACTTGCCAAAACCTAACAAGGTTTCTCCAGAGGACCCTGCATTATACCGT

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GAACTTCAATTAATCCAAGCTGGTGTGAAAGAGAAAGATTGGCCGGTAAGGCATCTTGGGGTGCTTTA
ATCACTGGTAAACCAAGAATCCTTGAAAGAGTTATTGTTGGAGGTATGTTGCAATCATTGCAACAATTG
ACTGGTGATAACTATTTCTTCTACTACAGTACCACCATTTTCAAGTCTGTCCGGTTAAATGATTCCTTC
GAAACATCTATTATCCTTGGTGTCACTCAACTTTGCTTCCACTTTTGTGGTATTTATGCCATTGAAAGA
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GGTTTCTTGATTTTCCTTCTTCACTTCATTTATCACTGATGCTATCCACTTCTATTATGGTTTTGTGTTT
ATGGGCTGTTTAGTGTTCATTTTCTTTGTTTACTTTATGATTTACGAACTAAAGGTCTTACTTTA
GAGGAAATTGATGAATTATACTCTACCAAGGTTGTTCCATGGAAATCAGCCGGTTGGGTTCCACCTTCT
GACGAAGAAATGGTTCGTGCAAAAGGCTATACTGGTGATATCCACGCAGATGAAGAGCAAGTTTAA

YDR345C_homolog 550aa (SEQ ID NO 580)

MSLDNSTENRDL EEKEEIPKNEHNEQGEQNNENHIPTLEDKPLKEYIGISILCFLIAFGGFVFGFDTG
TISGFINMTDFLERFGGTKADGTLFYSNVRTGLLIGLFNVGCAIGALFLSKVGD MYGRRVIMTAMI IY
IVGII VQIASQHA WYQIMIGRIITGLAVGMLS V LCLPFI SEVSPKHLRGTLVYCFQLMITLGI FLGYCT
SYGTKKYSDSRQWRIP LGLCFAWALCLLGGMV RMPESP RYLVGKDRIDDAKI SLAKTNKVSPEDPALYR
ELQLIQAGVERERLAGKASWGALITGKPRILERVIVGGMLQSLQQLTGDN YFFYYSTTIFKSVGLNDSF
ETSII LGVINFASTFVGIYAIERLGRRLCLLTGSVAMSICFLIYSLIGTQHL YIDQPGGPTRKPDGNAM
IFITALYVFFFASTWAGGVYSIVSELYPLKVRSKAMGFANACNWLWGFLISF FTSFITDAIHFFYGFVF
MGCLVFSIFFVYFMIYETKGLTLEEIDELYSTKVVPWKSAGWVPPSDEEMVRAGYTGDIHADEEQV

YDR545W_homolog 1194bp public: 1..1194 (SEQ ID NO 581)

ATGGCATCCGAAGGTATTACTGAAATCGACTCTGGTTTAATTGAAACCAATTACGATAACGTCGTCTAC
AAGTTCGACGATTTAACTTGAAACCAACATTGTTAGAGGTATTTTGGTTACGGGTATGAACTCCA
TCCGCTATTCAACAAAGAGCCATCTTGCCAATCACTGAAGGTAGAGATGTTTTGGCTCAAGCTCAATCC
GGTACTGGTAAAACCGCTACCTTTACCATTTCTGCATTACAAAGAATCAATGAAAATGAAAAAGCCACT
CAAGCTTTAATCTTGGCCCCAACAGAGAATTGGCTTTGCAAATCAAGAATGTTATCACTGCTATTGGT
TTGTACTTGAAGGTTACTGTCCATGCTTCTATTGGTGGTACCTCAATGAGTGACGATATTGAAGCTTTC
AGATCTGGTGTTCAAATTGTCTGTTGGTACTCCAGGTAGAGTCTTAGACATGATTGAAAGAAGATATTTT
AAAACCGATAAAGTCAAGATGTTTCAATTTGGATGAAGCTGATGAAATGTTATCAAGTGGATTTAAAGAA
CAAATTTACAACATTTTTCAGATTATTACCAGAAACCACCAAATTGTCTTATTATCTGCCACCATGCCA
CAAGACGTTTTTGAAGTCACCACCAAATTCATGAACAACCCAGTCAGAATCTTAGTCAAAAAAGATGAA
TTGACTTTGGAAGGTATCAAACAATTCTATATTAATGTTGAATTAGAAGATTACAAATTCGATTGTTG
TGTGATTTTGACGATTCTATTTCTGTCAACCAAGCCGTCATTTTCTGTAAACACTAGATCCAAAGTTGAA
TTTTTAACCAACAAATTGAGAGAACAACACTTTACTGTCTCTGCCATCCACGCTGATTGCCCACAAGCC
GAAAGAGACACCATTATGAAAGAATTGAGATCTGTTCTTCAAGAATCTTGATCTCTACTGATTGTTA
GCTAGAGGTATTGATGTCCAACAAGTTTCTTTAGTTATCAACTACGATTGCCAGCCAACAAGGAAAAC
TACATTATAGAAATTGGTAGAGGTGGTCTGTTTCGGTAGAAAGGGGGTTGCCATCAACTTTGTCACTGAC
AGAGATGTTGGTATGATGAGAGAAATTGAAAATTCTACTCTACTCAAATCGAAGAAATGCCAGCTGAT
ATTGGTGCCTTTATTGCTTAG

YDR545W_homolog 397aa (SEQ ID NO 582)

MASEGITEIDSGLIETNYDNVVKFDDLNLKPNIVRGIFGYGYETPSAIQQRAILPITEGRDVLAAQAS
GTGKTATFTISALQRINENEKATQALILAPTRELALQIKNVITAIGLYLKVTVHASIGGTSMSDDIEAF
RSGVQIVVGT PGRVLDMIERRYFKTDKVKMFI LDEADEMLSSGFKEQIYNIFRLLPETTQIVLLSATMP
QDVLEVTTKFMNPNVRILVKKDELTLLEGIKQFYINVELEDYKFDCLCDLYDSISVTQAVIFCNTRSKVE
FLTNNKLREQHFTVSAIHADLPQAERDTIMKEFRSGSSRILISTDLLARGIDVQVSLVINYLDPANKEN
YIHRIGRGGFRGRKGVAINFVTD R DVGMREIEKFYSTQIEEMPADIGALFA

YIL057C_homolog 606bp public: 1..606 (SEQ ID NO 583)

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CATTTACAACCAGTCCCTAAAACAAGATCATCATCAATTACCTCAATTGAAAGTGCTGATGAACCAGGT
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GTTTCGTGATGAACTTGGGATAATGATTTTGATTATTTCCATGGTAGATTACATTATTATCCACCATTT
GTTATGAAGAGTTGTCAAATAATCTTGAAAAATCAAGCCTACCATGAATAAAAACTCCAAGAAATTT
AGACGTGATTTACAACATCATATTCAAAAACATTTAATTAAAGATTTAGAAAAATGTTGTGGTTACGAG
TTGAATTTTGGTAAAGGAGAAGTTGTTGAGACTGATAATAAAGTTACTTGGAAATTTAAAGACGAAACT
GATCATGGTTTTAGTAAAGAAGAAGAAGATATGTATGATAGACATTGGAGATTGGAATTGGATGTTTCT
TGTACAAATGAATCAGCTATGGTTGATGTTGAATATAAATCCATTCCAATGTAA

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YIL057C_homolog 201aa (SEQ ID NO 584)

MAGKKKSKSEALPLDLNPKMDHLQVPKTRSSSITSIESADEPGTMKQVLLPPTIKEFDELEQFESF
VRDETWDNDFDYFHGRLHYYPFVMKSCQNNLEKIKPTMKNNSKKFRRDLQHHIQKHLIKDLEKCCGYE
LNFGKGEVVETDNKVTWKFKDETDHGFSSKEEDMYDRHWRLDVSCTNESAMVDVEYKSIPM

YKR097W_homolog 1662bp public: 1..1662 (SEQ ID NO 585)

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TTATACGAAGATGGTTTATTAGAAAAAGGTACTACTATCTCATCTACTGGTGCTTTAATGGCTTACTCT
GGTAACAAAACCGGTAGATCTCTTAAAGACAAGAGAATTGTCGACGAATCCACCTCATCCCATAACATT
TGGTGGGGTCCAGTGAATAAACAAGTTGACGAATTAACCTGGAAGATTTCTAGATCAAGAGCTTTGGAT
TACTTGAGAACTAGAGAAAAGTTGTTTGTGTGTTGACGCTTATGCTGGTTGGGATCCAAGATACAGAATC
AAGGTCAGAATTATCTGTGCTAGAGCTTACCATGCTTTGTTTCATGACCAATATGTTGATCAGACCAACT
GAAGAAGAATTAAAAAACTTTGGTGAACCAGATTTACCATCTACAATGCTGGTCAATTCCCAGCCAAC
ATCCACACTAAAGGTATGACTTCTGCCACTTCTGTTGAAATCAACTTTAAAGATATGGAAATGGTTATC
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AAACACAAGGTTTTGACTTTGCACTCCTCATGTAACCAAGGGGTTGAAAAAGGTGATGTCACTTTGTTC
TTTGGTCTTTCTGGTACTGGTAAGACCACTTTGTCTGCTGATCCACAAAGAAAGTTGATTGGTGATGAC
GAACATTGTTGGTCCGACAATGGTGTGTTCAACATTGAAGGTGGTTGTTACGCCAAATGTTTGGACTTG
TCTGCTGAAAAAGAACCAGAAATTTCAACTCCATCAAGTTTGGTGTATTTTGGAAATGTTGTCTAC
GACCAATACCAAGGTTGTTGACTACGAAGATTCAATCAATCACTGAAAACACTAGATGTGCATACCCA
ATTGATTTTCAATCCATCTGCCAAGATTCCATGTTTGGCCGACACCCATCCAACCAATATTTATCTTGT
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ATTTCTGGTTACACCTCCAAGATGGCAGGTACTGAAGAAGGTGTTACTGAACCACAAGCTACATTCTCC
GCATGTTTTCGGTCAACCATTTCTTGGTGTGTCACCCAATGAAATATGCTCAACAATTTGCTGACAAGATT
TCCGAACACAATGCCAACGCTTGGTTGTTGAACACTGGTTGGGTTGGTTCTTCTGTTGCTCAAGGTGGT
AAGAGATGTCCATTGAAATACACCAGAGCTATCTTGGATGCTATCCACTCTGGTGAATTGTCTAAAGTC
GAATACGAAAAAGTTCCAGTTTCAACCTTAATGTTCCAACTTCTTGTCTGGTGTTCAGGTGAAATT
TTGAACCCAATAAAGCTTGGACCCAAGGTACTGATTCATTCAACAAGGAAATCAAATCTCTTGCTACC
AAGTTTGCTGAAAACCTCAAGACATACGCTGATCAAGCTACTGCTGAAGTTAAAGCTGCTGGTCCAGAA
GCATAA

YKR097W_homolog 553aa (SEQ ID NO 586)

MAPPTAVESSINFGGHPTIKSTQDPLVQKLSLNTD TVIRHNAPPPTLYEDGLLEKGTTSSTGALMAYS
GNKTGRSPKDKRIVDESTSSHNIWWGPNKQVDEL TWKISRSRALDYLRTREKLFVVDAYAGWDPRYRI
KVRIICARAYHALFMTNMLIRPTEELKNFGEPDFTIYNAGQFPANIHTKGMTSATSEVINFKDMEMVI
LGTEYAGEMKKGIFTVMFYLMPIKHKVLT LHSSCNQGVKGDVTLFFGLSGTGKTTLSADPQRKLI GDD
EHCWSDNGVFNIEGGCYAKCLDLSAEKEPEIFNSIKFGAILENVVYDPITKVVDYEDSSITENTRCAYP
IDFIPSAKIPCLADTHPTNII LLTCDASGVLPPVSKLTNAQVMYHFISGYTSKMAGTEEGVTEPQATFS
ACFGQPFLVLHPMKYAQQLSDKISEHNANAWLLNTGWVGSSVAQGGKRCPLKYTRAILDAIHS GELSKV
EYKVPVFNLNVPTSCPGVPSEILNPTKAWTQGTDSFNKEIKSLATKFAENFKTYADQATAEVKAAGPE
A

YOL126C_homolog 1014bp public: 1..1014 (SEQ ID NO 587)

ATGGTCAAAGTCGCTATTTTAGGAGCTGCTGGTGGTATTGGTCAACCATTATCTTTATTGACCAAATTA
AACCCAAATGTTGATGAATTGGCATTATTTGATGTCTGTCATGTTCCAGGAGTTGGTGCTGATTTATCT
CATATCAATTTCTGATTCTAAACTCAATCATATTTACCAAAAGATAAAGAAGATAAACTGCATTAGCT
GCTGCATTAAAAAGGTTCTGATTTTAGTCATTATCCAGCTGGTGTTCAGAAAACCAGGTATGACCAGA
GATGATTTTATTCAATATTAATGCATCAATCGTTCAAGGTTTAGCTGAAGGTATTGCTGCCAATTTCTCCA
AAAGCTTTTGTCTTGGTGATTCTAATCCAGTCAATTCTACTGTACCAATTGTTGCCGAACTTTACAA
GCTAAAGGTGTTTATGATCCAGCTAGATTATTTGGTGTACTACTTTGGATATTGTTTAGAGCCAATACT
TTTATTTCTCAATTATTCCTAGATCAAACATAACCATCTGATTTCAATATTAATGTTGTTGGTGGCCAT
TCTGGTGAAACCATTTGTTCCATTATATTCATTAGGTAACCTAAACAATATTATGATATATTATCTGAA
GAACAAAAGAAGGAATTAATCAAAAAGGTTCAATTTGGTGGCGATGAAGTTGTTTCAAGCCAAGAATGGT
GCTGGTTCGCCCACTTTATCCATGGCTTATGCCGTTATAGATTAGCCGAATCAATTTTAGCTGCTGTT
AATGGTAAAAC TGATATTGTTGAATGTACTTTCTTGAAC TTGGATTCTTCAATTAAAGGTGCTTCTGAA
GCTAGAAAAATTGGTTAAAGATTTAGATTTCTTTTCATTACCAGTTCAATTAGGTAAAAACGGTATTACT
GAAGTTAAATATGATATCTTAAATCAAATTTCTGATGATGAAAAGAAATTGTTAGAAGTTGCCATTGAA
CAATTACAAAAGAATATTGAAAAAGGTGTTTCATTGCTAAGAAATAA

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YOL126C_homolog 337aa (SEQ ID NO 588)

MVKVAILGAAGGIGQPLSLLTKLNPVDELALFDVVNVPVGADLSHINSKTSYLPKDKEDKTALA
AALKGSDLVIIIPAGVPRKPGMTRDDLNFNINASIVQGLAEGIAANSPKAFVLVISNPVNSTVPIVAETLQ
AKGVYDPAFLFGVTTLDIVRANTFISQLFLDQTKPSDFNINNVGGHSGETIVPLYSLGNSKQYYDILSE
EQKKELIKRVQFGGDEVVQAKNGAGSATLSMAYAGYRLAESILAAVNGKTDIVECTFLNLDSSIKGASE
ARKLVKDLDFSLPVQLGKNGITEVKYDILNQISDDEKKLLEVAIEQLQKNIEKGVSFARK

YBL072C_homolog 621bp public: 1..621 (SEQ ID NO 589)

ATGGGTATTTCTAGAGATTCACGTCACAAAAGATCCGCCACTGGTGCCAAAAGAGCCCAATTCAGAAAG
AAGAGAAAGTTTGAATTAGGTAGACAACCAGCCACACCAAGATTGGTCCAAAAGAAATTCACCTCTGTC
AGAACCAGAGGTGGTAACCAAAAATTCAGAGCTTTGAGAGTTGAAACCGGTAACCTTCTCTTGGGGTTCC
GAAGGTGTTTCCAGAAAACCAGAAATTTGCTGGTGTCTGTTTACCATCCATCTAATAACGAATTTGGTTAGA
ACCAACACCTTGLACCAAACTCTGCTGTTGTTGTTGATGCTACTCCATTCAGACAATGGTACGAAAAAC
CACTACGGTGTCTACTTTAGGTAAAAAGAAGGGTGGTGTCTCATGCTGCTCACGCTGCTGAAGTTGCCGAT
GCCAAGAGATCAAGAAAAGTCGAAAGAAAATTTGGCTGTCTAGATCTGGTGTCTGCTGCCATTTGAATCCGCT
GTTGACTCTCAATTCGGTTCTGGTAGATTATACGCTGTCTATTTCTTCAAGACCAGGTCAATCTGGTAGA
TGTGATGGTTACATCTTGAAGGTGAAGAATTAGCCTTCTACTTGAGAAGATTAACTGCTAAGAAATAA

YBL072C_homolog 206aa (SEQ ID NO 590)

MGISRDSRHKRSATGAKRAQFRKKRKFELGRQPANTKIGPKRIHSVRTRGGNQKFRALRVETGNFSWGS
EGVSRKTRIAGVVYHPSNNELVRTNTLTKSAVVQIDATPFRQWYENHYGATLGKKKGGAHAHAHAEEVAD
AKRSRKVERKLAARSGAAIESAVDSQFGSGRLYAVISSRPGQSGRCDGYILEGEELAFYLRRLTAKK

YBR009C_homolog 318bp public: 1..318 (SEQ ID NO 591)

ATGTCAGGTACCGGTAGAGGAAAAGGTGGTAAAGGTTTAGGAAAAGGTGGTGTCTAAACGTCACAGAAAA
ATTTTAAGAGATAACATTCAGGTATTACAAAACCAGCTATCAGAAGATTGGCCAGAAGAGGTGGTGT
AAACGTATTTCTGCTTTGATTTATGAAGAAGTCAGAGTTGTCTTGAAACAATTTTGGAAAACGTTATC
AGAGATGCTGTACTTACACTGAACATGCTAAAAGAAAAACCGTCACTTCATTGGATGTTGTTTACGCT
TTGAAGAGACAAGGTAGAACCTTGTATGGTTTCGGTGGTTAA

YBR009C_homolog 105aa (SEQ ID NO 592)

MSGTGRGKGGKGLGKGGAKRHRKILRDNIQGITKPAIRRLARRGGVKRISALIYEEVRVVLKQFLENVI
RDAVITYTEHAKRKTVTSLDVVYALKRQGRITLYGFGG

YBR189W_homolog 489bp public: 1..489 (SEQ ID NO 593)

ATGGCCGGTGAAATACCGGTTTAAAAACAAGGGGGGAATCTACAGAATTGGGGTTCCAAATGTCCTAAA
ATCAGAAGAGCTGCTCGTGAAATTTGTAACCAAGAGGTGAAAAAGGCCCCAAAAAGATTATTCGGAAGGTA
ATGGCTTTGATCAGAAGATTAGTCAGATTCGGTTTCTTGTCTGAGGACAAAATGAAATTTGGATTATGTC
TTGGCTTGGAAACCCAGAAGTTTCTTGAACAGAAGATTCCAACCCCAAGTTTTCAAATTAGGTTTAGCT
AGATCTATCCCCCAGCCAGAGTTTGTATCACCACCAAGCCACATTTGCTGTTGGTAAACAAATTTGTTACC
ATCCCATCATTTACTGTCTAGATTGGACTCTCAAAAACACATTTGACTTTGCCCAACAATCTCCATACGGT
GGTGGTAGACCCGGTAGAGTTAAGAGAAAGAACCAAGGTAAAGGTGGTGAAGAAGGTGCCGAAGAAGAA
GAATAA

YBR189W_homolog 162aa (SEQ ID NO 594)

MAGEYRFKKQGGNLQNWGSKCPKIRRAAREFVTRGEKGPKKIIRKVMALIRRLVRFGLSEDKMKLDYV
LAWNPEVFLNRRFQPVFKLGLARSIPHARVLITQSHIAGVKQIVTIPSFTVRLDSQKHIDFAHNSPYG
GGRAGRVRKRNQKGGGEEGAEEEE

YBR191W_homolog 330bp public: 1..330 (SEQ ID NO 595)

ATGCCACACAAATACTACCACGGTAAGACTGGTATTGTTTACAACGTTACCAAATCCTCCGTTGGTGT
ATCATTAACAAAGTTGTTGGAAACAGATACATTGAAAAGAGAGTTAACTTGAGAGTTGAACATGTTAAA
CACTCTGCTTGTCTCAAGAAATCTTGAACAGAGTTAAATCTAACGCTGCTAAAAAGAGAGAAGCTAAA
GCTAACGGTGAAACCGTTTACTTGAAGAGACAAGCTGCCAAGCCAAGAGGTTCAGAAATTATCTCCACT
GAAGGTAACATTTCTCAAACTTTGGCTCCAGTCGCTTACGAACTTTTCATTAA

YBR191W_homolog 109aa (SEQ ID NO 596)

MPHKYYHGKTGIVYNVTKSSVGVIIINKVVGNRYIEKRVNLRVHVKHSACRQEFNLNRVKSNAKKREAK
ANGETVYLKRQAAKPRGSRIISTEGNIPQTLAPVAYETFI

YCL035C_homolog 384bp public: 1..384 (SEQ ID NO 597)

ATGATAGACAAAATGCTGCTGATTCTTGCCTGGGGATTCAATTTGTGGTATCAACCACCTCCACCTACT
GCACAAACTGAGAAAAGAAATCGAACACACTATTAACCTCTCACAAGATTGTTATTTATCTAAAACCTAT

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TGTCCATTTTGTGACCAAACCAAACATCTATTAAATGAACAATATCCACAAGAATCGTACGAAGTCATA
AACTTGAATATTCTCGATGACGGATTGACTATTGAGAATCAATTGTATGCTAATACTGGTCAATATATG
GTGCCATAATCTTCATAAACGGACAACACGTTGGAGGAAATTCAGAAGTTCAGCAATTGCACACCAAT
GGGAAATTGCAAGAATTATTGAATCCTCAGAAATATTGA

YCL035C_homolog 127aa (SEQ ID NO 598)

MIDKMSSILAWGFNLWYQPPPTAQTEKEIEHTINSHKIVYISKTYCPFCDDQTKHLLNEQYPQESYEVI
NLNILDDGLTIQNQLYANTGQYMPVPIIFINGQHVGGNSEVQQLHTNGKLQELLNPQKY

YDL004W_homolog 486bp public: 1..486 (SEQ ID NO 599)

ATGTTTCAGACAAGTTTTCCGTCAAGTTACCAAACAATCATTCACTGGGGTTAAGAGAACTTATGCCACC
GAGGCCGCCGTGTCTACAGATGCTTTGAAATTATCCTTGGCATTGCCACACCAAACCTTATACAACGAC
TCCGAAGTCCAACAAGTAAACTTGCCATCTGTCAACGGTGATTGGGTATTTTGGCCAACCACATTCCA
ATTGTGCAACAATTGAGACCAGGATTGTTAGAAATCATTTCAAAAACGGAGACTCTGACCAATACTTT
GTCAGCGGCGGTATCGCCATGGTCCAACCAGGAAACAAGTTGACTATTTCCGCCATCGAAGCATTTCAAG
ACCGACCAAATTGATCTCTCTGCCGTCAAAACTTGATTGCCGATGCCCAAAGAGAGCTGAATCTAGT
GATGAAAAGGTCGCTGCTGAAGCCAACATCGAATTGGAAGTGTTAGATGCTTTACAACATTTTACTAAG
TAA

YDL004W_homolog 161aa (SEQ ID NO 600)

MFRQVFRQVTKQSFTGVKRTYATEAAVSTDALKLSLALPHQTLYNDSEVQQVNLPSVNGDLGILANHIP
IVEQLRPLLEIIISKNGSDQYFVSGGIAMVQPGNKLITISAIEAFKTDQIDLSAVKNLIADAQKRAESS
DEKVAEEANIELEVLDAHQHFTK

YDR099W_homolog 795bp public: 1..795 (SEQ ID NO 601)

ATGCCAGCCTCCCGTGAAGATTCCGTTTACCTTGCTAAATTAGCCGAACAAGCAGAACGTTATGAAGAA
ATGGTTGAAAACATGAAAGCCGTTGCTTCTCTGGCCAAGAATTGTCTGTTGAAGAACGTAATTTATTA
TCTGTTGCTTACAAGAATGTCATTGGTGCTCGTCGCTTCTTGGAGAATTGTTTCATCAATGAACAA
AAAGAAGAAGCCAAAGGAAATGAGAGCCAAGTTGCTTTGATCAGAGATTACCGTGCCAAGATTGAAGCT
GAATTGTCTAAAATTTGTGAAGATATTCTCTCTGTGTTGAGCGACCATTTAATTACATCTGCCCAAAC
GGTGAATCAAAAGTATTTTACTACAAGATGAAAGGTGATTACCACAGATACTTGGCTGAATTTGCTATC
GCTGAAAACGTAAGGAAGCTGCTGATTTATCATTAGAGGCTTATAAAGCTGCTTCTGACGTTGCTGTG
ACCGAGTTGCCACCAACCCATCCAATCAGATTAGGTTTAGCATTGAACCTTCTCTGTTTCTACTATGAA
ATTTTGAACCTCCCAGATAGAGCTTGTCAATTTAGCTAAACAAGCTTTTCGATGATGCTGTTGCTGATTTA
GAAACCTTATCTGAAGATTATACAAGGATTCAACTTTGATTATGCAATTATTGAGAGATAACTTGACT
TTATGGACCGATTTATCTGAAGCCCCAGCTGCCACTGAAGAACAACAACATCCAGTCAAGCTCCAGCT
GCTCAACCAACAGAAGGTAAGGCTGATCAAGAATAG

YDR099W_homolog 264aa (SEQ ID NO 602)

MPASREDSVYLAKLAEQAERYEEMVENMKAVASSGQELSVEERNLLSVAYKNVIGARRASWRIVSSIEQ
KEEAKGNESQVALIRDYRAKIEAELSKICEDILSVLSDHLITSAQTGESKVFYKMKGDYHRYLAEFAT
AEKRKEAADLSLEAYKAASDVAVTELPPTHPIRLGLALNFSVFYYEILNPSDRACHLAKQAFDDAVADL
ETLSEDSYKDSTLIMQLLRDNLTLWTDLSEAPAATEEQQSSQAPAAQPTEGKADQE

YDR399W_homolog 642bp public: 1..642 (SEQ ID NO 603)

ATGTCTGAATCTGAGAAAATGTACATTTTCGTACAATAATATACACCAGTTATGTCAAGAAATAGCCCC
AAGATCAAAGAATTTAAGCCTGACTTGATCATTTGCTATTGGTGGCGGTGGTTTTATTCAGCTAGAATG
TTGCGTTTCTTCTTGAAAGAACCAGGTCAACCAAACGTTAGAATTATGGCTATCATATTTGCTTTATAC
GAAGAGATTGAGAGTGAAAACGGTATTGAAAAGCCAGGTACCCAAGTTGTGCGTACTCAATGGATTGAT
TATCATCAATCTAAAATTGACTTGGTTGGTAAAAATGTGTTAATTATTGATGAGGTTGATGATACCAGA
ACCACTTTGCATTACGCAGTCAGTGAATTGAAAAAGATGTGGAAGAGCAATCAAAAGCCAAAGGTGCA
GATCCTAAAGATACCAAGTTTGGTATTTTGTGTTGCACGACAAGCAAAAAGCAAAAAGAGCAGAAATTG
CCAGATGATATTATGAAGACTGGTAATTATTTGCTGCTCGTTCTGTCCCAGATAGCTGGATTGCATAC
CCATGGGAGTCTACTGACATTTTATCATCAAATGAAAGCTGAAGAACAAGGAAACGATGTGTTCTCT
CCTTCATCCACTTTAGAGTAA

YDR399W_homolog 213aa (SEQ ID NO 604)

MSESEKMYISYNNIHLQCEIAPKIKEFKPDLIIAIGGGGFIPARMLRSFLKEPGQPNVRIMAILLSLY
EEIESENGIEKPGTQVVRTQWIDYHQS KIDLVGKNVLIIDEVDDTRTTLHYAVSELKQDVEEQSKAKGA
DPKDTKFGIFVLHDKQKQKKAELPDDIMKTGNFYFAARSVPDSWIAYPWESTDIVYHQMKAEEQGNVFL
PSSTLE

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YDR418W_homolog 498bp public: 1..498 (SEQ ID NO 605)
ATGCCCTCCAAATTTGATCCAAATGAAGTTAAATTCCTTTACTTAAAGAGCTGTTGGTGGTGAAGTTGGT
GCTTCATCTGCTTTAGCTCCAAAGATTGGTCCATTAGGTTTATCCCCAAAGAAAGTTGGTGAAGATATT
GCCAAAGCCACCAAGAATACAAAGGTATTAAAGTTACTGTTCAATTGAGAATTCAAAACAGACAAGCT
ACTGCTTCTGTTGTTCCATCCGCTTCATCTTTAGTCATCACCAGCTTTGAAAGAACCAGTCAGAGACAGA
AAGAAGGAAAAGAACGTCAAACACTCTGGTAACAATTCATTAGATGAAATCTTTGAAAATTGCCAGAAAA
ATGCAACACAAATCATTCGGTAAGAATTTGGCATCTGCTTCCAAGGAAATCTTGGGTACTGCTCAATCT
GTTGGTTGTAGAGTTGATGGTAAGAACCCTCATGACATCATGACGCCATCAACGCTGGTGAATTTGAT
GTTCCAGAAAAC TAG

YDR418W_homolog 165aa (SEQ ID NO 606)
MPPKFDPNVVKFLYLRAVGGVEVGASSALAPKIGPLGLSPKKVGEDIAKATKEYKGKIKVTVQLRIQNRQA
TASVVPSSASLVITALKEPVRDRKKEKNVHSGNIPLDEIFEIARKMQHKSFGKNLASVSKEILGTAQS
VGCRVDGKNPHDIIDAINAGEIDVPEN

YDR513W_homolog 360bp public: 1..360 (SEQ ID NO 607)
ATGTTTCGTACATTATTAACCAAAAGACTATTCAATACATCAACAATGGTTTCATCTCAAGTTAAGAAC
AAGGTCGAACAATTTGATCAAAAACCAAAACAGTTTTCATTGGCTCCAAATCCTATTGTCCATACTGTAAG
GCTACCAAAAGCACAATTTGAAGCTATAACAAAGGATGCTTACATTCTTGAATTTAGACGAAGTTGACGAC
GGTGTGAAATCCAAGAAGCATTTATTGGAATCACTGGTCAAAGAACCCTTCCAAATGTCTTTATTGGT
GGTCAACATATTGGTGGCAATTCGGATGTGCAAGCTTTGAAGTCTAGTGACAAATTTAGATGACAAAATC
AAAGCTGCTTTATAA

YDR513W_homolog 119aa (SEQ ID NO 608)
MFRLLTKRLFNTSTMVSSQVKNKVEQLIKTKPVFIASKSYCPYCKATKSTIEAITKDAYILELDEVDD
GAEIQEALLEITGQRTVPNVFIGGQHIGGNSDVQALKSSDKLDDKIKAAAL

YEL009C_homolog 972bp public: 1..972 (SEQ ID NO 609)
ATGCCCTGCTACTACTCCTATTATTTATGAAGATTCTTTATTTGAATCTCAAGATTTATTTGCTTCTCCA
GTTAAACAACAACATCAAAAAGTTGATACCTGTTGCTACCAAAAACGAAATTTGGTTTGGAAATTAATTTA
GGTTTACCAGAAATGCAAAAGGCTTCAGAACTGTTTCCACTCCATTTCAAATCCATTCCAGTGATTTG
GAGTCGGGTTTTCAGCACCAATTTGGATGGAGTCAATGATATTGATCATACTCCAATGTTTGTATGAATTG
GATTTGATTATGGACGGAGCCAAAGTCAATTCATCAGAAGATTGGGTTGCTCTTTTTTGGAGATGACAAT
GATGATGGTGTGCTATAGCTGGTGTCTACTAGCAAAGAACCAATGTTTATCATTTGAATGAAGATAACGAG
AACAAATGATGACGACGCTGATGACGCTGATGATGATGATGATGCTCTTGTTCGAAGAGAAGATACTATT
GAAGCTTTTATTATTGGAACCATCACCAATCGTACCATTCTGCTGCTACTTCTGCTTCTACTTTCATCA
TTAAACAGTCCAGAAAGTACTATTGCTACCACAGTCACTGCTGGTGGTGAAGTTGTTGTTGCAAGTAAA
AAGCAATTTCAATTGGTAACACCAATCCTTCATCCACTTTACCAACACCATTATTGGATTCTAAAAAT
TCTAAAAAAGAGTTAAAGTTGATCATTTGGGTTGTGTTACCTATTTCGAAAAAACATAGATCTCAACCT
TTACAACCGATTGTTGTTGATGACATTAAAGATGCTGCTGCTTTTGAAAAGAGCTAAAAATACTGAAGCT
GCTAGAAGATCCAGAGCTCGTAAAAATGGAAGAATGAGTCAATTGGAAGATAAAGTTGAGAATTTGATT
AATGAAAAGCAAGCTTTTACAAGATCAAGTTGAAAGATTACAAGAAATTTGTTAAGAGTTAATGGTATTCAA
TTTTAA

YEL009C_homolog 323aa (SEQ ID NO 610)
MPATTPPIIYEDSLFESQDLFASPVKQQHQKVDTVATKNEIGLELNLGLPEMQKASETVSTPFIHSSVL
ESGFSTNLDGVNDIDHTPMFDELDLIMDGAKVNSSSEDWVAFGDDNDGVAIAGATSKEPMLSLNEDNE
NNDDDDADDADDALVPREDTIEALLLEPSNRTISAATSASTSSLNSPESTIATTVTAGGEVVVASK
KQFQLVTPNPSSLTPLPLDSKNSKKRVKVDHLGCVTYSKKHRSQPLQPIVDDIKDAAALKRAKNT
ARRSRARKMERMSQLEDKVENLINEKQALQDQVERLQELLRVNGIQF

YGL123W_homolog 750bp public: 1..750 (SEQ ID NO 611)
ATGTCAGCTGAAGCCCCAAAAGACAATTTGGTGATAGAAGAAGAGGTGGTGAAGAGGTGGTAGAAGA
GATGGTGAAGAAAAGGTTGGACTCCAGTCACCAAGTTAGGTAGATTAGTCAAAGCTGGTAAAAATCACC
AGTGTGAACAAATCTACTTGCCTCTTTGCCAGTCAAGGAATACCAATCATTTGATTTGTTATTGCCA
GACTTGAAAGATGATGTCATGAAGATCAGATCTGTCCAAAACAAACCAGAGCTGGTCAAAGAACCAGA
ATGAAGGCTGTTGTCGTCATTGGTGACTCTAACGGTCACGTTGGTTTGGGTATCAAGACCGCTAAAGAA
GTTGCTTCTGCCATTAAAGCTGCTATTGTTATTGCCAAATTATCCATCATCCCAATCAGAAGAGGTTAC
TGGGGTTCTAACTTGGGTCAACCACACTCTTTGCCATTAAGTCACTGGTAAATGTGGTTCCGTTGCC
GTTAGATTAAATCCCAGCCCCAAGAGGTAAAGGTATTGTTGCTTCTCCAGTTGTCAAGAGATTAAATGCAA
TTGGCTGGTGTGAAGATGCTCTATACTTCTCTTCTGGTTCTACCAGAACTACCGAAAACACCTTGAAA
GCTGCTTCTCGCTGCTATCGGTAACACTTACAGTTTCTTGACTCCAAACTTGTGGGCTGAAACTCCATTA
GCTGCTTCTCCATTGGAAGTTTACGCTGAAGAAGCTGCTGCTGGTAAAAAGAGATACTAA

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YGL123W_homolog 249aa (SEQ ID NO 612)
MSAEAPKRQFGDRRRGGRRGGRRDGEKGWTPVTKLGRVLKAGKITSVEQIYLHSLPVPKEYQIIDL LLLP
DLKDDVMKIRSVQKQTRAGQRTRMKAVVVGDSNGHVGLGIKTAKEVASAIAAIVIAKLSIIPIRRGY
WGSNLGQPHSLPCKVTGKCGSVAVRLIPAPRGKGIVASPVVKRLMQLAGVEDVYTSSSGSTRTTENTLK
AAFAAIGNTYSF LTPNLWAETPLAASPLEVYAE EEAAGKKRY

YGR209C_homolog 312bp public: 1..312 (SEQ ID NO 613)
ATGGTTCACGTTGTCACTGAAGTTAACGAATTCCAAACCTTTTAAAGGAAAACAACCTTAGTTATTGTT
GACTTTTTTGCCACTTGGTGTGGTCCATGTAAAATGATTGCTCCATTATTAGAAAAATTCAAAAATGAA
TATTCTAATATTAAATTTTTGAAAATTGATGTTGATCAATTGGGTCTTTAGCACAAGAATATAATGTT
AGTTCTATGCCAACTTTGATTTTATTCAAAAATGGTGAAGAAGTCAATCGTGTCAATTGGTGTCAACCCA
GCTGCTATTAAACAAGCTTTGGCTTCTCTTGCTTAA

YGR209C_homolog 103aa (SEQ ID NO 614)
MVHVVEVNEFQTLLENLIVDFVFATWCGPCKMIAPLLEKFQNEYSNIKFLKIDVDQLGSLAQEYNV
SSMPTLILFKNGEEVNRVIGANPAAIKQALASLA

YHR039C-B_homolog 342bp public: 1..342 (SEQ ID NO 615)
ATGTCATCTGGTATCCAATCATTATTGAAAACCGAAAAAGAAGCTGCAGAAATTGTTAATGAAGCTAGA
AAATATAGAACCACACGTTTGAAGTCTGCAAAACAAGATGCTCAAGCTGAAATTGATAACTATAAAAAAG
CAAAAGGAAGAAGAATTAAAAAATTTGAAAAAGAACACGAAGGGTTAAATGAAAAGATCGATAAAGAA
GCTGATGCTGAAGTTGAAAAGGAATTGACCAGTATCAAATCCACTTTTGAAAAGAAAAAGAGTGCAGTT
GTTAAATTGTTAGTTGACGCTACTGTCAAGCCAACACCAACTTTACACATAAATGCATCTCAATAA

YHR039C-B_homolog 113aa (SEQ ID NO 616)
MSSGIQSLLKTEKEAAEIVNEARKYRTTRLKSAKQDAQAEIDNYKKQKEEELKNFEKEHEGLNEKIDKE
ADAEVEKELTSIKSTFEKKKSAVVKLLVDATVKPTPTLHINASQ

YJL138C_homolog 1194bp public: 1..1194 (SEQ ID NO 617)
ATGGCATCCGAAGGTATTACTGAAATCGACTCTGGTTTAATTGAAACCAATTACGATAACGTCGTCTAC
AAGTTCGACGATTTAACTTGAAACCAAAACATTGTTAGAGGTATTTTTGGTTACGGGTATGAACTCCA
TCCGCTATTCAACAAAGAGCCATCTTGCCAATCACTGAAGGTAGAGATGTTTTGGCTCAAGCTCAATCC
GGTACTGGTAAAACCGCTACCTTTACCATTTCTGCATTACAAAGAATCAATGAAAATGAAAAAGCCACT
CAAGCTTTAATCTTGGCCCCAACAGAGAATTGGCTTTGCAAATCAAGAATGTTATCACTGCTATTGGT
TTGACTTTGAAGGTTACTGTCCATGCTTCTATTGGTGGTACCTCAATGAGTGACGATATTGAAGCTTTC
AGATCTGGTGTTCAAATTGTCGTTGGTACTCCAGGTAGAGTCTTAGACATGATTGAAAAGAAGATATTTTC
AAAACCGATAAAGTCAAGATGTTTCAATTTTGGATGAAGCTGATGAAATGTTATCAAGTGGATTTAAAGAA
CAAATTTACAACATTTTCAGATTATTACCAGAAACCACCCAAATTGTCTTATTATCTGCCACCATGCCA
CAAGACGTTTTTGAAGTCACCACCAAATTCATGAACAACCCAGTCAGAATCTTAGTCAAAAAAGATGAA
TTGACTTTTGAAGGTATCAACAATTTCTATATTAGTTGAATTAGAAGATTACAAATTCGATTGTTTG
TGTGATTTGTACGATTCTATTTCTGTCAACCAAGCCGTCATTTTCTGTAAACACTAGATCCAAAGGTTGAA
TTTTTAACCAACAAATTGAGAGAACAACACTTTACTGTCTCTGCCATCCACGCTGATTTGCCACAAGCC
GAAAGAGACACCATTATGAAAGAATTCAGATCTGGTTCTTCAAGAATCTTGATCTCTACTGATTGTGTA
GCTAGAGGTATTGATGTCCAACAAGTTTCTTTAGTTATCAACTACGATTTGCCAGCCAACAAGGAAAAC
TACATTATAGAAATTGGTAGAGGTGGTCTGTTTCCGGTAGAAAGGGGGTTGCCATCAACTTTGTCACTGAC
AGAGATGTTGGTATGATGAGAGAAATTGAAAATTTCTACTCTACTCAAATCGAAGAAATGCCAGCTGAT
ATTGGTGCTTTATTGCTTAG

YJL138C_homolog 397aa (SEQ ID NO 618)
MASEGITEIDSGLIETNYDNVVKFDDLNLKPNIVRGIFGYGYETPSAIQQRAILPITEGRDVLAAQAS
GTGKTATFTISALQRINENKATQALILAPMRELALQIKNVITAIGLYLKVTVHASIGGTSMSDDIEAF
RSGVQIVVGTGPRVLDMIERRYFKTDKVKMFI LDEADEMLSSGFKEQIYNIFRLLPETTQIVLLSATMP
QDVLEVTTKFMNPNVRILVKKDELTLLEGIKQFYINVELEDYKFDCLCDLYDSISVTQAVIFCNTRSKVE
FLTNNKLREQHFTVSAIHADLPQAERDTIMKEFRSGSSRILISTDLLARGIDVQVSLVINYDLPANKEN
YIHRIGRGRFRGKGVAINFVTD RDVGMREIEKFYSTQIEEMPADIGALFA

YKL060C_homolog 1080bp public: 1..1080 (SEQ ID NO 619)
ATGGCTCCTCCAGCAGTTTAAAGTAAATCCGGTGTTATCTACGGTAAAGACGTCAAAGACTTGTTTGAC
TATGCTCAAGAAAAAGGTTTTGCCATTCCAGCTATCAATGTCACTTCATCTCAACTGTTGTTGCTGCT
TTAGAAGCTGCCAGAGACAACAAGGCTCCAATCATCTTGCAAACCTTCTCAAGGTGGTGCTGCCTACTTT
GCCGGTAAAGGTGTCGACAACAAGATCAAGCTGCTTCCATTGCTGGTTCAATTGCTGCCGCTCACTAC
ATTAGAGCCATTGCTCCAACCTTATGGTATCCAGTTGTTTTACACACTGATCACTGTGCCAAAAAATTA

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TTGCCATGGTTTGTATGGTATGTTGAAAGCCGATGAAGAATTCTTTGCTAAGACCGGTACTCCATTGTTCTCATCCACATGTTGGATTATCTGAAGAAACCGATGACGAAACATTGCTACTTGTGCCAAATATTTTGAAAGAATGGCTAAAATGGGTCAATGGTTAGAAATGGAAATTTGGTATCACTGGTGGTGAAGAAGATGGTGTCAACAACGAACACGTTGAAAAAGATGCTTTATACACTTCTCCAGAACTGTTTTCGCTGTCTACGAATCTTTTACACAAGATTCTCCAACTTTTCTATTGCTGCTGCTTTTGGTAACGTCCACGGTGTTTACAAACAGGTAATGTGCAATTGAGACCAGAAATCTTGGGTGACCACCAAGTTTACGCTAAGAAACAAATTGGTACTGATGCTAAACACCCATTATACTTGGTTTTCCACGGTGGTTCTGGTTCTACTCAAGAAGAATTCAACACTGCTATCAAGAATGGTGTGTCAAGGTCAACTTGGACACTGATTGTCAATATGCTTACTTGACTGGTATCAGAGATTACGTACCAACAAGATTGAATACTTGAAAGCACCAGTTGGTAACCCAGAAGGTGCTGACAAACCAACAAGAAATACTTTGACCCAAGAGTCTGGGTTAGAGAAGGTGAAAAGACCATTGTCCAAGAGATTGCTGAAGCTTTGGATATTTCCACACCAAGGACAATTGTAA

YKL060C_homolog 359aa (SEQ ID NO 620)

MAPPVAVLSKSGVIYKDVKDLFDYAQEKGFAPAINVTSSSTVVALEAARDNKAPIILQTSQGGAAAYFAGKGVNDKQDAASIAGSIAAAHYIRAIAPTYGIPVVLHTDHC AKLLPWFDGMLKADEEFFAKTGTPLFSSHMLDLSEETDDENIATCAKYFERMAKMGQWLEMEIGITGGEEDGVNNEHVEKDALYTS PETVFVAYE SLHKISPNFSIAAAFNVHGVYKPGNVQLRPEILGDH QVYAKQIGTDAKHPLYLVFHHGSGSGSTQEEFN TAIKNGVVKVNLDTDCQYAYLTGIRDYVTNKIEYLKAPVGNPEGADKPNK KYFDP RVVWVREGEKTM SKRIAALDIFHTKGQL

YKL150W_homolog 906bp public: 1..906 (SEQ ID NO 621)

ATGTTGACTCATCATTTATCGAAATTGGCTACTCCAAAATTCTTAGTACCATTTCGCTGGTGCCACTGCTTTGTCAATTGGTTTGGCATTGCAATATTCTACTTCCAACAATTACATTGCTAACGAAACTGGTAAAACTTCACTGATAGCAATGAATGGGTGGACTTGAAATTATCTAAGTCAATTGATTGACTCATAACACCAAACTCTGGTTTTCAAGTTAAAAGATGAGAATGATGTTTTCTGGTTTGATCACTGCTTCATGTTTGTGACCAATTTGTACACCAAAGGGTAACAATGTTATTCGTCCATATACCCCTGTCTCTGATGTTAACCAATCTGGTGAAATTGATTTCTGTGATTAAAAAATACGACGGAGGTAAAATGTCAAGTCACATTTTCGATTTGAAAGAAGGTGAAACCTTATCATTTCAAAGGACCAATTGTTAAATGGAATGGGAACCAATCAATTCAAGTCCATTGCTTTGATTGGTGGTGGTACTGGTATTACTCCATTATACCAATTGTTGCATCAAATCACTTCTAATCCAAAGGACAAACCAAAGTTAATTTGATTACGGTAACTTGACTCCAGAAGATATCTTGTTAAAGAAA GAAATCGATGCTATTGCTTCTAAACACAAGGACCAAGTTAAAGTTCATTACTTTGTTGACAAGGCAGATGAAAAGAAATGGGAAGGTCAAATTGGTTTCAATTACTAAAGAATTCTTACAAAAGAATTAGAAAAACCA GGTCTGATTTCAAGGTTTTTGTGTTGGTCCACCAGGTTTATACAAGGCTATATCAGGTCCCTAAAGTT TCCCCAACTGATCAAGGTGAATTGACTGGTCTTTGAAAGATTTGGGTTTCGAAAAAGAACATGTCTTT AAATTTTAG

YKL150W_homolog 301aa (SEQ ID NO 622)

MLTHHLSKSLATPKFLVPFAGATALSIGLALQYSTSNYYIANETGKTFTDSNEWVDLKLKSIDLTHNTKHLVFKLKDENDVSGELITASCLLTKFVTPKGNVIRPYTPVSDVNQSGEIDFVIKKYDGGKMSSHIFDLKEGETLSFKGPVWKWEPNQFKSIALIGGGTGITPLYQLLHQITSNPKDNTKVNLIYGNLTPEDILLKKEIDAIASKHKDQVKVHYFVDKADEKKWEGQIGFITKEFLQKELEKPGSDFKVFVCGPPGLYKAISGPKVSPTDQGELTGALKDLGFEKEHVFKF

YLR029C_homolog 615bp public: 1..615 (SEQ ID NO 623)

ATGGGTGCCTACAAATATTTAGAAGAATTGCAAGAAAGAAGCAATCTGATGTTATGAGATTCTTGTATCGTGTGATGTTGGGAATACAGACAAAAGAATGTCATCCACAGAGCTTCCAGACCATTAGACCAGACAAGGCTAGAAGATTAGGTTACAAAGCTAAACAAGGTTTCGTTATCTACAGAATCAGAGTTAGAAGAGGTGGTAGAAAGAGACCAGTTCCAAAGGGTGCCACTTACGGTAAACCAACCAACCAAGGGGTTAACCAATTGAAATACCAAAAATCATTGAGATCTACTGCTGAAGAAAGAGTTGGTCGTCGTGCTTCTAACTTGAGAGTCTTGAACTCATACTGGGTAAACCAAGATTCCACCTACAAATACTTTGAAGTTATTTTAGTCGACCCATCTCACAAAGCTATCAGAAGAGATGCTAGATACAACCTGGATCGTTAACCAGTTCACAAACACAGAGAAGCCAGAGGTTTGACTTCTGCTGGTAAGAAATCCAGAGGTATTAACAAGGGTCATTTGTTCAACAAAACCAAGCTGGTAGAAGACACACCTGGAAGAAGCACACACCTTATCTTTATGGAGATACAGATCTTAA

YLR029C_homolog 204aa (SEQ ID NO 624)

MGAYKYLEELQRKKQSDVMRFLYRVRCWEYRQKNVIHRASRPSRPDKARRLGKAKQGFIYRIRVRRGRKRPVPGATYGPPTNQGVNQLKYQKSLRSTAEERVGRRASNLRLVNSYVWNQDSTYKYFEVILVDPSHKAIRRDARYNWI VNPVHKHREARGLTSAGKKS R GINKGHLFNKTKAGRRHTWKHKHNTLSLWRYRS

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YNL030W_homolog 318bp public: 1..318 (SEQ ID NO 625)
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AGAGATGCTGTTACTTACACTGAACATGCTAAAAGAAAAACCGTCACTTCATTGGATGTTGTTTACGCT
TTGAAGAGACAAGGTAGAACCCTTGATGGTTTCGGTGGTTAA

YNL030W_homolog 105aa (SEQ ID NO 626)
MSGTGRGKGGKGLGKGGAKRHRKILRDNIQGITKPAIRRLARRGGVKRISALIYEEVRVVLKQFLENI
RDAVTYTEHAKRKTVTSLDVVYALKRQGRTRYLGFGG

YOR285W_homolog 546bp public: 1..546 (SEQ ID NO 627)
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GCCGATGTTAAGGATGTGGCCGTACACCCGTGAAAACACCCCTGATTCTGTTTTAGTGGATGTTAGAGAA
CCAACTGAATTTGGAGATGGTCATATACCAGGAGCTTTGAATATTTCCATTTAAAGTAGTCCCGGCGCA
TTGGATTGTGCAGAAGAAGATTTCCAAGAACATTTTGGATTTCCTAAACCAAGTACTGATAAAGAATTG
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AAAAGAGGAAATTTATCTTGGAAAGTTGGGAAGATTGGGTAAAACATGAAAATAAAAAAGAACTAA

YOR285W_homolog 181aa (SEQ ID NO 628)
MFAFKKSTTSILKTVVAPTSSRYLSTVTLRSIPRTFHNATKVSILFNLRTTTPRFYSVLTESPEAKVYKY
ADVKDVAVHPENHPDSVLVDVREPTFEFGDGHIPGALNIPFKSSPGALDLSEEDFQEHFGFPKPKSTDKEL
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YOR327C_homolog 603bp public: 1..603 (SEQ ID NO 629)
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GTATCCCAAAGAACTCAACCTGGACAGAGACAAAGTGTTGAAGAAGGTAATTATATTGGTCATACATTAT
ACCAGATCAGAAGGAATTTCTGGTATCATTATAACGGACAAAGATTACCCTGTAAGACCAGCATATACA
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GCAATGAAACTTTACAATATGGACAATTAGAAGCATATTTGAAAAAATATCAAGATCCCACTCAAGCT
GATTCAATCATGAAAGTTCAACAAGAATTAGATGATACTAAGGTTGTTTTACACAAAACATTGAAAGGG
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YOR327C_homolog 200aa (SEQ ID NO 630)
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YPL037C_homolog 474bp public: 1..474 (SEQ ID NO 631)
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AACAGAGTTGGTGTTCAGGTGCTCCAGCTTCTAATACTTTTGCCTTCACTGGTTACCCACAAGAAAAG
AATATTACTCAATTGATCCCACAAAATTTTACCACAATTTGGGTGCTGAAAACCTTGGAAATCTTGAGACAA
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YPL037C_homolog 157aa (SEQ ID NO 632)
MPVDPEKLAKLQKSSAKKVGGSRVKAKKNIKTEQDDTKLIEALGKLKATKIEGVVEANFFREDGKVLHF
NRVGVQGAPASNTFAFTGYPQEKNTITQLIPQLPQLGAENLEILRQLAEQIQAGKTPKDFNTGSANAAA
DAGGEDIPDLVDQKFDDVE

YPL079W_homolog 330bp public: 1..330 (SEQ ID NO 633)
ATGCCACACAAATACTACCACGGTAAGACTGGTATTGTTTACAACGTTACCAAATCCTCCGTTGGTGT
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CACTCTGCTTGTCTGCAAGAATTTCTTGAACAGAGTTAAATCTAACGCTGCTAAAAAGAGAGAGCTAAA
GCTAACGGTGAAACCGTTTACTTGAAGAGACAAGCTGCCAAGCCAAGAGGTTCAAGAATTATCTCCACT
GAAGGTAACATTCCTCAAACTTTGGCTCCAGTCTGCTTACGAAACTTTCATTAA

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YPL079W_homolog 109aa (SEQ ID NO 634)

MPHKYVHGKGTGIVYNVTKSSVGVIIINKVVGNRYIEKRVNLRVEHVKHSACRQEFNLNRVKSNAKKREAK
ANGETVYLKRQAAKPRGSRIISTEGNIPQTLAPVAYETFI

YBR089C-A_homolog EMBL_entry 279bp public: 1..279 (SEQ ID NO 635)

ATGGCTCCAGGTGAAAAGAAAGAGTCTCTAGAAAAGAAAGGATCCAGATGCTCCAAAAAGATCCCTTA
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GGTCAAGTTGGTAAATTATTAGGTGAAAAATGGAAGGCTTTAAACAGTGAAGATAAATTACCTTACGAA
AACAGGCTGAAGCTGATAAAAAGAGATATGAAAAAGAAAAGGCTGAATACGCTAAAAAGAAATTCGCC
TAA

YBR089CA_homolog SWISS-PROT_entry 92aa (SEQ ID NO 636)

MAPGERKKSSRKKKDPDAPKRSLSAYMFFANENRDIVRAENPGISFGQVGKLLGEKWKALNSEDKLPYE
NKAEDKKRYEKEKA EYAKKNSA

YBL092W_homolog EMBL_entry 396bp public: 1..396 (SEQ ID NO 637)

ATGGCTACTTCTGTTCCACACCCAAAAATTTGTTAAGAAATACACCAAGAAATTCAGAGACACCATTCT
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GCTGGTTACAAAGTTTACTTGGTTAAAAACGTTAAAGACTTAGATGTCTTGTATTGTCACACTAAATCT
TATGCTGCTGAAATTGCCTCTTCTGTCTCATCTAGAAAAAGAGTTGAAATCGTTGCTAAAGCTAAGAAA
CTCGGTGTTAAAGTCACTAATCCAAAGGGTAAATTTGAACTTGAAGCTTAA

YBL092W_homolog SWISS-PROT_entry 131aa (SEQ ID NO 638)

MATSVPHPKIVKKYTKKFKRHHSRDYHRVAENWRKQKIDSCVRRRFRGTIPQPNIGYGSNKKTKFLNP
AGYKVYLKVNKVDLVDVLLHSTKSYAAEIASVSSRKRVEIVAKAKKLGVKVTNPKGKLNLEA

YDL059C_homolog 2791bp PathoSeq: 1..2791 (SEQ ID NO 639)

TATCCATTGGTAATGAATCAGTTAATACCCTACCAAACTGTTTTATTAAATCTAGAGCAGATTTTAATACTG
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CTCAATTATGTCGTGATATTGAAGTTTCTTTTAAAGAAGATACTCAACAATATGAAGCTTTTGGGATTTCTCGAA
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ATTTATATATCATATTCAGGAGCAAATGTTTCATCAATTGTTCTTGTTCATATTCAAGATAAAGATCACGTAAC
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ATATTTGTAGATTCTGCTTGTCCAGTTGTTCTCTAAAAGTACCATCTTTCAATATTAATCGTATTTTCTACTACA
ACAAGGGCAGAATACTTGTTCATCTTTATTTTCCCGTTTGGGTTAAATACCAATCCCAAAATTTGTCGGG
GTGACCATTCATCCA

YDL059C_homolog_1 67aa PathoSeq: 1..67 (SEQ ID NO 640)

ENKYSALVVVKIRLILKDGTFREQSGQAESTNMPYKHCYASARKKAVTDAIKNAIVGLRLDLYLEYE

YDR377W_homolog 24076bp PathoSeq: 1..24076 (SEQ ID NO 641)

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TGGTAGCACTAGGCGAATTAGAGTTTTCAGTTTTCATCTTATTGTTAAGTGTGATTGAGCAACATAAAAAAGCC
TTGTCCACTTTCTCGAGGCAGTTACCGGAATATTACGTATTCTCCTCTCTCCCTATTTTCTAAACCAACAAA
CAAAAAATAAATATCATGAGAAGTTAAAGAAAATAAATCGCTCAAAGTTTATCTACGCAAACTATGCTAAAAA
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ACCCCTCTAGCACCCCAAGGAACAATCGAATGTTTCTCTCTCTCTTGAACATTTCTTAATAATACGTATGTA
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AAGAATATATCACCAAATGGTATGTCGTTATACCTACTTTGTTTGTGCTATCAGGTTGTTGATTTCTTCATG
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YDR377W_homolog_1 80aa PathoSeq: 1..80 (SEQ ID NO 642)

NLGSNPNAKRMAEVVKFYNNKLPGQPAPAAKKSNNPFARYRAAYFDGDNASGKPLVHLAIAVVIFGYSLEYQHLKH
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YGR008C_YLR327C_homolog 8405bp PathoSeq: 1..8405 (SEQ ID NO 643)

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YGR008C_YLR327C_homolog_1 79aa PathoSeq: 1..79 (SEQ ID NO 644)

MTRTNKWTVHEKRPQEPKWFTHNGHSDTDPTKVKNKGAGKNNWGQPGDELDDNEVRHYQKSSGRNNSNHEMNQER
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YGR034W_homolog 2004bp PathoSeq: 1..2004 (SEQ ID NO 645)

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YGR034W_homolog 120aa PathoSeq: 1..120 (SEQ ID NO 646)

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YMR273C_homolog 935bp PathoSeq: 1..935 (SEQ ID NO 647)

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YMR273C_homolog_1 98aa PathoSeq: 1..98 (SEQ ID NO 648)

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YPR028W_homolog 3616bp PathoSeq: 1..3616 (SEQ ID NO 649)

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YPR028W_homolog 149aa PathoSeq: 1..149 (SEQ ID NO 650)

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YFR033C_homolog 24142bp PathoSeq: 1..24142 (SEQ ID NO 651)

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YHR001WA_homolog 1949bp PathoSeq: 1..1949 (SEQ ID NO 653)
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YHR001WA_homolog 63aa PathoSeq: 1..63 (SEQ ID NO 654)
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YJL166W_homolog 15790bp PathoSeq: 1..15790 (SEQ ID NO 655)
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YJL166W_homolog_1 93aa PathoSeq: 1..93 (SEQ ID NO 656)

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YPL271W_homolog 7123bp PathoSeq: 1..7123 (SEQ ID NO 657)

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YPL271W_homolog_1 50aa PathoSeq: 1..50 (SEQ ID NO 658)
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YJR115W_homolog 81440bp PathoSeq: 1..81440 (SEQ ID NO 659)
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[illegible]

YDL075W_homolog 513bp PathoSeq: 1..513 (SEQ ID NO 661)

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YDR064W_homolog 5975bp PathoSeq: 1..5975 (SEQ ID NO 663)

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YDR064W_homolog 143aa PathoSeq: 1..143 (SEQ ID NO 664)

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YKL156W_homolog 2002bp PathoSeq: 1..2002 (SEQ ID NO 665)

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YKL156W_homolog_1 81aa PathoSeq: 1..81 (SEQ ID NO 666)

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CSFRRK

YLR038C_homolog 8469bp PathoSeq: 1..8469 (SEQ ID NO 667)

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YLR038C_homolog_1 74aa PathoSeq: 1..74 (SEQ ID NO 668)

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YNL131W_homolog 15251bp PathoSeq: 1..15251 (SEQ ID NO 669)

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TACCAATTTGTGATAATTCTTATTCTAATTTGAAATTTGATTTAATGAATGTGCTAAAAATAAAAATTCCTGA
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TCCCACAAAAATATTTTGCTAATTGTATATTACCAGAGAATTTACCACCAAGTTTTAAACATGTAATATTTCCC
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CAACAATTTCCGCCAGTAGTAATATGAAGAAGTTGAATTAAGATGTTCAAATATTAAGTATTAAGTGGATTAC
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TAGCCAGCAGCAGGATCAAGGTCAGGTCAGCACCCTGGGAGAGAACACAAGATTTCTTAGGACATCATCTA
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YNL131W_homolog 150aa PathoSeq: 1..150 (SEQ ID NO 670)

MVKLTQIDDETQQQFENQSVAKNNHIIDEASSEESDDDDSDLDLDFENETLLERIVALKDIVPPEQRE
SIYNLSSTIGDLFKSSVQNGGKFLWTLTSSSLLLGVPLALAILSETQLQEMERGMSEKSAQDVLAPGSEA
AFGNENKK

YHR161C_homolog 4220bp PathoSeq: 1..4220 (SEQ ID NO 671)

ATCCAGTTTACTTAAATTTAAATGGACAATTATCTTAATAGACAAACATCCCAGATTATTATCATCTATCTTTCAT
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CATGGTTCACAAATGGTTCATCTCCCCATGGTAAATTTTGTGTTGTTGATGTACGAGATTCTGATTTTGTGGAG
GTCATATAAAAGGCTGTTATCATTATCCTGCAGCCAATTTCCACTACACATTGAATGAATTATATCAAAAAATAT
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GCAATTGTGAAAACAAAGCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT
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ACAAATCATTTGACCAATAATCTAAATGCAGTTAAGACAATGTCATTATTTATCTCGTTTTCCATGAAATTATTCT
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TTCCCAATTTGTAATATTGGATAACCATGGATGGTATAACATGATACGAATGCATGATTTCGGCATCCCTTTTGT
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ATATACTCCCCGAATCTTTGATGGTTAGCAATGAGTTCTTGTGTTGAAAGGAATTGTATCGATTGGAGATGGAACA
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TCTTTAAGTCTCACAGTTAAAGTTGTAGTACCCTTCCATAAGAGCCTGATGATGTCGTGTACGAAAACCTTGTGA
TTGATTCCATGAAATACCTT

YHR161C_homolog 609aa PathoSeq: 1..609 (SEQ ID NO 672)

MTTYEKIVKGATKVKVAAPKPKYIEPILMATSLNHSLSKENFNTIMRTLQARLHDSWSVYKALIVIHLMIRE
GDKNVTLDYLSNQASPNLLNLNNNNIKNSNSFNSDIKFITRYAKYLHTRVKQFESTGVDYVRDERSNNNTNQGG
GRLRLLDVDKGLLREVESVQKQIDSLLKNNFMENEINNDIVLTAFLRLVNDLLALFQELNEGVINILEHYFEMSK
IDAERSLKIYKKFVDQTKFVIDYLRVAKHLEYATKLHVPTIKHAPTALTSSLEEYLDNPNFEINRKQYLAEEKGK
DNIVLKPTQSILNKKSKNEPGQQQQQPREQQQKLGSTSSDLNRHSSLVQQTYPWNTMFVPIVGVVDPLQQDQA
QQQAQQQAQQQAQQQALQQQVQLQQAQQQALQQQATQQATQQQQQQTFLFSQLPSISQGGTQLQSTFTGVGFGGYGS
QPQQLQAQHTNPFIQPTPQLQQPQQPQQPVGLQRSNTNPFSSMATGQHQSQQQFAQPYSQLNMNQPPQLQAQS
TNPFANTRFASTSHTTAFTLDNGSIQPPQQQQQONQKIQANATGNNPFKVSQTTQLQFDNYALTQQQNQHQQCLKP
QATAGGLEH

YDR544C_homolog 1700bp GeneSeq: 1..1700 (SEQ ID NO 673)

CTAAAGTCCAAAGTTGGTTCAATTTTGGCAGAAAAAGAGAAGGAAAAATTCAGTGGAGCTGATTCAATTGCTG
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AACTAGAAAGATCTTTTATTGACCGCTTCCATAGAGATGAGTCTAGCAC'TGGCATTAGCAGACAACATGAGCAGCAC
CAGCAGCCTTTGAGTGATCCTTTGCCTCACGCAGAGAAGCCTCAACCGGAAATTCCTCAATCACCAGAAGCTCCAC
AGGCCAAATCAGTAGAGCTGTATCAGAAGTACTAAAAGAACTGTTCCACCTATGCAAAACGGGTCCGAAGGAA
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TCAACCGCCAGCACCTGTGCCACAAGAATCCAGATCTAGACAAAGCAGTGATGGCATT'TACTCGTTTGAAGCGGGT
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GAAGCAACATCTGCTTCTCAAAGCCTCAAGGTGCGTTTAATAAGAGAAAAACAGAATAACATGGAGATATCCAC
AGTCCCTCGCATTTGAATGGTGTAGAGCGTTGATAGCTAGATTTATGACTAATGGATTGGGTTCCGAACCTGATC
TGGTGTGCAGATTAAATTTCAAGTTAAGGATCCACAAGTCAAGTACTGTAGTATTTACAGTGAGAATGGCGAAGAG
ATTCTTACGTTTAGAAATTTGGTTAGCGGTAGTTATAGTGGTCATCTTTAAGTTATCTGTTTTGAGATTAGTCTCT
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YDR544C_homolog 548aa GeneSeq: 1..548 (SEQ ID NO 674)

LKSKVGSIFGRKKKKKEKFTGADSLAEDESLEVSLLPPTTRTRNSSVLSRSNSTRRSFIDRFHRDESSTGISRQHEQH
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GGSVKPLPEPVDSPNVIKYNDSDDSSTEERRGSLLEKHNLEVQPVSSPFTTQPPAPVPQESRSRQSSDGIYSFEAG
DDSNPISATPRSEQNVFGQMPDPNLSPEKTLAPPPPPSRKVLHHEEPTVRDSALFHNLPAAASHGRDSVMAPLASQ
DRGHSLLKNDFKHENLASTLGLSSSIAEVINASFKDGLIKSQVVGEVAFNYNGNASDPLVVTIPNSFDKVLVNKT
FIEDLGQSKYKVNPTSITSKTLGGLKYLKPTQVPVVIQQIWKFEHPHQSSLMVSIRSTTPLVLENFVVSVALNQDI
EATSASSKPQGAFFNKEKNRITWRYPQSLALNGVERLIARFMTNGLGSEHESGVQIKFQVKDPQVKYCSIYSENGEE
IPTFRNLVSGSYSGHL

YHR094C_homolog 1653bp public: 1..1653 (SEQ ID NO 687)

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AGTTACGGTACTAAGAAATATTCTGACTCCAGACAATGGAGAATTCATTGGGTATTATGCTTTGCTTGG
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ATTGACGATGCTAAGATTTCACTTGCCAAAACCTAACAAGGTTTCTCCAGAGGACCCTGCATTATACCGT
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GAGGAAATTGATGAATTATACTCTACCAAGGTTGTTCCATGGAAATCAGCCGGTTGGGTTCCACCTTCT
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YHR094C_homolog 550aa (SEQ ID NO 688)

MSLDNSTENRDLEEKEEIPKNEHNEQGEQNNENHIPTLEDKPLKEYIGISILCFLIAFGGFVFGFDTG
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IVGIIVQIASQAWYQIMIGRIITGLAVGMLSVLCLPFISEVSPKHLRGTLVYCFQLMITLGLIFLGYCT
SYGTTKYSRQWRIPLGLCFAWALCLLGGMVRMPESPRYLVGKDRIDDAKISLAKTNKVSPEDPALYR
ELQLIQAGVERERLAGKASWGALITGKPRILERVIVGGMLQSLQQLTGDNYFFYYSTTIFKSVGLNDSF
ETSIILGVINFASFVGIYAIERLGRRLCLLTGVSAMSICFLIYSLIGTQHLYIDQPGGPTRKPDGNAM
IFITALYVFFFASTWAGGVYSIVSELYPLKVRSKAMGFANACNWLWGFLISFFTSFITDAIHFFYGFVF
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YBL099W_homolog 1344bp public: 1..1344 (SEQ ID NO 717)

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GTTGATGGTTTTAGGTAACCAATTGATGGTAAAGGTCCAATCAAGGCTGCTGCTTACTCCAGAGCTCAA
GTTAAAGCTCCAGGTATTTTACCAAGAAGATCCGTCCACGAACCAATGCAAACCGGTTTGAAATCTGTT
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GCCGTTGCCTTGATGCCATCTTGAACCAAAAGAGATGGAACAATGGTTCTGACGAAAAGAAGAAATTG
TACTGTGTTTACGTTGCCGTTGGTCAAAGAGATCCACTGTTGCTCAATTGGTCCAACTTTGGAACAA
CACGACGCTCTTAAATACTCTGTTATTGTTGCTGCTACTGCTTCTGAAGCTGCTCCATTGCAATACATT
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GATGATTTGTCAAACAAGCTGTTGCTTACCGTCAATTGTCAATTATTGTTGAGAAGACCACCAGGTAGA
GAAGCTTACCCTGGTGATGTTTTCTACTTACATTCCAGATTATTGGAAAGAGCTGCTAAGATGTCTGAT
GCTTACGGTGGTGGTTCTTTGACTGCTTTGCCAGTTATTGAAACCAAGGTGGTGATGTCTCTGCTTAT
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TTGGACAATGTTGCTCTTGACAGAATTGGTGAATTCGAAGAAGCTTTCTTGGGTCATTGAAATCTAAC
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YBL099W_homolog 447aa public: 1..447 (SEQ ID NO 718)

MALNLEADQVGVLFGSDRLVKEGETVKRTGQIVSVPIGPELLGRVVDGLGNPIDKGPIKAAAYSRAQ
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YCVYVAVGQKRSTVAQLVQTLQHDALKYSVIVAATASEAAPLQYIAPFTACAIGEWFRDNGRHALIVY
DDLKQAVAYRQLSLLLRPPGREAYPGDVFLHSRLLERAAMKMSDAYGGGSLTALPVIETQGGDVSA
IPTNVISITDQIFLEAEIFYKGRPAINVGLSVSRVGSAAQVKAMQVAGSLKFLAQYREVAFAQF
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YEL032W_homolog 2637 bp public: 1..2637 (SEQ ID NO 719)

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GACCCTAACCAGCAATACTATTTATCATTCAAGGGAGCATTGTTGGGGACATTTCGCTCACTCCTAGATCG
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CAAACAACATCCTTTGATGCAATTGCTACTCCGGCTATATATCCAACCTGAAGATATGGAAGGTAATAAAA
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GAAAGAAGATTGGAGGCTGGTGCAATGGTATTGGCTGACAGAGGTATTGTTGTATTGATTGAATTTGAT
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YEL032W_homolog 878 aa public: 1..878 (SEQ ID NO 720)

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YHR135C_homolog 1488 bp public: 1..1488 (SEQ ID NO 721)

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YHR135C_homolog 495 aa public: 1..495 (SEQ ID NO 722)

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YJL060W_homolog 1362 bp public: 1..1362 (SEQ ID NO 723)

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YJL060W_homolog 453 aa public: 1..453 (SEQ ID NO 724)
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YML028W_homolog 591 bp public: 1..591 (SEQ ID NO 725)
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YML028W_homolog 196 aa public: 1..196 (SEQ ID NO 726)
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YOL100W_homolog 2835 bp public: 1..2835 (SEQ ID NO 727)
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YJL166W_homolog 288bp Pathoseq: 1..288 (SEQ ID NO 729)

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YJL166W_homolog 95aa PathoSeq: 1..95 (SEQ ID NO 730)

MAGAPHPTYMGWWSLGSQPKQYITQYTISPAAKPLKGAAYNAVFNTFRRTKNQFLYVAIPFVVVWS
IWTRARDYNEYLYTKEGREELERVNV

YLR038C_homolog 252bp PathoSeq: 1..252 (SEQ ID NO 731)

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YLR038C_homolog 83aa PathoSeq: 1..83 (SEQ ID NO 732)

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Human homologues

>YGL080W_homolog, CDS: 1-330 bp (SEQ ID NO 675)

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>YGL080W_homolog, 109 aa (SEQ ID NO 676)

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>YGR243W_homolog, CDS: 1-384 bp (SEQ ID NO 677)

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>YGR243W_homolog, 127 aa (SEQ ID NO 678)

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>YGR183C_homolog, CDS: 1-399 bp (SEQ ID NO 679)

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>YGR183C_homolog, 132 aa (SEQ ID NO 680)

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>YBR009C_homolog, CDS: 1-312 bp (SEQ ID NO 681)

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>YBR009C_homolog, 103 aa (SEQ ID NO 682)

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>YGR209C_homolog, CDS: 1-318 bp (SEQ ID NO 683)

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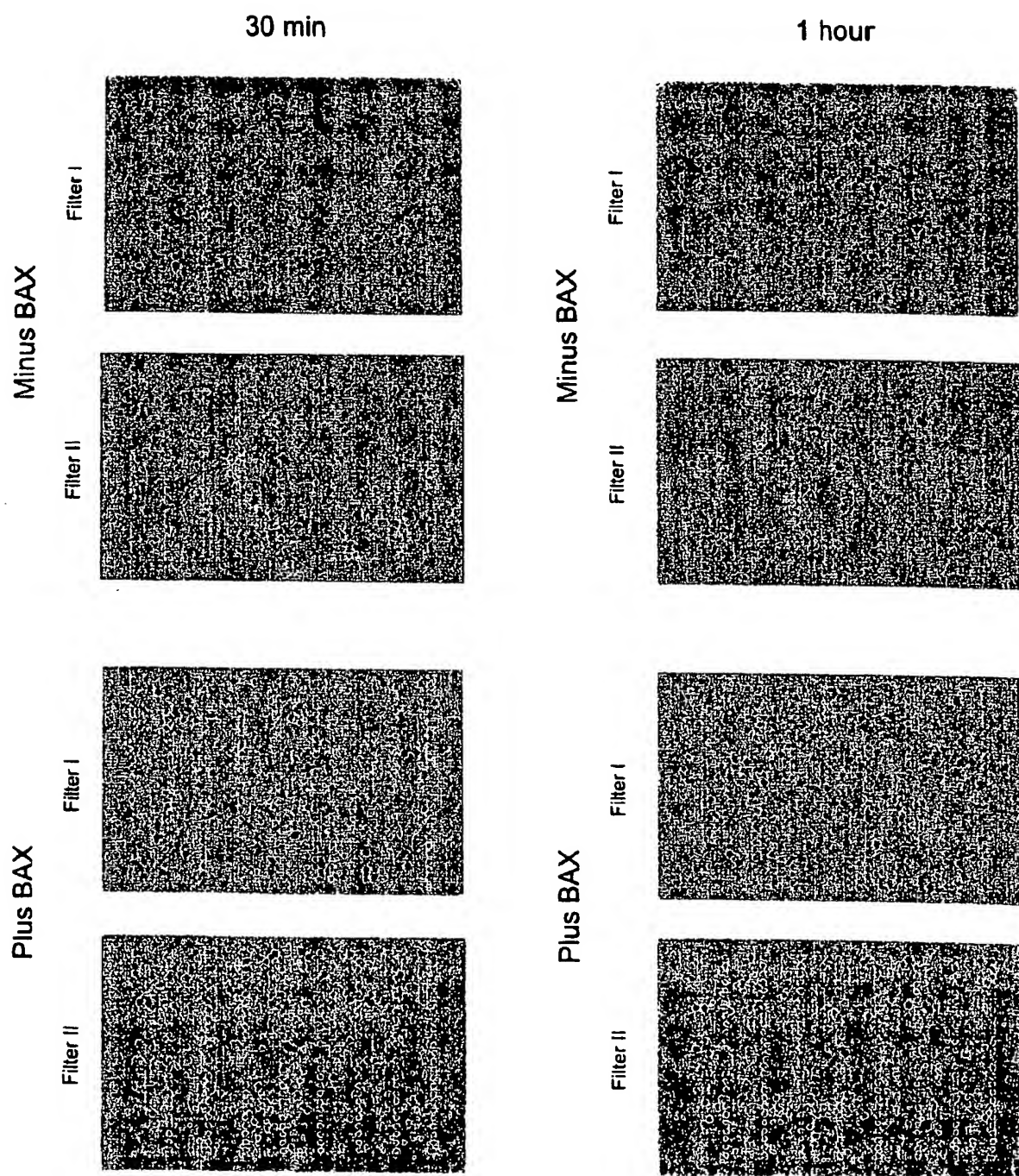
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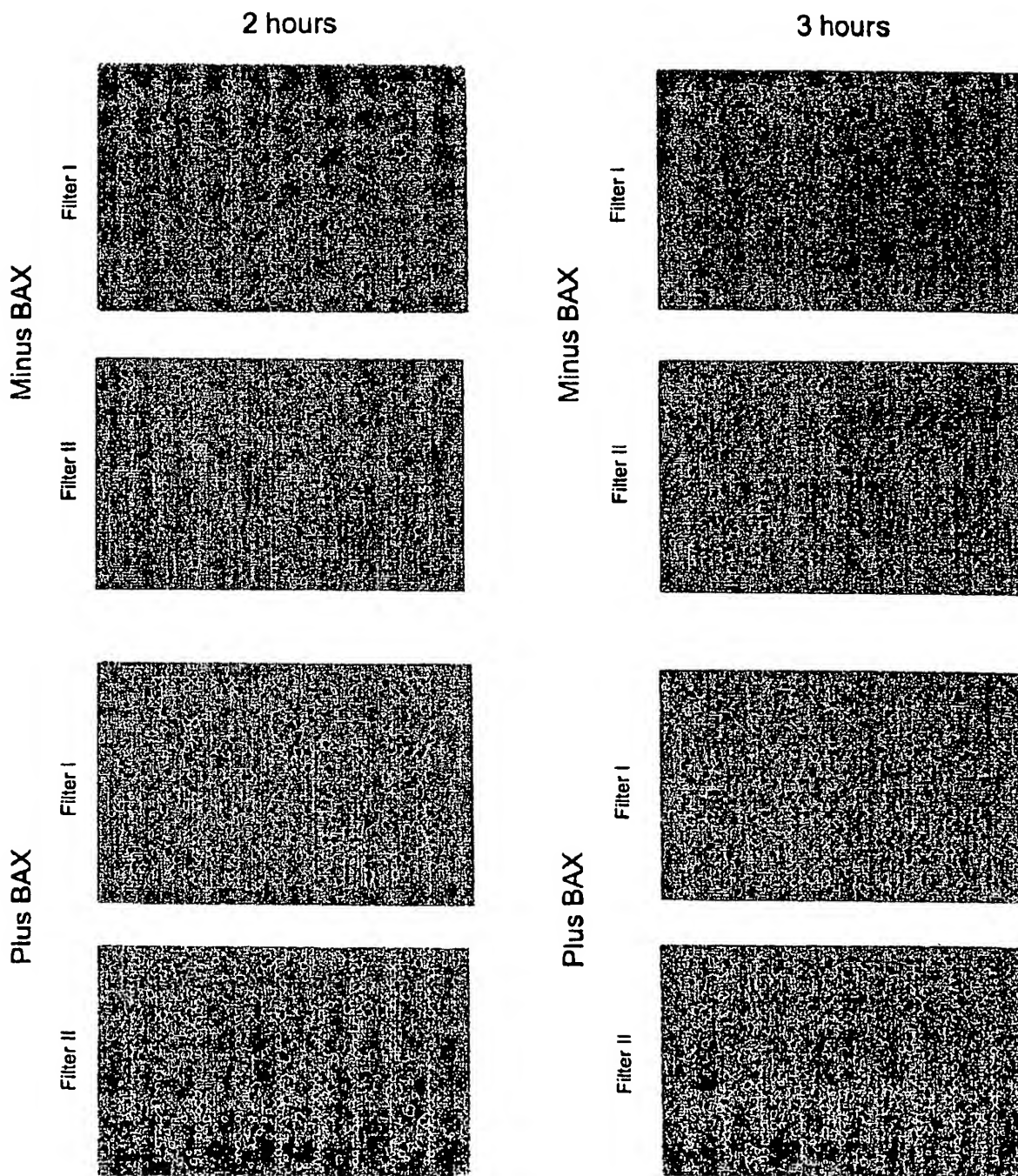
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>YPR028W_homolog, 197 aa (SEQ ID NO 686)

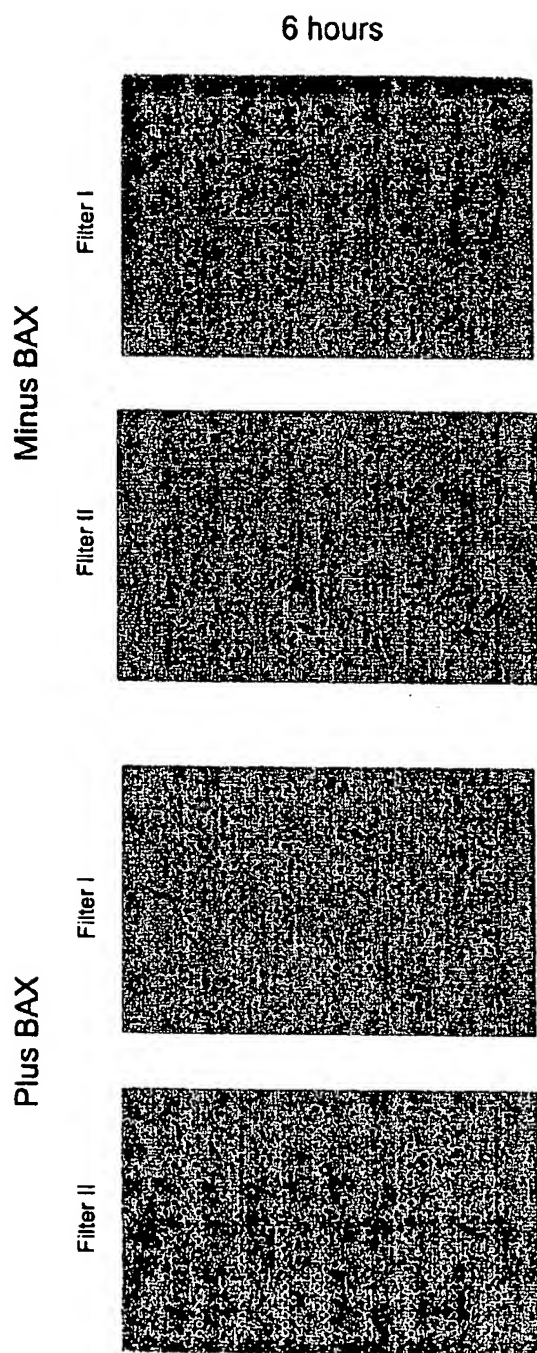
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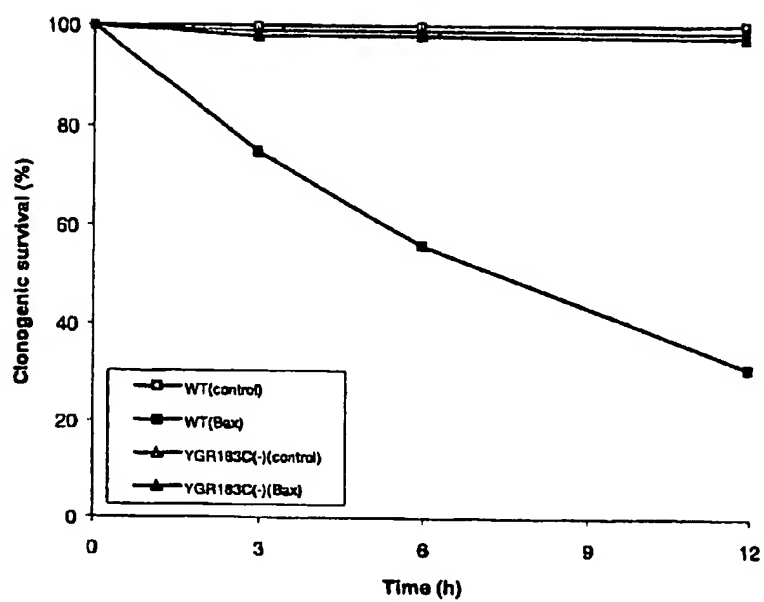
Figuur 3 - 1



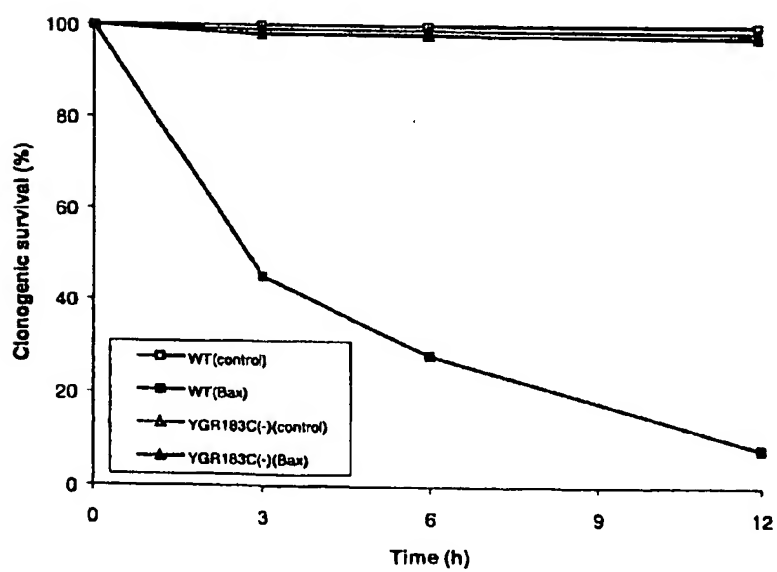
Figuur 3 - 2



Figuur 3 - 3



(A)



(B)

Figure 4

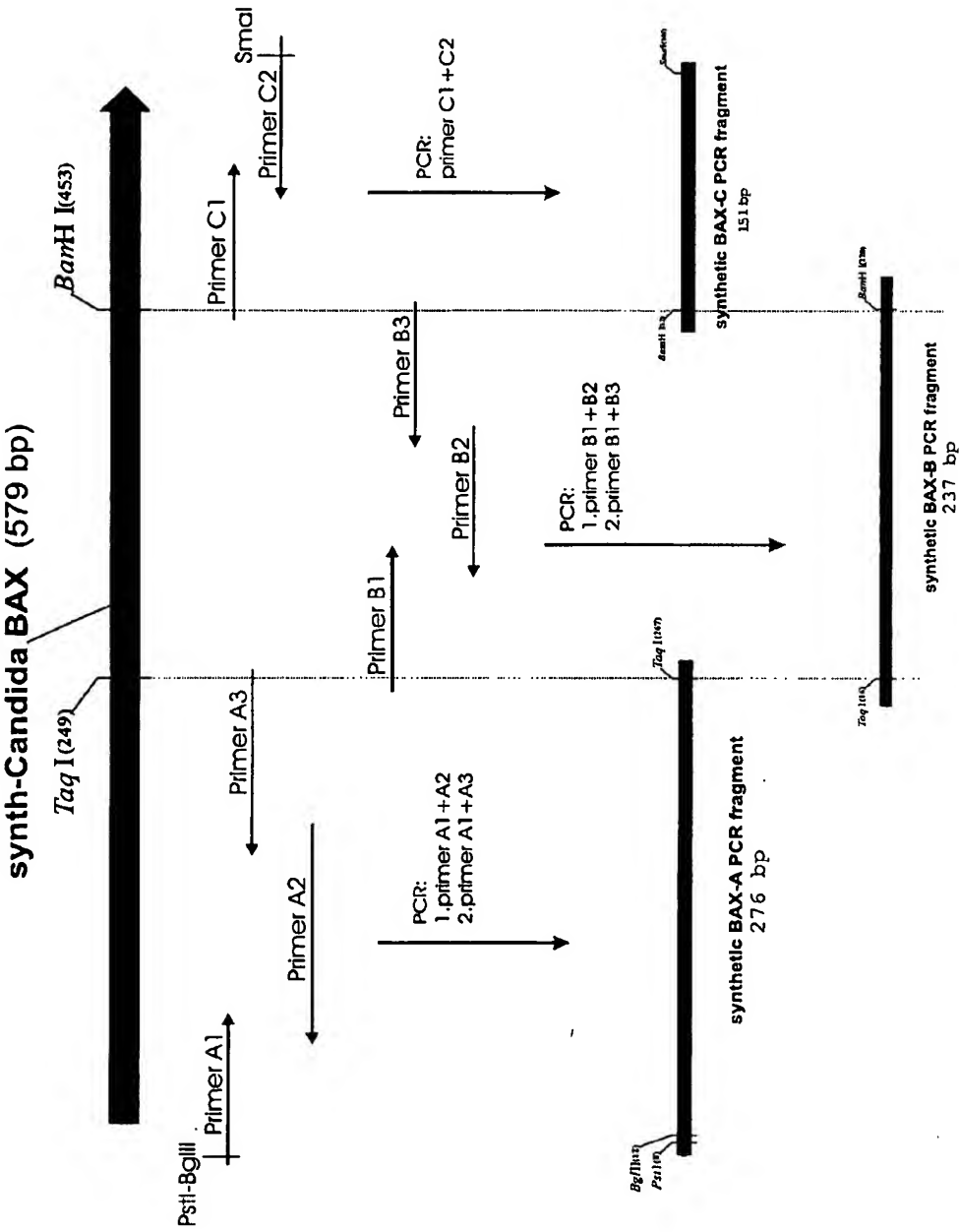


Fig. 5

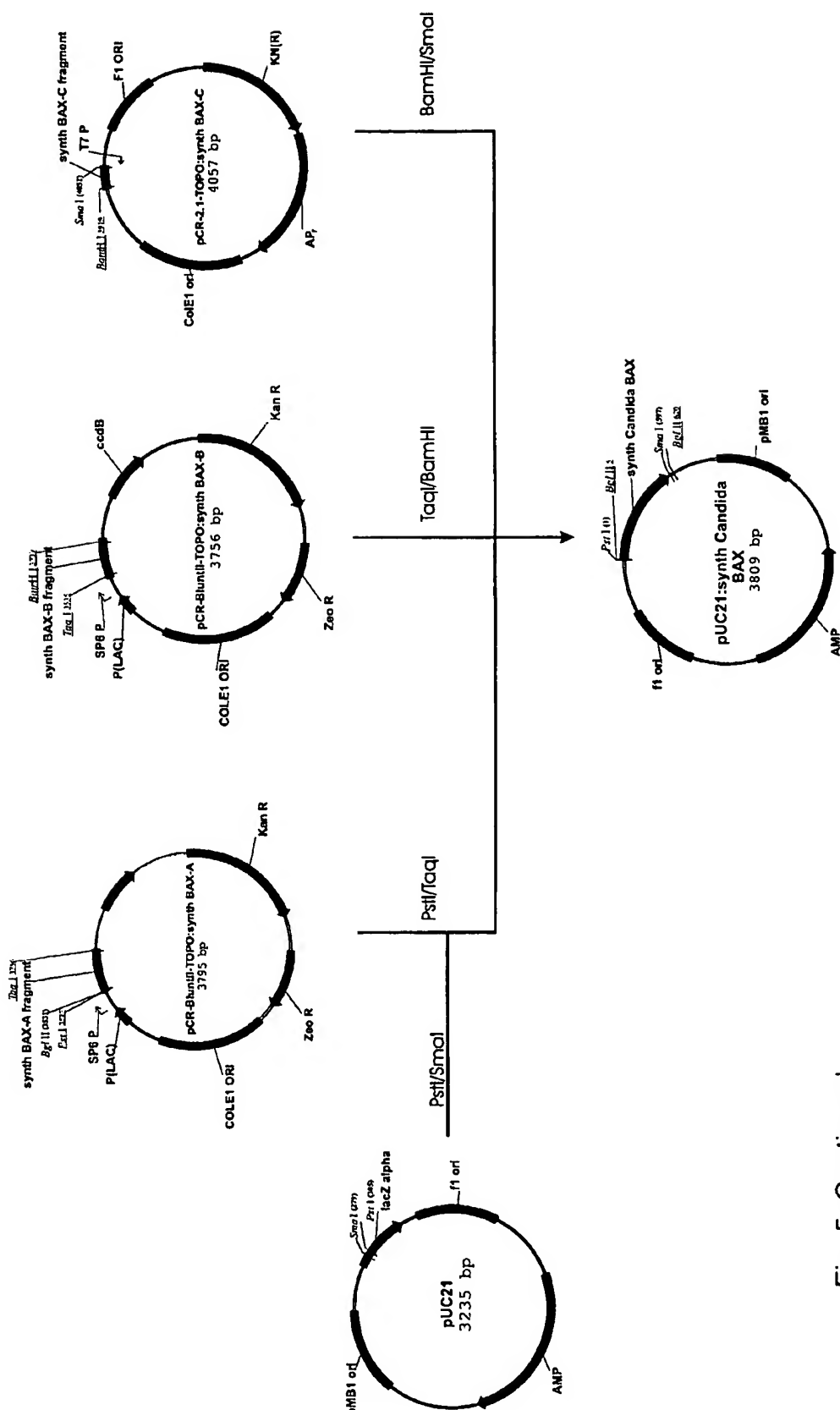


Fig. 5. Continued

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Glu Thr Pro Glu Leu Thr Leu Glu Gln Pro Pro Gln Asp Ala Ser Thr Lys Lys Leu Ser
121 GAA ACC CCA GAA TTG ACC TTG GAA CAA CCA CCA CAA GAT GCT TCT ACC AAA AAA TTG TCT

Glu Cys Leu Arg Arg Ile Gly Asp Glu Leu Asp Ser Asn Met Glu Leu Gln Arg Met Ile
181 GAA TGT TTG AGA AGA ATC GGT GAT GAA TTG GAT TCT AAC ATG GAA TTG CAA AGA ATG ATC

Ala Asp Val Asp Thr Asp Ser Pro Arg Glu Val Phe Phe Arg Val Ala Ala Asp Met Phe
241 GCT GAT GTC GAT ACC GAT TCT CCA AGA GAA GTC TTC TTC AGA GTC GCT GCT GAT ATG TTC

Ala Asp Gly Asn Phe Asn Trp Gly Arg Val Val Ala Leu Phe Tyr Phe Ala Ser Lys Leu
301 GCT GAT GGT AAC TTC AAC TGG GGT AGA GTC GTC GCT TTG TTC TAC TTC GCT TCT AAA TTG

Val Leu Lys Ala Leu Cys Thr Lys Val Pro Glu Leu Ile Arg Thr Ile Met Gly Trp Thr
361 GTC TTG AAA GCT TTG TGT ACC AAA GTC CCA GAA TTG ATC AGA ACC ATC ATG GGT TGG ACC

Leu Asp Phe Leu Arg Glu Arg Leu Leu Val Trp Ile Gln Asp Gln Gly Gly Trp Glu Gly
421 TTG GAT TTC TTG AGA GAA AGA TTG TTG GTC TGG ATC CAA GAT CAA GGT GGT TGG GAA GGT

Leu Leu Ser Tyr Phe Gly Thr Pro Thr Trp Gln Thr Val Thr Ile Phe Val Ala Gly Val
481 TTG TTG TCT TAC TTC GGT ACC CCA ACC TGG CAA ACC GTC ACC ATC TTC GTC GCT GGT GTC

Leu Thr Ala Ser Leu Thr Ile Trp Lys Lys Met Gly (SEQ ID NO 2)
541 TTG ACC GCT TCT TTG ACC ATC TGG AAA AAA ATG GGT TAA (SEQ ID NO 1)

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Fig. 6

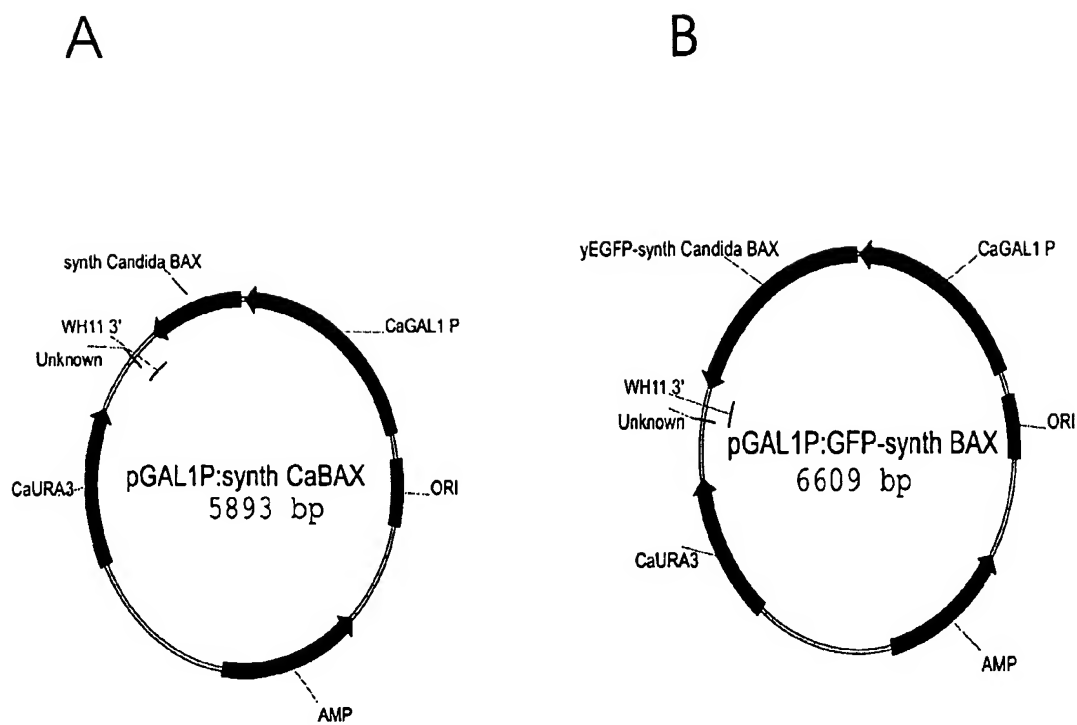


Fig. 7.

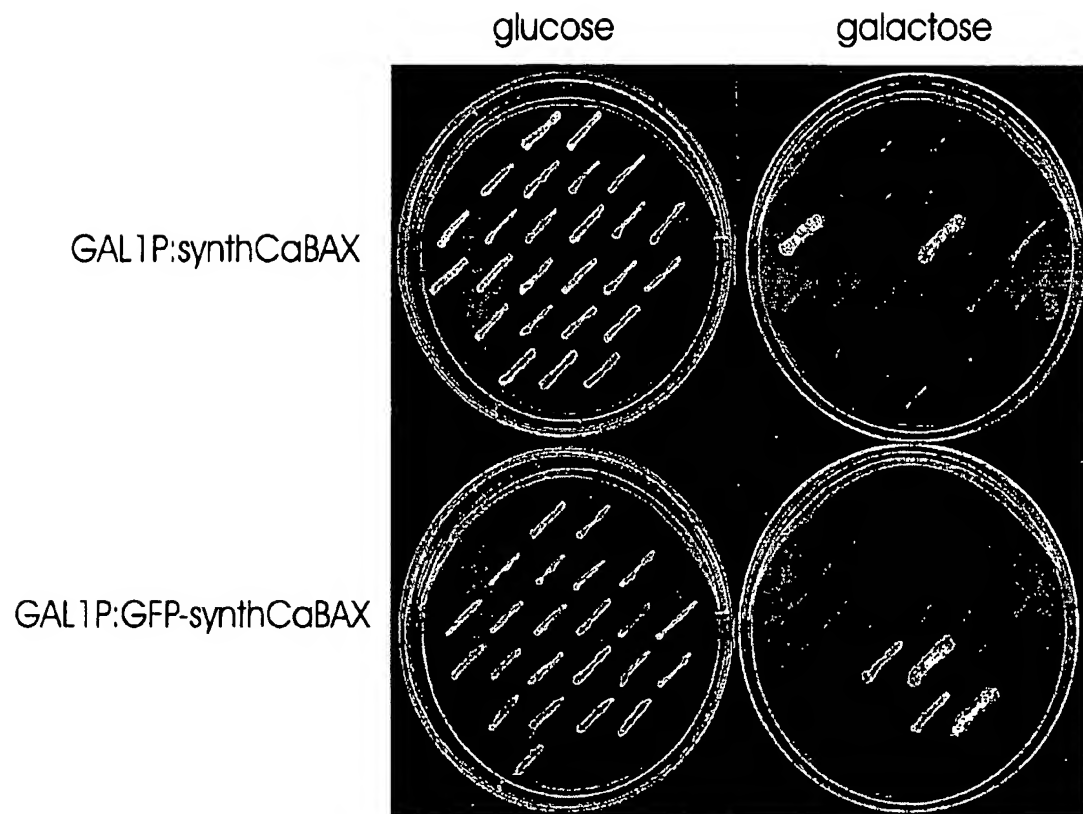


Fig. 8.

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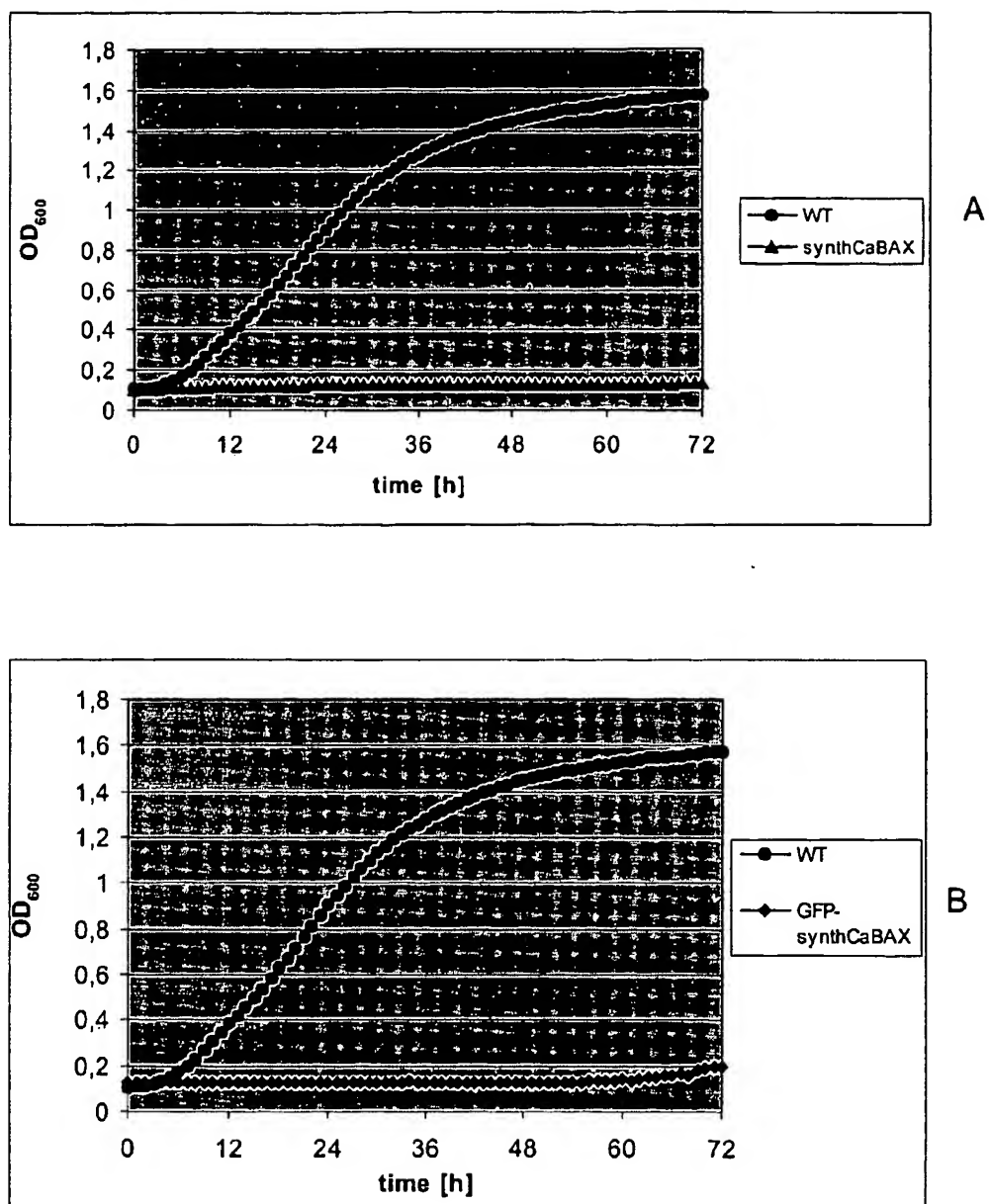


Fig. 9.

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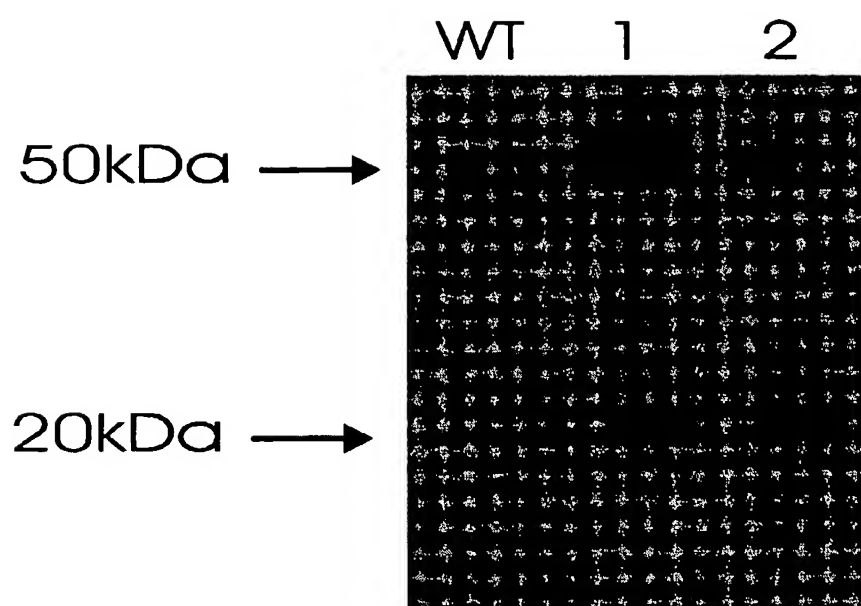


Fig. 10.

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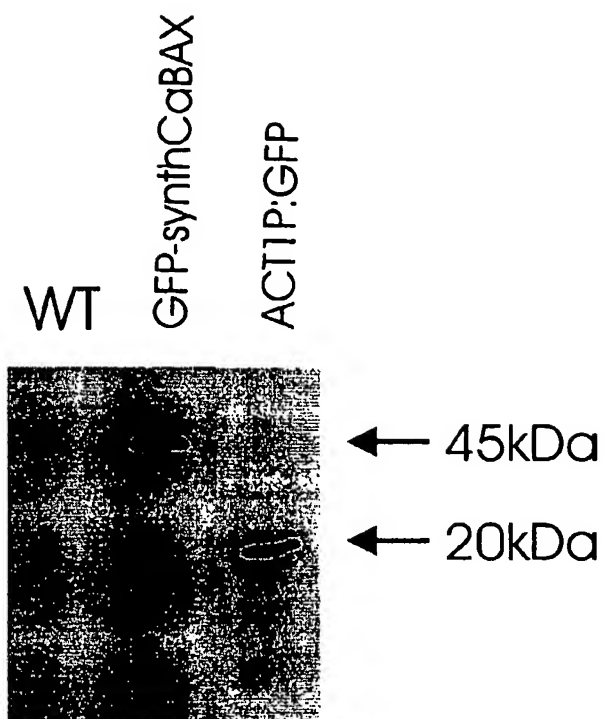


Fig. 11.

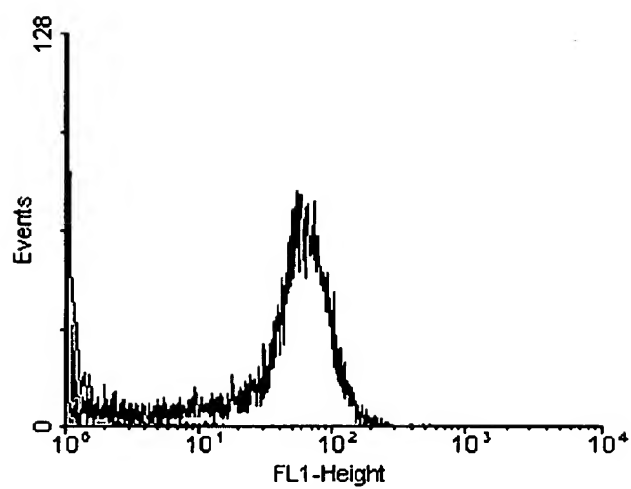
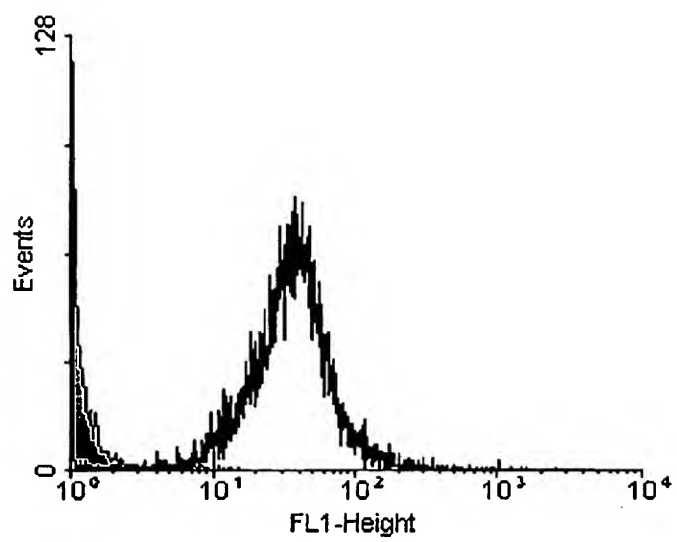


Fig.12.

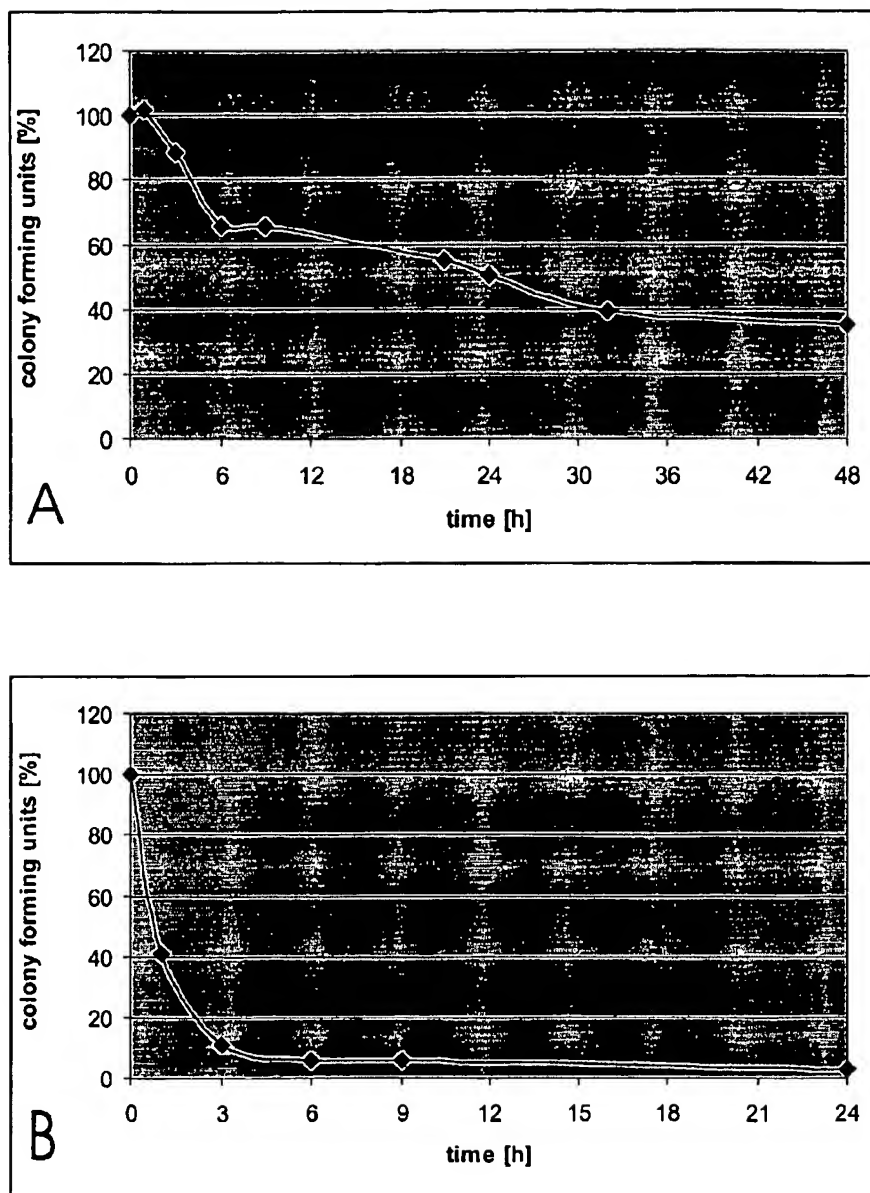


Fig. 13.